

91478

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From: Turner, Sharon  
Sent: Monday, April 14, 2003 2:23 PM  
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Backtranslation of SEQ ID NO:12 standard and oligomer search  
Standard and Oligomer search SEQ ID NO:11

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CITE

priority 60/225,919 8-16-00  
file 8-15-01

POINT OF CONTACT:  
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Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: 4/16  
Date Completed: 4/24  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

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| 23: | /SDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT * |
| 24: | /SDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT *  |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

| SUMMARIES  |       |             |        |             |                     |
|------------|-------|-------------|--------|-------------|---------------------|
| Result No. | Score | Query Match | Length | ID          | Description         |
| 1          | 2007  | 99.9        | 6030   | 24 AAD32844 | Human ion channel   |
| 2          | 1970  | 98.1        | 5932   | 24 AAD32845 | Human ion channel   |
| 3          | 1733  | 86.3        | 8378   | 22 AAH55763 | Human adult form c  |
| 4          | 1545  | 76.9        | 6027   | 24 AAD27266 | Human transporter   |
| 5          | 1447  | 72.0        | 8378   | 22 AAH55764 | Human neonatal foet |
| 6          | 1444  | 71.9        | 4362   | 24 AAD32846 | Human ion channel   |
| 7          | 1382  | 68.8        | 4179   | 24 AAD32847 | Human ion channel   |
| 8          | 1332  | 66.3        | 4197   | 24 AAD32848 | Human ion channel   |
| 9          | 1326  | 66.2        | 5997   | 24 AAD32839 | Human ion channel   |
| 10         | 1289  | 64.2        | 5889   | 24 AAD32840 | Human ion channel   |
| 11         | 947   | 47.1        | 8131   | 24 ABL36889 | Human sodium chanm  |
| 12         | 763   | 38.0        | 4339   | 24 AAD32841 | Human ion channel   |
| 13         | 701   | 34.9        | 4166   | 24 AAD32842 | Human ion channel   |
| 14         | 670   | 33.5        | 4164   | 24 AAD32843 | Human ion channel   |
| 15         | 392   | 19.5        | 1992   | 22 AAK02861 | Human brain expres  |
| 16         | 392   | 19.5        | 1992   | 22 AAI02784 | Probe #2775 used t  |
| 17         | 385   | 19.2        | 1194   | 22 ABA48040 | Human breast cell   |
| 18         | 385   | 19.2        | 1194   | 22 ABA65925 | Human fetal liver   |
| 19         | 385   | 19.2        | 1194   | 22 ABA33014 | Probe #11480 for g  |
| 20         | 385   | 19.2        | 1194   | 22 AAK14344 | Human brain expres  |
| 21         | 385   | 19.2        | 1194   | 22 AAK40073 | Human bone marrow   |
| 22         | 385   | 19.2        | 1194   | 22 AAI20854 | Probe #10787 for g  |
| 23         | 385   | 19.2        | 1194   | 22 AAI46090 | Probe #14776 used   |
| 24         | 385   | 19.2        | 1194   | 22 AAI06565 | Probe #6536 used t  |
| 25         | 385   | 19.2        | 1194   | 22 AAB14511 | Human genome-deriv  |
| 26         | 379   | 18.9        | 1178   | 22 AAK15629 | Human brain expres  |
| 27         | 379   | 18.9        | 1178   | 22 AAI07805 | Probe #7796 used t  |
| 28         | 322   | 16.0        | 969    | 22 ABA42812 | Human breast cell   |
| 29         | 322   | 16.0        | 969    | 22 ABA53333 | Human foetal liver  |
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| 32         | 322   | 16.0        | 969    | 22 AAK27041 | Human bone marrow   |
| 33         | 322   | 16.0        | 969    | 22 AAI11841 | Probe #1574 for ge  |
| 34         | 322   | 16.0        | 969    | 22 AAI32838 | Probe #1624 used t  |
| 35         | 322   | 16.0        | 969    | 22 AAI01568 | Probe #1559 used t  |
| 36         | 322   | 16.0        | 969    | 24 ABS01620 | Human genome-deriv  |
| 37         | 318   | 15.8        | 3403   | 22 AAH55792 | Human SCN1A genom   |
| 38         | 277   | 13.8        | 1456   | 22 ABA08930 | Human N channel F   |
| 39         | 139   | 6.9         | 8349   | 22 AAH55793 | Human adult form c  |
| 40         | 139   | 6.9         | 8349   | 22 AAH55794 | Human neonatal foet |
| 41         | 119   | 5.9         | 1425   | 22 AAHS8462 | DNA encoding novel  |
| 42         | 119   | 5.9         | 3700   | 22 AAHS5822 | Human SCN2A genom   |
| 43         | 99    | 4.9         | 6822   | 24 ABR63697 | Rat sequence diffre |
| 44         | 96    | 4.8         | 965    | 22 AAH53777 | Human SCN1A genom   |
| 45         | 94    | 4.7         | 606    | 23 ABV58235 | Human prostate exp  |

| RESULT   | ALIGNMENTS |
|--|------------|
| 1  |            |
| AAD32844   |            |
| ID AAD32844 standard; CDNA; 6030 BP.                       |            |
| XX   |            |
| AC AAD32844;   |            |
| XX   |            |
| DT 01-JUL-2002 (first entry)                               |            |
| XX   |            |
| DE Human Ion Channel cDNA #6.                              |            |
| XX   |            |
| KW Human; novel human protein; NHP; voltage-               |            |
| KW gene therapy; dihydropyridine receptor; mental disorder |            |
| KW gene; medical disorder; ss.                             |            |
| XX   |            |
| OS Homo sapiens.   |            |
| XX   |            |
| XX   |            |
| FT Key   |            |
| CD Location/Qualifiers                                     |            |
| 1..6030  |            |



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FT      /tag- a
FT      /product- "Human ion channel protein #6"
FT      /transl_except- (pos:2974..2976, aa:Xaa)
FT      /transl_except- (pos:3199..3201, aa:Xaa)
FT      /note- "Xaa - any amino acid"
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XX      WO200214498-A2.
XX
XX      21-FEB-2002.
XX
XX      15-AUG-2001: 2001MO-US25650.
XX
XX      16-AUG-2000: 2000US-225989P.
XX
XX      (LEXI-) LEXICON GENETICS INC.
XX
XX      Turner CA, Mathur B, Mathur D;
XX      WPI; 2002-280757/32.
XX      P-PSDB; AAE20515.
XX
XX      Novel polynucleotides encoding human sodium channel proteins,
XX      particularly voltage-gated sodium channel proteins useful for drug
XX      screening, diagnosis and in gene therapy of biological disorders.
XX
XX      Claim 2; Page 55-57; 83pp; English.
XX
XX      The present sequence is a cDNA encoding novel human protein (NHP), ion
XX      channel protein. NHP share structural similarity with mammalian sodium
XX      channel proteins particularly voltage-gated sodium channel proteins.
XX      NHP oligonucleotides are useful as hybridisation probes for screening
XX      libraries and assessing gene expression patterns. Sequences derived
XX      from regions adjacent to the intron/exon boundaries of NHP gene can be
XX      used to design primers for use in amplification assays to detect
XX      mutations within the exons, splice sites, introns that can be used in
XX      diagnostics and pharmacogenomics. NHP nucleotide sequences are useful
XX      for drug screening effective in the treatment of symptomatic or
XX      phenotypic manifestations of perturbing the normal function of NHP in
XX      the body, and nucleotide constructs encoding NHP products are useful to
XX      genetically engineer host cells to express NHP products in vivo. These
XX      genetically engineered cells function as bioreactors in the body
XX      delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion
XX      protein to the body. Nucleotide construct encoding NHP products are
XX      also useful in gene therapy for modulating NHP expression and to
XX      produce genetically engineered host cells to express NHP products in
XX      vivo. NHP nucleotide sequences may also be used as part of ribozyme
XX      and/or triple helix sequences that are useful for NHP gene regulation.
XX      The NHP polypeptides are useful for generating antibodies, as
XX      reagents in diagnostic assays, for identifying other cellular gene
XX      products related to NHP and as reagents in assays for screening for
XX      compounds that are useful in the treatment of mental, biological or
XX      medical disorders and diseases.
XX
XX      Sequence 6030 BP; 1786 A; 1190 C; 1345 G; 1706 T; 3 other:
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XX      Alignment Scores:
XX      Pred. No.: 0 Length: 6030
XX      Score: 2007.00 Matches: 2009
XX      Percent Similarity: 100.00% Conservative: 0
XX      Best Local Similarity: 100.00% Mismatches: 0
XX      Query Match: 99.90% Indels: 0
XX      DB: 24 Gaps: 0
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XX      21 SerLeuAlaIleGluArgArgIleAlaGluGluValAlaLysAsnProLysProAsp 40
XX      61 TCTCTTGGGGCTTATGAAAGACCATTTGCCAGAGAAAGGCAAGATATCCCAACAGAC 120

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QY      181 CTTCATTTATTTATGAGACATCTCCAGAGATGCTGACAGCCCTGGAGAGACTG 240
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QY      261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTyr 280
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701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720  
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DB 3481 GCACCTGTAGAGAAAGCCCGTAGTGAACTGAGAACTCTTGAACCAAGAGCTGT 3540  
QY 1181 PheThrGluLysCysValGlnArgPheLysCysGlnIleAsnValGluGluArg 1200  
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QY 1381 ThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIle 1400  
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QY 1841 LeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSerGlyAsp 1860  
DB 5521 CTGCCACAACCAAACTCCAGCTCATGTCATGATTTGGCCATGAGTGGTGGTGCAG 5580  
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QY 1981 ALACSPROPROSEPTYRSPARGVALTHRLYSPROILEVALGLULYSHISGLINGLU 2000
DB 5941 GCTTGCCACCTTCTATGACCGGTGACAAAGCCCAATGTGTGAAAAACATGAGCAAGAA 6000
QY 2001 GLYLYASAPGLULYVALALYSGLYLYS 2009
DB 6001 GGCMAAGATGAAAAAGCCAAAGGAAA 6027

RESULT 2
AAD32845
ID AAD32845 standard; cDNA; 5922 BP.
XX
XX AAD32845;
XX
XX 01-JUL-2002 (first entry)
XX
XX Human ion channel cDNA #7.
XX
XX Human; novel human protein; NHP; voltage-gated sodium channel;
XX gene therapy; bioelectro; mental disorder; biological disorder;
XX gene; medical disorder; ss.
XX
XX Homo sapiens.
XX
XX Location/Qualifiers
XX Key 1..5922
XX CDS
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XX /transl_except= (pos:2974..2976, aa:Xaa)
XX /transl_except= (pos:3199..3201, aa:Xaa)
XX /note= "Xaa = any amino acid"
XX
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XX
XX 21-FEB-2002.
XX
XX 15-AUG-2001; 2001WO-US25650.
XX
XX 16-AUG-2000; 2000US-225989P.
XX
XX (LEXI-) LEXICON GENETICS INC.
XX
XX Turner CA, Mathur B, Mathur D;
XX
XX WPI: 2002-280757/32.
XX
XX P-PSDB: AAE20516.
XX
XX Novel polynucleotides encoding human sodium channel proteins,
XX particularly voltage-gated sodium channel proteins useful for drug
XX screening, diagnosis and in gene therapy of biological disorders
XX

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XX
XX Claim 1, Page 62-64; 83pp; English.
XX
XX The present sequence is a cDNA encoding novel human protein (NHP), ion
XX channel protein. NHP share structural similarity with mammalian sodium
XX channel proteins particularly voltage-gated sodium channel proteins.
XX NHP oligonucleotides are useful as hybridisation probes for screening
XX libraries and assessing gene expression patterns. Sequences derived
XX from regions adjacent to the intron/exon boundaries of NHP gene can be
XX used to design primers for use in amplification assays to detect
XX mutations within the exons, splice sites, introns that can be used in
XX diagnostics and pharmacogenomics. NHP nucleotide sequences are useful
XX for drug screening effective in the treatment of symptomatic or
XX phenotypic manifestations of perturbing the normal function of NHP in
XX the body, and nucleotide constructs encoding NHP products are useful to
XX genetically engineer host cells to express NHP products in vivo. These
XX genetically engineered cells function as bioreactors in the body
XX delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion
XX protein to the body. Nucleotide construct encoding NHP products are
XX also useful in gene therapy for modulating NHP expression and to
XX produce genetically engineered host cells to express NHP products in
XX vivo. NHP nucleotide sequences may also be used as part of ribozyme
XX and/or triple helix sequences that are useful for NHP gene regulation.
XX The NHP polypeptides are useful for generating antibodies, as
XX reagents in diagnostic assays, for identifying other cellular gene
XX products related to NHP and as reagents in assays for screening for
XX compounds that are useful in the treatment of mental, biological or
XX medical disorders and diseases.
XX
XX Sequence 5922 BP; 1746 A; 1166 C; 1320 G; 1687 T; 3 other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 0 Length: 5922
XX Score: 1970.00 Matches: 1972
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 98.06% Indels: 0
XX DB: 24 Gaps: 0
XX
XX US-09-930-871-12 (1-2009) x AAD32845 (1-5922)
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XX 1 ATGAGCAAAACAGTGTCTGTACCAACGAGACGTCGACGCTTCACTTCCACAGAGAA 60
XX
XX QY 21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluValAlaLysAsnProLysProAsp 40
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XX QY 41 LysLeuAspAspAspGluAsnGlyProLysProAspSerPheGluAlaGlyLysAsn 60
XX 121 AAAAAGATACAGACGAAATGGCCCAAAAGTGTACTGTGAAAGTGGAAAGAAC 180
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XX QY 61 LeuProPheIleTyrGlyAspIleProGluMetValSerGluProLeuGluAspLeu 80
XX 181 CTTCATTTATTTATGAGACATTCCTCCAGAGATGCTGCAGAGCCCGGAGAGACTG 240
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XX 241 GACCCCTACTATATCAATAAGAAACTTTATGTATGAAATTAAGGAGAGCCACTCTTC 300
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XX 301 CGGTTCAGTCCACCTGCGCTGTACATTTTAACTCCCTCAATCTCTTAGGAAATA 360
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XX QY 121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
XX 361 GCTATTAAAGATTTTGGACATTCATTTATAGCATGCTAATTTATGCGCACTATTGACA 420
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XX QY 141 AsnCysValPheMetThrMetSerAsnProProAspTyrThrLysAsnValGluTyrThr 160
XX 421 AACTGTGTGTTTATGACAAATGAGTAACCCCTCGATTTGACAAAGAAATGTAATACACC 480
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Db 3721 TATATGTACAGGAAAGCGATTAAGAGATGTGGATATAGCTACAGAGGTTTCACT 3780

Qy TyrIlePheIleLeuGluMetLeuLysTyrValAlaTyrGlyTyrGlnThrTyrPhe 1280  
Db 3781 TACATTTTCATTCGGAAGACTTCTTAATAGGGGCGCATATGCGTATCAAAACATATTC 3840  
Qy ThrAsnAlaTyrCysTyrPheAspPheLeuIleValAlaAspValSerLeuValSerLeuThr 1300  
Db 3841 ACCAATGCTGTGTGTGCTGTGACTCTTAATTTGTGATGTTTCAATGTGATCA 3900  
Qy AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320  
Db 3901 GCAAATGCTGTGTGTGCTGTGACTCTTAATTTGTGATGTTTCAATGTGATCA 3960  
Qy LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValAlaValAsnAlaLeu 1340  
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Qy ThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIle 1400  
Db 4141 ACTGTGACAGTGTGATCATGACGACGAAATATCATACATGATGCTTAATAATTA 4200  
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Qy GlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTyrMetAspIleMetTyrAla 1440  
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Qy AlaValAspSerArgAsnValGluLeuGlnProLysTyrGluGluSerLeuTyrMetTyr 1460  
Db 4321 GCAGTGTATCCAGAAATGTGAACTCCAGCTTAAGTATGAAGAAAGTGTGACATGAT 4380  
Qy LeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIleGly 1480  
Db 4381 CTTACTTGTATTTTCAATCTTTGGGCTCTTCTTCACTTGAACCTGTATTTGAT 4440  
Qy ValIleIleAspAsnAspAsnGlnGlnLysLysPheGlyGlyGlnAspIlePheMet 1500  
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Qy LysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheValThrArg 1540  
Db 4561 AAGCTATACCTCGACACAGAAACAAATTTCAAGAGATGTGTACTGCAACACACA 4620  
Qy GlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMetVal 1560  
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QY 1621 LeuAlaGluLeuIleGluIuYsTyPheValSerProThrLeuPheArgValIleArgLeu 1640
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QY 1661 PheAlaLeuMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuPheLeuVal 1680
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QY 1721 ThrThrSerAlaGlyTPAspGlyLeuLeuAlaProIleLeuAsnSerLysProProasp 1740
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QY 1741 CysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsnProSer 1760
DB 5221 TGTACCTTAATAAGTTAACCCTGGAAGCTCACTTAAGGAGAGCTTGGGAACCCATCT 5280
QY 1761 ValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValValAsnMet 1780
DB 5281 GTTGGAATTTCTTTTGTTCAGTTACATCATATCCTCTGTTGGTGGTGAACATG 5340
QY 1781 TyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGluProLeu 1800
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QY 1801 SerGluAspAspPheGluMetPheTyrGlyValTyrGlyLysPheAspProAspAlaThr 1820
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QY 1821 GluPheMetGluPheGluLysLeuSerGluPheAlaAlaLeuGluProProLeuAsn 1840
DB 5461 CAGTTCATGGAATTTGAAAAATATCTCAGTTGACCTCGCTTGAACCGCTCTCAAT 5520
QY 1841 LeuProGluProAsnLysLeuGluLeuIleAlaMetAspLeuProMetValSerGlyAsp 1860
DB 5521 CTGCCAACAACCAACAACCTCCAGCTCATGATGATGATGATGATGATGATGATGATG 5580
QY 1861 ArgIleCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGluGluSerGly 1880
DB 5581 CGGATCCACTGCTGTTGATATCTTATTTGCTTTTACAAAGCGGGTCTTAGAGAGAGTGA 5640
QY 1881 GluMetAspAlaLeuArgIleGluMetGluLysArgPheMetAlaSerAsnProSerLys 1900
DB 5641 GAGATGATGCTCTACAAATACAGATGAGAGAGATGATGATGATGATGATGATGATG 5700
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DB 5701 GTTCTCATATGAGCAATCACTACTACTTTTAAACGAAAGAGAGATGATGCTGCTC 5760
QY 1921 IleIleGluArgAlaTyArgArgHISLeuLeuLysArgThrValLysGluAlaSerPhe 1940
DB 5761 ATATTTCAGGCTGCTTACAGACCGCACTTTTAAAGGAACTTAAACCAAGCTTCTCTT 5820
QY 1941 ThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuIleLysGluAspMetIle 1960
DB 5821 ACCTACAAATAAAAAACAAGAGAGGCGCTAACTCTTATTAAGAGAGAGATGATA 5880
QY 1961 IleAspArgIleAsnGluAsnSerIleThrGluLys 1972
DB 5881 ATTGACGAAATTAATGAAAACTATTAAGAGAAAA 5916

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AAH5763
ID AAH5763 standard; cDNA; 8378 BP.
AC
XX
AC AAH5763;
XX
DT 04-SEP-2001 (first entry)
XX
DE Human adult form of SCN1A nucleotide sequence SEQ ID NO:1.
XX
KW Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;
XX diagnosis; mutation; chromosome 2q23-q31; neurological disorder;
XX anticonvulsant; neuroprotective; ss.
OS Homo sapiens.
PN WO200138564-A2.
PD 31-MAY-2001.
PE 24-NOV-2000; 2000MO-CA01404.
PR 26-NOV-1999; 99US-0167623.
PA (UYN-C) UNIV MCGILL.
PI Rouleau GA, Lafreniere RG, Rochefort D, Cossette P, Ragsdale D;
XX WPI; 2001-355945/37.
DR P-PDB; AAB99674.
XX
PT Determining a predisposition to epilepsy and/or development of epilepsy
PT comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a
PT DNA variant, equivalent, or mutation which shows a linkage
PT disequilibrium.
XX
PS Disclosure; Page 90-93; 26pp; English.
XX
XX The present invention describes a method (M1) of determining an
XX individual's predisposition to epilepsy and/or development of epilepsy,
XX as well as predicting the individual's response to medication. The
XX method comprises determining the genotype of at least one gene selected
XX from SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation
XX which shows a linkage disequilibrium. SCN1A, SCN2A and SCN3A are all
XX sodium channel genes located on chromosome 2. The idiopathic generalised
XX epilepsy (IGE) gene is more specifically localised on chromosome
XX 2q23-q31. Compounds identified as modulators of the biological activity
XX of SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating
XX epilepsy or other neurological disorders. They have anticonvulsant and
XX neuroprotective activities. AAH5763 to AAB56164 and AAB99674 to
XX AAB99679 represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR
XX primers, oligonucleotides and proteins given in the exemplification of
XX the present invention.
SO Sequence 8378 BP; 2496 A; 1575 C; 1782 G; 2525 T; 0 other;

Alignment Scores:
Pred. No.: 0 Length: 8378
Score: 1733.00 Matches: 2006
Percent Similarity: 99.758 Conservative: 0
Best Local Similarity: 99.758 Mismatches: 3
Query Match: 86.268 Indels: 5
DBs: 22 Gaps: 0

US-09-930-871-12 (1-2009) x AAH5763 (1-8378)
QY 1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
DB 266 ATGGAGCAACAACAGTGTGTTGACACACAGGACCTGACAGCTTCAACTCTTACACAGAA 325
QY 21 SerLeuAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
DB 326 TCTCTTGGCGCTATTGAAAGACCATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 385

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RESULT 3

QY 41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60  
DB AAAAAGATGACGACGAAATATGGCCCAAGCAATATGACTTGGAGGCTGGAAGAAGAC 445  
QY 61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAsnLeu 80  
DB CTTCATTTATTTATGAGACATTCCTCAGAGATGGTGTGAGACCCCTGGAGACCTCG 505  
QY 81 AspProTyrTyrIleAsnLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100  
DB GACCCCTACTATCAATCAAGAAACTTTATGATGAAATAAAGGAGGCCATCTTC 565  
QY 101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120  
DB CGGTTCACATGGCACCTCGCCCTGACATTTAACTCCCTCAACCTCTTAGAAAAATA 625  
QY 121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140  
DB GCTATTAAAGATTTGGTACATTCATTATTCAGCATGCTAAATATGTGACATTTTGGACA 685  
QY 141 AsnGlyValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160  
DB AACTGTGTGTATGACATGATGTAACCTCTGATGTGACAAAGAAATGTAATACACC 745  
QY 161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180  
DB TTTCACAGCAATATATACCTTTGCAATCACTTAAATAATTTATGCAAGGGATCTGTTTA 805  
QY 181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200  
DB GAAGTTTTACTTCTCTCGGATCCAGATGAACTGGCTGATTTGACGTCTTACATTT 865  
QY 201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220  
DB GCGTACGTCACAGATTTGTGACCTGGGCAATGTCTCGGCTTGAAGAACATTCAGAGT 925  
QY 221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240  
DB CTCGAGAGATTTGAAGACATTTCACTCACTTCAGGCCCTGAAACATGTTGGAGACCCG 985  
QY 241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260  
DB ATCCAGTCTGTGAAGAACCTCTCAGATGTAATGATCCGACGTCTGTCTGTGACGCTA 1045  
QY 261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280  
DB TTTCGCTAAATTTGGCTGACGTCTGATGGCAACCTGAGGAAATATGTTACAAATGG 1105  
QY 281 ProProThrAsnAlaSerLeuGluGluHisSerIleGlyLysAsnIleThrValAsnTyr 300  
DB CCTCCACCAATGCTTCTCTTGAGAGACATGATATGAAAAAGAAATATACCTGAAATTT 1165  
QY 301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320  
DB AATGGTACACTTATTAAGAACTGTCTTGAAGTTGACTGGAAGTCAATATTCAGAGAT 1225  
QY 321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340  
DB TCAAGATATCTATTTCTCTGAGAGGTTTTTATGATGACATATGTGGAAATAGCTCT 1285  
QY 341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360  
DB GATGACAGCCCAATGCTCCAGAGAGATATATGTGTGAAAGCTGTGTAAGAAATCCCAATTT 1345  
QY 361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380  
DB GGTACACAAAGCTTTGATACCTGAGTTGGGCTTTTGTCTCTGCTTTCGACTATATGACT 1405  
QY 381 GluAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400  
DB CAGGACTTCTGGGAAAACTTATATCACTGACATTCAGTGTGCTGGGAAAAAGCTACATG 1465  
QY 401 IlePhePheValIleValIlePheLeuGlySerPheTyrIleAsnLeuIleLeuAla 420

DB 1466 ATATTTTGTATTTGGTCAATTTCTTGGGCTCATATTCACCTAAATTAATTTGCTGGCT 1525  
QY 421 ValValAlaMetAlaTyrGluGluGlnInsnGlnAlaThrLeuGluGluAlaGluGlnLys 440  
DB GTGGTGGCCATGCTGCTCAGAGACAGAAATCAGGACCTTGGAGAACAGCAACAGAA 1585  
QY 441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460  
DB GAGGCCGATTTTCACAGATGATTTTAAACGCTTAAATAAAGCAACAGAGAGCTACAG 1645  
QY 461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480  
DB GCAGCAAGGCACTGCTCAGAAACATTCAGAGAGCCGAGGCGAGGAGGCTGTCA 1705  
QY 481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500  
DB GACAGCTCATCTGAAGCCCTTAAGTTGAGTTCCAAAGAGTGTCAAGGAAAGAAATCGG 1765  
QY 501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520  
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QY 521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540  
DB CAAAATCTGATCTGAGAGACAGATCAGAGAGAAAGTTTCGCTTCCATTTGAAGGG 1885  
QY 541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560  
DB AACCATTTGACATATGAAAGAGGATCTCCCTCCACACACATCTTTGTTGGATCTCGT 1945  
QY 561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgLysArg 580  
DB GGCTCCCTATTTTCACCAAGGCAATATGCAACAAGCCTTTTACGCTTTAGAGGGCA 2005  
QY 581 AlaLysAspValGlySerGluAsnAspPheAlaAspGluHisSerThrPheGluAsp 600  
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QY 601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620  
DB AACGAGAGCCGTAGAGATCTCTTTGTCGCCACGACGACGAGAGAGAGCAACAGC 2125  
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DB ATGCACAGACACTGTGATTTGCAATGTGTGTCTCTGTTGGTGGACCTTCACTTCTCT 2245  
QY 661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680  
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QY 681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerPheHisValSer 700  
DB AATGGAAACACCTGAAACTGAAATGAGAAAGAAAGAGGTCAAGTCTTCTCCACTTTC 2365  
QY 701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720  
DB ATGACATTTCTAGAGATCTCTCCAAAGGCAAGAGCAATGATATGACCGCATTTCTTA 2425  
QY 721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740  
DB ACAATATACAGTGAAGAACTGAAGATCCAGGCAAGGCAATGATATGACCGCATTTCTTA 2485  
QY 741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpPheLysValLysHisVal 760  
DB TTTTCAACATATTTCTTATCTGGGACGTGTCTCATATTTGTTAAAGTGAACATGTT 2545  
QY 761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780



Db 2546 GTCACCTGGTGTGATGAGACCATTTGGTACCTGGCCATCACCATCTGATTTGCTTA 2605  
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Db 2606 AATACCTTTTCATGGCCATGGAGCACTATCATATGACGACCATTTCAATATATGCTT 2665  
QY 801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuValIle 820  
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QY 1000 ValAlaIleThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetIle 1020  
Db 3265 TGCAGCCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3324  
QY 1020 GlyGlyValAlaIleTyrValIleArgGlyIleTyrGluPheIleGlnIleSerPheIleLeu 1040  
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QY 1080 snGlyThrThrSerGlyIleGlyThrGlySerSerValGluTyrIleIleAspGlu 1100  
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Db 3564 GTGATTTACATGATCATTAACCAACCCAGCTTACTGTGATGATGATGATGATGATGATG 3623  
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QY 1140 LysSerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleG 1160  
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QY 1180 LysPheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGlyAla 1200  
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Db 4163 CAGCAAAATGCTGT 4222  
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QY 1340 LeuLeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTyrLeu 1360  
Db 4283 TTTTACGACCAATTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 4342  
QY 1360 IePheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThr 1380  
Db 4343 TTTTACGACCAATTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 4402  
QY 1380 hThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeu 1400  
Db 4403 CAACCTGTACAGCTTGTGATCTGAAAGCTGTAATATATATGATGATGATGATGATG 4462  
QY 1400 LeGluTyrGlnGlnThrAlaArgTyrLysAsnValLysValAsnPheAspAspValGly 1420  
Db 4463 TAGAAAGAAATGAGCTGCTCGATGGAATAATGTAAGTAATCTTGTATATGTGAT 4522  
QY 1420 hGlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTyrPheAspIleMetTyr 1440  
Db 4523 TTGGGATCTCTCTTGTCTTCAAGTTGCCACATTAAGAGATGAGATATATATGATG 4582  
QY 1440 LysAlaValAspSerArgAsnValGluLeuGlnProLysTyrGluGluSerLeuTyrMet 1460  
Db 4583 CAGCACTTATTTCCAAATAATGTAAGTCAAGCTCAAGTATGTAAGAAAGTCTGTACAT 4642  
QY 1460 LysLeuTyrPheValIlePheIleIlePheGlySerPheThrLeuAsnLeuPheIleG 1480  
Db 4643 ATCTTTACTTTGTATTTTCAATCATCTTTGGGCTCTTCACTTCACTTCACTTCACTT 4702  
QY 1480 LysValIleIleAspAsnPheAsnGlnGlnLysLysLysPheGlyGlyGlnAspIlePhe 1500  
Db 4703 GTGTATCATATGATTAATTTCAACCAACGAGAAAGAAAGTGTGAGGTCAAGACATCTT 4762



XX Thornton M, Walla NK, Yue H, Nguyen DB, Lai P, Gandhi AR;  
 PI Tribouley CM, Yao MG, Ramkumar J, Au-Young J, Lu Y, Tang YT;  
 PI Azimzai Y, Bruns CM, Griffin JA, Yang J, Sanjanwala MS;  
 PI Raumann BE, Lee EA, Hafalia A, Baughn MR, Green BD, Khan FA;  
 PI Kearney L, Elliot VS, Selhammer JT, Policky JL, Borowsky ML;  
 PI Burford N, Ding L, Lu DM, Hillman JL;  
 XX WPI: 2002-122055/16.  
 DR P-PSDB: AAE1676.  
 XX  
 PT New human transporters and ion channels (TRICH) polypeptides useful for  
 PT diagnosing, treating or preventing disorders associated with aberrant  
 PT expression of TRICH  
 XX  
 PS Claim 11: Page 196-197, 210pp: English.  
 XX  
 CC The invention relates to human transporters and ion channels (TRICH)  
 CC polypeptides and their cDNA molecules. The nucleic acid and polypeptide  
 CC sequences are useful in the diagnosis, treatment, and prevention of  
 CC disorders associated with transport (akinesia, cystic fibrosis, Bell's  
 CC palsy, amyotrophic lateral sclerosis); neurological (Alzheimer's disease,  
 CC amnesia, dementia); muscle (cardiomyopathy, myocarditis, Duchenne's  
 CC muscular dystrophy); immunological (AIDS, Addison's disease, allergies,  
 CC asthma); cell proliferative disorders (cancers, leukemia, psoriasis);  
 CC cardiac disease (angina, hypertension, or bradycardia) and in the  
 CC assessment of the effects of exogenous compounds on the expression of  
 CC nucleic acid and amino acid sequences of transporters and ion channels.  
 CC The polynucleotides may be used to detect and quantify gene expression  
 CC in biopsied tissues in which TRICH expression may be correlated with a  
 CC disease, to generate hybridization probes for mapping naturally occurring  
 CC genomic sequence, and in drug screening. The present sequence is human  
 CC TRICH-13 cDNA.  
 CC  
 XX  
 SO Sequence 6027 BP: 1785 A; 1189 C; 1348 G; 1705 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 0 Length: 6027  
 Score: 1545.00 Matches: 2004  
 Percent Similarity: 99.50% Conservative: 0  
 Best Local Similarity: 99.50% Mismatches: 5  
 Query Match: 76.90% Indels: 10  
 DB: 24 Gaps: 0  
 US-09-930-871-12 (1-2009) x AAD27266 (1-6027)  
 QY 1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhenPheThrArgGlu 20  
 DB 1 ATGGAGCAAAAGAGCTGCTTACACAGACCTGACACCTTCACTTCTCAGCAGAGAA 60  
 QY 21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluValAlaLeuValProGlyProAsp 40  
 DB 61 TCTCTGGGGCTATTGAAAGAGCGCTTGCAGAGAAAGGCAAGAAATCCCAACCAAC 120  
 QY 41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60  
 DB 121 AAAAAAGATGACGACGAAATATGGCCCAAGCAAAATAGTACTGACTGGAAGCTGAGAAAG 180  
 QY 61 LeuProPheIleTyrglyAspIleProProGluMetValSerGluProLeuGluAspLeu 80  
 DB 181 CTTCATTATTATTATGAGACATCTCCAGAGATGATGAGAGCCCTCGAGAGACCTG 240  
 QY 81 AspProTyrglyIleAsnLysLys-ThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100  
 DB 241 GACCCCTATATCAAAACCA-GACTTTTATAGTATTAAGAAAGGAGGCACTTT 299  
 QY 100 eArgPheSerAlaThrSerAlaLeuTyrglyLeuThrProPheAsnProLeuArgLysIle 120  
 DB 300 CCGGTTCAGTCCACCTGCTGCTGATCACTTAACTCCCTCAATCTCTTAAAGAAAT 359  
 QY 120 eAlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140  
 DB 360 AGCATATTAAAGATTGGTACATTCATTATCAGCATGCTAATTATATGTCACATATTGAC 419

QY 140 fAsnGlyValPheMetThrMetSerAsnProProAspIleThrLysAsnValGluTyrrh 160  
 DB 420 AAAGTGTGTATTATGACAAATGATGATACCTCTGATGAGCAAAAGATGATGATAC 479  
 QY 160 rPheThrGlyIleTyrrhPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLe 180  
 DB 480 CTTCAGAGAAATATATATCTTGTGAATCACTATAAAATATATGCAAGGGGATTCGT 539  
 QY 180 uGluAspPheThrPheLeuArgAspProProAsnProPheAspPheThrValIleThrPh 200  
 DB 540 AGAGATTTTACTTCTCTCGGATTCATGAGACTGCTCGATTTCACTGTCATTAACNT 599  
 QY 200 eAlaTyrglyValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArg 220  
 DB 600 TGGTACGTCACAGAGTTTGGGACCTGGGCAATGCTCGGCAATGAGAACTTGAAGT 659  
 QY 220 lLeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAla 240  
 DB 660 TCTCCGACCAATGAAAGAGATTTCACTATCCAGGCTGAAACCATTGTGGAGCCCT 719  
 QY 240 uIleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVa 260  
 DB 720 GATCCAGTCTGGAAGAGCTCTCAGATGATATGATCCTGACTGTTCTGTGAGGCT 779  
 QY 260 lPheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTr 280  
 DB 780 ATTGCTTATATGTCGTCGAGAGCTTCTCATGCGCACTGAGAGATTAATGATACATG 839  
 QY 280 pProProThrAsnAlaSerLeuGluGlnHisSerIleGluLysAsnIleThrValAsnTy 300  
 DB 840 GCCTCCACCAATGCTCTCTGAGAGAAATATGATATAAAGATATATACCTGAAATTA 899  
 QY 300 fAsnGlyThrLeuIleAsnGluThrValPheGluPheAspThrLysSerTyrrhIleGlnAs 320  
 DB 900 TAAATGTAACCTTATTAATATGAAAGCTCTTGTGAGTTGACTGGAAGTATATATCAAGA 959  
 QY 320 pSerArg-TyrrhIleTyrrhPheLeuGluGlyPheLeuAspAlaLeuLeuGlyAsnSer 340  
 DB 960 TTC-AGATATCATATATTTCTCGAGAGGCTTTTATGATGACACTATATGTAATTA 1018  
 QY 340 eArgPheAlaGlyGlnCysProGluGlyTyrrhMetCysValLysAlaGlyArgAsnProAsn 360  
 DB 1019 CTGATGACGAGGCAATGTCAGAGGATATATGCTGTAAGACTGCTGTAATCCCAATT 1078  
 QY 360 TyrglyTyrrhSerPheAspThrPheSerThrPheLeuSerLeuPheArgLeuMet 380  
 DB 1079 ATGGCTACACAAGCTTTATATACCTTCACTGAGTTGCTTGTGCTGACTAATGA 1138  
 QY 380 hArgLysPheThrPheGluAsnLeuTyrglyIleLeuThrLeuArgAlaIleGlyLysThrTyrrh 400  
 DB 1139 CTCAGAGATTCGCGAAATATCTTATCAACGACATTCAGCTGCTCTGGGAAAAGTACA 1198  
 QY 400 eTllePhePheValLeuValIlePheLeuGlySerPheTyrrhLeuIleAsnLeuIleLeu 420  
 DB 1199 TGATATTTTGTATGTGCTATTTCTTGGGCTCATCTTCACTAATTAATTTGATCTGG 1258  
 QY 420 lValValAlaMetValTyrglyGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGln 440  
 DB 1259 CTGTGCTGCGCATGCTGACGAGAGAAACAGAACAGCCACTGGAGAAAGCAGAAAGCA 1318  
 QY 440 yGluValAlaGluPheGlnIleMetIleGluGlnLeuLysGlnGlnGlnAlaIleGln 460  
 DB 1319 AAGAGCGCGAATTCAGAGAGATGATGAACAGCTTAAAGCAACAGAGAGAGCTGAC 1378  
 QY 460 lAlaAlaIleThrAlaThrAlaSerGluHisSerArgGluProSerAlaIleGlyArgLeu 480  
 DB 1379 AGGAGAGCAACGCAACTGCTCCAGAACTCCAGAGAGAGAGAGAGAGAGAGAGAGAG 1438  
 QY 480 eArgPheSerSerSerGluLysLeuSerSerLysSerAlaLysGlnArgArgAsn 500  
 DB 1439 CAGACAGCTCATGTGAAGCTCTTAAGTTGAGTTCAGAGAGAGAGAGAGAGAGAGAG 1498

OY 500 rGArGLySLySArGLySGlnLysGlnInSerGIyGLyGLuLyuYAspGluAspGluP 520  
 DB 1499 GGAGGAAAGAAAGAAAGAAAGCACTGCTGGGGAAAGAAAGATGAGAGAT 1558  
 OY 520 heGlnLysSerGlnSerGlnAspSerIleArgArgLysGlyPheArgPheSerIleGluG 540  
 DB 1559 TCCAAATCTGAATCTGGAGCAGACATCAGAGAAAGCTTTGCTCTCCATTCGAAG 1618  
 OY 540 LysAsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnInSerLeuSerIleA 560  
 DB 1619 GGAACCGATGACATATGAAAGAGTACTCTCCACACACAGCTTTGTTGAGATCC 1678  
 OY 560 rGGLySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgLysA 580  
 DB 1679 GTGGCTCCCTATTTTCACCAAGCCAAATAGCAGAAACCTTTTCACCTTTAGAGGGC 1738  
 OY 580 rGAlaLysAspValGlySerGlnAsnAspPheAlaAspAspGluHisSerThrPheGluA 600  
 DB 1739 GAGCAAGAGATGTGGATGTGAAAGCACTTCGAGATGATGAGCACACACCTTTGAGG 1798  
 OY 600 sPAsnGlnSerArgArgAspSerLeuPheValProArgArgHisGlyLysGluArgAsnS 620  
 DB 1799 AATAAGAGAGCCGTAGAGATCTCTGTTGTCCTCCCGACACAGAGAGAGACGACAA 1858  
 OY 620 eRAsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValPheProAlaAsnGlyL 640  
 DB 1859 GCACCTAGATGACAGCACTAGATGCTATCCCGATGCTGCGAGCTTTCCAGCAATGGGA 1918  
 OY 640 ySMetHisSerThrValAspCysAsnGlyValAlaSerLeuValGlyGlyProSerValP 660  
 DB 1919 AATGCACAGCACTGTGGATGCAATGCTGTGCTCTGTTGTTGAGCTTCAGTTC 1978  
 OY 660 rOfThSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspA 680  
 DB 1979 CTACATCGGCTGTGAGAGCTCTGCGCAGAGTGATTAATAGTAAAGCCAGCTACGATG 2038  
 OY 680 sPAsnGlyThrThrGlnThrGlnLysMetArgLysArgArgSerSerPheHisValS 700  
 DB 2039 ACMAAGGAAACCACTGAAACTGAAATGAGAAAGAAAGGTCMAATCTTTCCAGCTT 2098  
 OY 700 eZMetAspPheLeuGlnAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleL 720  
 DB 2099 CCATGACATCTTCTAGAAAGATCTTCCCAAGGCAAGCAGCAATGATATGCCAGATTC 2158  
 OY 720 eUrThAsnThrValGlyGlnLeuGlnLeuSerArgGlnLysCysProProCysTrpTyrL 740  
 DB 2159 TACCAATTCAGTAGAAGAACTTGAAAGATCCAGGCAAAATGCCACCTGTTGGTATA 2218  
 OY 740 ySPheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisV 760  
 DB 2219 AATTTTCCAACTATTTCTTAATCTGGGACTGTTCTCAATTTGGTTAAAGTAAACATG 2278  
 OY 760 aLValAsnLeuValAlaMetAspProPheValAspLeuAlaIleThrIleCysIleValL 780  
 DB 2279 TTGTCAACCTGTTGTGATGAGACCCATTTGTTGACTGGCCATCAACATCTGTAATGCT 2338  
 OY 780 eUAsnThrLeuPheMetAlaMetGlnHisTyrTrpMetThrAspHisPheAsnAsnValL 800  
 DB 2339 TAAATTACTTTTTCATGAGCCATGAGCACTATTCATGAGCAGCAATTTTCAAAATGTC 2398  
 OY 800 eUrThValGlyAsnLeuValPheThrGlyIlePheThrAlaGlnMetPheLeuLysIleI 820  
 DB 2399 TTACAGTAGGAAACTTGATTTCTACCTGGATCTTTACAGCAGAAATGTTTCTGAAATTA 2458  
 OY 820 LeAlaMetAspProTyrTyrTyrPheGlnGlnGlyTrpAsnIlePheAspGlyPheIleY 840  
 DB 2459 TTGGCATGATCTTACTATTTATTTCCAAAGAGCTGGAATATCTTTGAGAGGTTTATG 2518  
 OY 840 aLThrLeuSerLeuValGlyLeuGlyLeuAlaAsnValGlyGlyLeuSerValLeuArgS 860  
 DB 2519 TGAACGTTTGCTGTGAGAACTGAGACTGCCAATGTGGAAGATTAATCTGTTCTCCGTT 2578  
 OY 860 eRPheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuI 880

DB 2579 CATTTGATGTGCTGCAGATTTTCAAGTTGCAAAATCTGGCCAAAGCTTAATATCTTA 2638  
 OY 880 LeLysIleIleGlyAsnSerVal-GlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIle 899  
 DB 2639 TAAAGATCAATCGGCAATTCGGG-GGGGGCTGTGGGAAATTAACCTCGCTGGGCCATC 2697  
 OY 900 IleValPheIlePheAlaValAlaGlyMetGlnLeuPheGlyLysSerTyrLysAspCys 919  
 DB 2698 ATCGTTTATTTTTCCTGCTGCGCATGCACTCTTTGGTAAAGCTCAAAAGTTGT 2757  
 OY 920 ValCysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPheHis 939  
 DB 2758 GTCTGCAAGATGCCAGATGATGTGCAATCCCGACGCTGGACATGATGACTCTTCCAC 2817  
 OY 940 SerPheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCys 959  
 DB 2818 TCCTTCTGATTTGTTGCTCCGCTGTGTGGAGTGATACAGACATGTGGACTGT 2877  
 OY 960 MetGluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGly 979  
 DB 2878 ATGGAGTTGCTGTGTAAGCATGTGCTTACTGTCTTCAATGATGATGATGATGGA 2937  
 OY 980 AsnLeuValAlaLeuAsnLeuPheLeuAlaLeuLeu\*\*\*-SerSerPheSerAlaAspS 999  
 DB 2938 AACCTAGTGTGATGAATCTTTGCGCTTCTCT- GAGCTCATTTTAGTCACAGAA 2996  
 OY 999 nLeuAlaAlaThrAspAspAsnGlnMetAsnAsnLeuGlnIleAlaValAspArgHe 1019  
 DB 2997 CCTTGCAGCCACTGATGATGATGAATGAATATCTCCAAATTCCTGTGATGATGAT 3056  
 OY 1019 tHISLysGlyValAlaIleTyrValLysArgLysIleTyrGlnPheIleGlnInSerPheI 1039  
 DB 3057 GCACAAAGAGATGCTATGTAGAAAGAAATATGAAATTAATCAACAGCTTCAT 3116  
 OY 1039 eArgLysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAs 1059  
 DB 3117 TAGGAAACAAAGATTTTGAATGAATTAACCACTGATGATCAACAAAGAAAGA 3176  
 OY 1059 pSerCysMetSerAsnHisThr\*\*\*-GluIleGlyLysAspLeuAspTyrLeuLysAspV 1079  
 DB 3177 CAGTTGATCTCCAAATCATCTACAGC-AGAAATTTGGGAAAGTCTTGACTATCTAAAGATG 3235  
 OY 1079 aLAsnGlyThrThrSerGlyIleGlyThrGlySerValGlyLysTyrIleIleAspG 1099  
 DB 3236 TAAATGAACTACAAAGGATAGAGAACTGCGAGCTGTGAAATTAATTAATTTAGATG 3295  
 OY 1099 lUsErAspTyrMetSerPheIleAsnAsnProSerLeuThrValIleValProIleAlaV 1119  
 DB 3296 AAAGTATTAATCATGATTCATTAACAAACCCAGTCTTACTGTGACTGACCAATGCTG 3355  
 OY 1119 aLelGlyLysAspPheGlnAsnLeuAsnThrGlnAspPheSerSerGlnSerAspLeuG 1139  
 DB 3356 TAGAGAGATCTGACTTTGAAATTTAAACAGGAAAGCTTTAATAGTAATCGCATCTGG 3415  
 OY 1139 lUGlUsErLysGlnLysLeuAsnGlnUsErSerSerSerSerGlnLysSerThrValAspI 1159  
 DB 3416 AAGAAAGCAAGAAAGAACTAAATGAAGAGAGTCACTATAGAAAGGATGAGCAGTGGACA 3475  
 OY 1159 lEGLyAlaProValGlnGlnGlnProValAlaGlnProGlnGlnThrLeuGlnProGlnA 1179  
 DB 3476 TCGGGCGAGCTGTAGAAAGAACCCGCTAGTGAAGCTGAAGAACTTTGAACGAGAG 3535  
 OY 1179 lAcysPheThrGlnGlyCysValGlnArgPheLysCysGlnIleAsnValGlnGluG 1199  
 DB 3536 CTGTGTTCACTGAGAGGTGTGTACAAAGATTCAGAGTTTCAAAATCAATGTGAAGAG 3595  
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 DB 3596 GCAGAGGAAACATGATGTGAGACCTGAGAGAGAGGTTTCCAAATGATTTGAACATTA 3655  
 OY 1219 rPheGlnThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluA 1239

D 3656 GGTGTGACCTTCATGTTTCATGATTCCTTAGTAGTGTGCTGTGCATTGTGAAG 3715  
Q 1239 SPIETRYIIEASPGIARGLYSHRIIELYSTRMETLEUGLUTRYALASPLYSVALP 1239  
D 3716 ATAAATATATGATCAGCAAGAAAGCATTAAGACGATGTGGAAATATGCTCAACAAGTTT 3775  
Q 1259 hehryrlylephelieleuglunetleuleuylstrpvalalalytglytyriginhr 1279  
D 3776 TCACTTCATTTTCATCTGGAATTCCTTCAAAATGGGTCGATATGGCTATCAACAT 3835  
Q 1279 yrpherhrasnalatrpcysrtrleuaspheleuilevalasplaserleuvalserl 1299  
D 3836 ATTTCACCAATAGCTGGTGTGGCTGACCTTAATGTGATGTTTCATGTGTCAGTT 3895  
Q 1299 eutrralialasnalaleuglytyrisercluleuglyalalieleyserserleuarghrleua 1319  
D 3896 TAAACGAAATGCTTGGGTACTCAGACACTTGAGCCATCAAAATCTCTCAGACACTAA 3955  
Q 1319 rgalaleuarproleuaralaleuaserargphlegluglymetargvalalvalasna 1339  
D 3956 GAGCTCTGAGACCTCTTAGACCTTATCTGATTTGAAGGATGAGGATGTTGTGATG 4015  
Q 1339 laleuleuglyalalaleproserilemetasnalaleuleuvalcysleuilephetrpl 1359  
D 4016 CCCTTTAGAGGCAATTCATCCATCATGAAATGCTTGCTTGCTTATATTCGCGC 4075  
Q 1359 euliepheserilemetglyvalasleuuphealaglylyshphetryhiscysileasnt 1379  
D 4076 TAAATTTTCACCATCATGCGGATTAATTTGTTGCTGCAAAATCTTACCACATGATTTAA 4135  
Q 1379 hrthrhrthglaspariphasprilegluasprvalasnasnlsthraspcysleuylsl 1399  
D 4136 CCACACTGTGTGACAGGTGTGACATCGAAGACGGAATTAATCAATACGATTTGCTTAAAC 4195  
Q 1399 euliegluasnasnluhrthalartrpshasnalalyvalasnpheaspsanvalg 1419  
D 4196 TAAATAGAAAGAAATGACACGTGCGATGGAATAATGGAAGTAATTTGATATATAG 4255  
Q 1419 lyphleglytyrleuserleuenglnalalathrphelyrglytrpmetcapilemet 1439  
D 4256 GATTTGGGTATCTCTCTCTTCTTCACCTTCCACATTCACAAAGATGATGATTAATGT 4315  
Q 1439 yralaalavalaspsarargasnalgluleuglnprolystrylugluserleuylrm 1459  
D 4316 ATGCAGACAGTTGATTCAGAAATGTAGAACTCCAGCTTAAGTAAAGAAAGTGTGACA 4375  
Q 1459 eutryrleuylrphelialephelielephleglyserphetrhrleuansleupher 1479  
D 4376 TGTATCTTACTTGTATTTTCATCATCTTGGGTCTCTTCACTTGACCTGTTA 4435  
Q 1479 leglyvalalieleaspsanpheasnglnulyslyshphleglyglinaapllep 1499  
D 4436 TTGGGTGCACATAGATTAATTTCAACACGCAAGAAAGATTTGGGTGCAAGACATCT 4495  
Q 1499 hehethrthgluglnulyslystrtyrasnalametlyslenglyserlyslsyp 1519  
D 4496 TTTTGCAGAAAGAAAGAAATATACATATATGCAATGAAATTAATTAAGTTCGAAAAAAC 4555  
Q 1519 roglulysproileproargprogllyasnllyshphenglnlymetvalpshaspphevalr 1539  
D 4556 CGCAAAAAGCTATACCTGACGACGAAACAAATTTCAAGAAATGGTCTTGACCTGTAA 4615  
Q 1539 hrtrrglnvalpheaspliserlilemetleuleuilecysleuasnmvetalithmetk 1559  
D 4616 CCAAGCAAGTTTTTGCATATAGATCATGTATTCATCTCTTCAACATGTGCACATGA 4675  
Q 1559 etvalglutrraspspserglutryalthrthrileuserargileasnlleuyl 1579  
D 4676 TGGTGGAAAGATGACAGAGATGATATGTGATACATTTTGTCAAGCATCAATCTGG 4735  
Q 1579 alpheilevalleuupherhglylucysvalleuylleuylserleuarghrhistr 1599  
D 4736 TGTTCATGTGTATTTACTGAGAGAGTGTACTGAAACATCTCTCTACGCAATTAAT 4795

Q 1599 yrpherhrileglytrpasmilepheasphelvalvalilleuserlilevalglym 1619  
D 4796 ATTTCACATGATGATGAATTTTGTATTTTGTGTGTGATCTCTCCATGTAGTA 4855  
Q 1619 etpheleualagluenileglulysrtrphevaserprothrleuupheargvalillea 1639  
D 4856 TGTTCCTTCCGACCTGATTAABAAAGTATTTGTGTGCTCCCTACCTGTCGAGATGCC 4915  
Q 1639 rgleualarglileglyarglileuuarqleuileylsglyalalyseglylilearghr 1659  
D 4916 GTCTGTGATGATGGCGAATCTTACGTCTGATCAAAAGAGCAAGGATCCGACAGC 4975  
Q 1659 eulieuphealaleuemetserleuoproalaleupheasnlileglyleuileuuphel 1679  
D 4976 TGCCTTGTGCTTGTATGATGTCCTTCTGCTGCTGTTTAAACATCGGCTCTACTCTCC 5035  
Q 1679 euvalmetpheleletrralalephegylmetserasnphealatrvallysharggluy 1699  
D 5036 TAGTCATGTCATCTACGCCATCTTGGGATGTCACACTTGTGCTATGTTAAGAGGGAAG 5095  
Q 1699 alglyleaspsametpheasnpheglutrrpshglasnsrmetilecysleupheg 1719  
D 5096 TTGGGATCGATGACATGTTCATCTTGAGACCTTGGCAACAGATGATCTGCTATATCC 5155  
Q 1719 lnlierhrtrseralaglytrpaspolyleuualaproilleuasnserylserp 1739  
D 5156 AAATTAACACTCTGCTGCTGGGATGATGATGATGATGATGATGATGATGATGATGATG 5215  
Q 1739 roaspasparproasnllyshasnploglyserservallyshgllyaspcysglysnp 1759  
D 5216 CCGACTGTGACCTTAATAAGTTTAACTTGAACCTGAACTGATTAAGGAGACGTGGGAAC 5275  
Q 1759 roservalglylephasphelvalserlyrileileleserphelenuvalalalya 1779  
D 5276 CATCTGTGGAATTTCTTTTCTCAGTTACATCATCATCTCTCTCTGCTTGTGTA 5335  
Q 1779 smettrylilealavalilleuglnasnpheasvalalathrthglugluseralaglu 1799  
D 5336 ACATGTACATCGCGGTATCTCTGGAAGAACTCACTGTTGCTAAGAAAGTGCAGAGC 5395  
Q 1799 roleusergluaspspshglumetphetryglvalaltrpglulysphasproaspa 1819  
D 5396 CTCTGACTGAGGATGATTTGATGATGATTTGATGATTTGATGATTTGATGATTTGATG 5455  
Q 1819 lathrthgluphemelglupheglulysleusergluphealalalyaleugluproprol 1839  
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Q 1839 euasnlleuprogluproasnllyseuglnleuilealameasplleuprometvalserg 1859  
D 5516 TCAATCTGCACAAACCAAACTCAGCTCATGTCATGATTTGCCATGTGAGTG 5575  
Q 1859 lyasparglylehlscysleuasplleleuphealathrthrlyshargvallyslus 1879  
D 5576 GTGACGGATCCACTGCTGTGATATCTTAATTTGTTTAAACAGGGGCTCTAGAGAGA 5635  
Q 1879 erglylumeasplaleualarglileglumetgluglnuargphemelaserapros 1899  
D 5636 GTGAGAGAGATGATGCTTCAGAAATACAGATGGAAGCCATTCATGCTTCCATCTT 5695  
Q 1899 erlyshasrtyrtrgluproillethrthrleuylsharglysglnulvalsera 1919  
D 5696 CCAAGGTCTCTACAGCCATCACTCACTTAAACGAAACAAAGAGAGATATCTG 5755  
Q 1919 lavalilleleuglnargalalyrarghrghisleuuleuylshargthvallyslas 1939  
D 5756 CTGTCAATTTACGCGGTGTACAGAGCCACCTTTAAAGCAAGTAAACCAACCTT 5815  
Q 1939 erpherhrtrrasnllyshasnllyshgllyalaleuuleuilelysglunsp 1959  
D 5816 CTTTACGTGATTAATAAACAAATCAAAAGTGGGCTATCTTCTTATTAAGAAAGACA 5875

QY 1959 ettlelleaspargilleangluanserlethrgulysrhraspleuthrmetsetr 1979  
 DB 5876 TGATTAATGACAGATAATGAAAACTATACAGAAAACTATCGACCACTCA 5935  
 QY 1979 hrtaialicysproprosertrrparavvalthrlyseprollevalglulysrhrslgug 1999  
 DB 5936 CTGACGCTTGCCACCTCTCTTGACCGGGTACAAAGCCATTGTGAAAAACATGAC 5995  
 QY 1999 lnglulysaspqlulysalalygllys 2009  
 DB 5996 AAGAGCAAGATGAAAAAGCCAAAGGAAA 6027  
 RESULT 5  
 AAH5764  
 ID AAH5764 standard; cDNA; 8378 BP.  
 XX AAH5764;  
 AC  
 XX 04-SEP-2001 (first entry)  
 DT  
 XX Human neonatal form of SCN1A nucleotide sequence SEQ ID NO:2.  
 DE  
 XX Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;  
 KW diagnosis; mutation; chromosome 2q23-q31; neurological disorder;  
 KW anticonvulsant; neuroprotective; ss.  
 XX  
 OS Homo sapiens.  
 XX WO200138564-A2.  
 PN  
 XX 31-MAY-2001.  
 PD  
 XX 24-NOV-2000; 2000WO-CA01404.  
 XX  
 PR 26-NOV-1999; 99US-0167623.  
 XX  
 XX (UTMC-) UNIV MCGILL.  
 PA  
 XX Rouleau GA, LaFreniere RG, Rochefort D, Cossette P, Ragsdale D;  
 PI  
 XX WPI; 2001-355945/37.  
 DR  
 XX P-PSDB; AAB99675.  
 DR  
 PT Determining a predisposition to epilepsy and/or development of epilepsy  
 PT comprising determining the genotype of SCN1A, SCN2A and/or SCN3A, or a  
 PT DNA variant, equivalent, or mutation which shows a linkage  
 PT disequilibrium.  
 PT  
 PS Disclosure; Page 93-96; 268pp; English.  
 PS  
 CC The present invention describes a method (M1) of determining an  
 CC individual's predisposition to epilepsy and/or development of epilepsy,  
 CC as well as predicting the individual's response to medication. The  
 CC method comprises determining the genotype of at least one gene selected  
 CC from SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation  
 CC which shows a linkage disequilibrium. SCN1A, SCN2A and SCN3A are all  
 CC sodium channel genes located on chromosome 2. The idiopathic generalised  
 CC epilepsy (IGE) gene is more specifically localised on chromosome  
 CC 2q23-q31. Compounds identified as modulators of the biological activity  
 CC of SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating  
 CC epilepsy or other neurological disorders. They have anticonvulsant and  
 CC neuroprotective activities. AAH5763 to AAH56164 and AAH99674 to  
 CC AAH99679 represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR  
 CC primers, oligonucleotides and proteins given in the exemplification of  
 CC the present invention.  
 CC  
 SQ Sequence 8378 BP; 2498 A; 1571 C; 1775 G; 2534 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 0 Length: 8378  
 Score: 1447.00 Matches: 2002  
 Percent Similarity: 99.40% Conservative: 0  
 Best Local Similarity: 99.40% Mismatches: 7

Query Match: 72.03% Indels: 12  
 DB: 22 Gaps: 0  
 US-09-930-871-12 (1-2009) x AAH5764 (1-8378)  
 QY 1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhenethrArgGlu 20  
 DB 266 AAGGAGCAAGACAGTGTGTGTACACGAGCCTGACAGCTTCAACTCTTCACACAGAA 325  
 QY 21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40  
 DB 326 TCTCTTGGCGCGATTGAAAGACCATTCGACAGAGAAAGCAAGATCCAAACACAGAC 385  
 QY 41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60  
 DB 386 AAAAAAGATGACAGCAAGAAATGCGCAAAAGCCAAATAGACTGTGAACCTGGAAGAAC 445  
 QY 61 LeuProPheIleTyrlGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80  
 DB 446 CTTCATTTATTTATGAGACATTCCTCCAGAGATGTGTGACAGCCCTGGAGGACCTG 505  
 QY 81 AspProTyrrTrIleAsnLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100  
 DB 506 GACCCCTACTATATCATCAATAGAAACTTTATAGATTGAATTAAGAGGAGGACCATCTTC 565  
 QY 101 ArgPheSerAlaThrSerAlaLeuTyrlIleLeuThrProPheAsnProLeuArgLysIle 120  
 DB 566 CGGTTCAGTCCACCTCTGCTGACATTTTAACTCCCTTCAATCTTTAGAAAAATA 625  
 QY 121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140  
 DB 626 GCTATTAAGATTGTTGGTATCATTCATATTCACAGATGCTAATATATGACACTTTTGACA 685  
 QY 141 AsnGlyValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGlyThr 160  
 DB 686 AACTGTGTATGACAAATGAGTAACTCTGATGGACAAAGATGTAAATACAC 745  
 QY 161 PheThrGlyIleTyrrThrPheGluSerLeuIleLysIleAlaAlaGlyPheCysLeu 180  
 DB 746 TTCACAGCAATATATATCTTTGATATCATTATTAATATATGCAAGGGGATTCGTGTTA 805  
 QY 181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200  
 DB 806 GAAGATTACTTCTCTGGGATCCATGAGAACTGGCTGATTCACGTATACATTT 865  
 QY 201 AlaTyr-ValThrGluPheValAsp-LeuGlyAsnVal-SerAlaLeuArgThrPheArg 219  
 DB 866 GCGTT-TGTAAACGAAATTTGTAAA-CTTAGCAATTT-TTCAGCTCTTGGCACTTTCACA 922  
 QY 220 ValLeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAla 239  
 DB 923 GCTTGTAGAGCTTTGAAAACTATTTGGAATTCAGGGCTGAAACCAATGTGGAGGC 982  
 QY 240 LeuIleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSer 259  
 DB 983 CGATGCAATCGTGTGAAGAGCTCTCAGATGTAATGATCTGACGTGTCTGTGTGAGC 1042  
 QY 260 ValPheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGln 279  
 DB 1043 GATATTGCTCTAATGGGCTGTGACAGCTGTTCATAGGGCAACCTGAGGAATATAAGTATACA 1102  
 QY 280 TrpProProThrAsnAlaSerLeuGluGluLysSerIleGluLysAsnIleThrValAsn 299  
 DB 1103 TGGCTCCACCAATGCTCTTGGAGAACATGATGAAAGAAATTAATGATGCAAT 1162  
 QY 300 TyrAsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrlIleGln 319  
 DB 1163 TATATGATGACACTATAATAGAACTGCTTGTGATTTGACTGGAAGCATATATTCOA 1222  
 QY 320 AspSerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuGlyLysSer 339  
 DB 1223 GATTCAGATATCATATATTTCTGTGGAGGCTTTTATAGAGCACTACTATGTGAAATATAC 1282



QY 340 SerAspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsn 359  
 DB 1283 TCGATGACAGGCCAATGTCAGAGGATATATGTGTGAAGCTGGTAAACATCCCAAT 1342  
 QY 360 TyrGlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMet 379  
 DB 1343 TATGGGTACACAAAGCTTGTGATACCTTCAGTTGGCTTTTGTCTTGTTCAGCTAATG 1402  
 QY 380 ThrGlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyr 399  
 DB 1403 ACTCAGAGACTTGGGAAATCTTTATCACTGACATTAGCTGCTGCTGGGAAACGTAC 1462  
 QY 400 MetIlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnIleIleu 419  
 DB 1463 ATATATATTTTTTATATGGTCATTTTCTTGGCTCATTTCACTCAATCAATTAATTTGATCTG 1522  
 QY 420 AlaValAlaIleMetAlaTyrGluGluGluGlnAsnGlnAlaThrLeuGluGlnAlaGluGln 439  
 DB 1523 GCTGTGGTGGCCATGGCTTCAGAGAACACAAATCAGGCCACTTGGAAAGACAGAACAG 1582  
 QY 440 LysGluAlaGluPheGlnGlnMetIleGluGlnLeuLysGlnGlnGlnAlaAlaGln 459  
 DB 1583 AAGAGGCCCAATTTCCAGAGATGATGAACAGCTTAAAGCAACAGAGGACAGCTCAG 1642  
 QY 460 GlnAlaIleAlaThrAlaThrAlaSerGlnIleHisSerArgGluProSerAlaAlaGlyArgLeu 479  
 DB 1643 CAGCAGCAACAGGCACTGCTCAGAACATTCAGAGAGCCACTGACAGAGGAGCTC 1702  
 QY 480 SerAspSerSerSerGlnAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsn 499  
 DB 1703 TCAGACAGCCTCATCTGAAGCTCTTAAGTTGACTTCCAAAGAGTGTAAAGAAAGAAAT 1762  
 QY 500 ArgArgLysLysArgLysGlnLysGlnLysSerLysGlyGluLysAspGluAspGlu 519  
 DB 1763 CGGAGGAGAAAGAAACAGAAAGACAGCTGCTGGGAGAAAGAAAGTGAAGATGAA 1822  
 QY 520 PheGlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGlu 539  
 DB 1823 TTCCAAAATCTGATCTGAGGACATCAAGAGAGGAAAGTTCCTTCTTCATTGAA 1882  
 QY 540 GlyAsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuSerIle 559  
 DB 1883 GGGAAACGATTCATATGAAAAAGAGTACTCCCTCCACACACAGCTTTGTGTAGCATC 1942  
 QY 560 ArgGlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGly 579  
 DB 1943 CGTGGCTCCCTATTTCCACCAAGGCGAAATAGCAAGAACCCCTTTCACCTTTAGAGG 2002  
 QY 580 ArgAlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGlu 599  
 DB 2003 CGAGCAAGAGATGGGATCTGAGAACGACTTCGCAATGATGAGCC-ACCACCTTTGAG 2061  
 QY 600 AspAsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsn 619  
 DB 2062 GATTAAGAGAGCCGTAGATTCCTTGTGTGTGCCCGAGAGACAGGAGAGAGAGCGAAC 2121  
 QY 620 SerAsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValPheProAlaAsnGly 639  
 DB 2122 AGCAACTGTGAGACACCACTAGGTCAATCCCGATGCTGCGACAGTGTTCACAGCAATGGG 2181  
 QY 640 LysMetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerVal 659  
 DB 2182 AAGATGACAGCACTGGGATGCAATGGTGGTTTCTTGTGTGGTGAACCTTCAGTT 2241  
 QY 660 ProThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAsp 679  
 DB 2242 CTAACATCGGCTGTGGACAGCTTCTGCCAGAGGTGATTAATAGTTAAGCCAGCTACTGAT 2301  
 QY 680 AspAsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerPheHisVal 699  
 DB 2302 GACAATGCAACCACTGAAGTGAAGTGAAGAAAGAGAGTCAATTTCTTCCACAGCT 2361  
 QY 700 SerMetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIle 719

DB 2362 TCCATGACCTTCTAGAAAGTCTTCCAAAGGCAAGAGCAATGATATAGCCAGATT 2421  
 QY 720 LeuThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyr 739  
 DB 2422 CTAAACAATACAGTAGAAGAACTTGAAAGATCCAGGACAGAAATCCACCTGTGGTAT 2481  
 QY 740 LysPheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHis 759  
 DB 2482 AAATTTCCAAACATATCTTAATCTGGAGAGCTTCCTCAATATGTGTTAAAGTGAACAT 2541  
 QY 760 ValValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleVal 779  
 DB 2542 GTTGTCACTGGTGTGGAGGACCACTTGTGACCTGGCCACACACATCTGATATGTC 2601  
 QY 780 LeuAsnThrLeuPheMetAlaMetGlnHisTyrProMetThrAspHisPheAsnVal 799  
 DB 2602 TTTAAATCTCTTTCATAGCCCATGAGACATATCCATGACGACCTTTCATATATGTG 2661  
 QY 800 LeuThrValGlyLysLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIle 819  
 DB 2662 CTTAACAGTAGAAACCTGTTTCACAGGATCTTTACACAGAAATGTTCTGAATAT 2721  
 QY 820 IleAlaMetAspProTyrTyrTyrPheGlnGlnGlyTyrTrpAsnIlePheAspGlyPheIle 839  
 DB 2722 ATTCAGATGATCTTATCTATATTTCCAAAGGCTGGAATATCTTGAAGGTTTAT 2781  
 QY 840 ValThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArg 859  
 DB 2782 GTACAGCTTACCGCTGAGAGAACTTGACCTGCCAATGTGAAAGATATATCTCTCCGT 2841  
 QY 860 SerPheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeu 879  
 DB 2842 TCAATTCGATGGCGGACAGTTTTCAGTGGCAAAACCTTGGCCCAAGTTTAAATATCTA 2901  
 QY 880 IleLysIleIleGlyAsnSerValGlyAlaLeuGlyLysLeuThrLeuValIleAlaIle 899  
 DB 2902 ATTAAGATCAATCGCAATTCGCTGGGGCTGTGGAAATTAACCTCGCTTGGCATC 2961  
 QY 900 IleValPheIlePheAlaValAlaGlyMetGlnLeuPheGlyLysSerTyrLysAspCys 919  
 DB 2962 ATGCTCTTCAATTTTGGCGGTGGGATGAGCATGAGCTCTTGTGTAACATCAAGATTTGT 3021  
 QY 920 ValCysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPheHis 939  
 DB 3022 GTCTGCAAGATCCGCACTGATTTGCAACTCCACGCTGCACAGATGACTTCTTCAC 3081  
 QY 940 SerPheLeuIleValPheArgValLeuCysGlyLysIleTrpIleGluThrMetTrpAspCys 959  
 DB 3082 TCTTCTCGATTTGTTCGCGCTGCTGTGGGAGTGAATAGACCATGTGGACTGT 3141  
 QY 960 MetGluValAlaGlyGlnAlaMetCysLeuThrValPheMetValIleGly 979  
 DB 3142 ATGAGAGTCTGCTGCAAGCATGCTGCTTACTCTCATGATGATGATGATGATGATGATG 3201  
 QY 980 AsnLeuValValLeuAsnLeuPheLeuAlaLeuLeu\*\*\*SerSerPheSerAlaAspAs 999  
 DB 3202 AACCTAGTGTCTGATATCTTCTTGTGCTGCTGTCT- GAGCTCATTTAGTGACAGCAA 3260  
 QY 999 IleuAlaIleAlaThrAspAspAsnGluMetLysAsnLeuGlnIleAlaValAspArgMe 1019  
 DB 3261 CTTTGCAGCCACGATGATATATTAAGAAATGAATTAATCTCCAAATTCCTGTGGTAGAT 3320  
 QY 1019 ThrLysGlyValAlaLysArgLysIleTyrGluPheIleGlnIleSerPheIle 1039  
 DB 3321 GCACAAGAGGTAGCTTATGTGAAGAAATTAATTAATTAATTAATTAATTAATTAATTA 3380  
 QY 1039 eArgLysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnLysLysAs 1059  
 DB 3381 TAGGAACCAAAAGATTTATATGAATTAACCACTGATGATCTAAACAAAGAAAGA 3440  
 QY 1059 pSerCysMetSerAsnHisThr\*\*\*GluIleGlyLysAspLeuAspTyrLeuLysAsp 1079

Db 3441 CAGTTGATGTCCATCATACAGC-AGAAATTGGGAAAGATCTTGAATCTTAAAGATG 3499  
Oy 1079 aAaaglyThrTherSerGylleGlyThrGlySerSerValGlyUlySerThrIleIleaspG 1099  
Db 3500 TAAATGGAACACACAGAGGTGTATGAGAACTGCACACAGCTTGAAATAATCATATATGATG 3559  
Oy 1099 luserAspTyrMetSerPheIleAaAsnProSerLeuThrValThrValProIleAlav 1119  
Db 3560 AAATGATACATCATCTTAAACAAACCCAGCTTACTGTGACTGTACCAATGTGCTG 3619  
Oy 1119 aGlyGlySerAspPheGlyUaAsnleuAnthrGlyUaAspPheSerSerUlySerAspLeuG 1139  
Db 3620 TAGAGAGATCTGACTTGAATAATTAACACGGAAGACTTATGATGTAATCGGATCTGG 3679  
Oy 1139 lugiSerLeuGlyUlySerUaAsnGlySerSerSerSerGlyUlySerThrValAspI 1159  
Db 3680 AAGAAAGCAAGAAAGAACTGAAATGAAAGCACTAGCTCATCGAAAGGTAGCACTGGACA 3739  
Oy 1159 lGlyAlaProValGlyUaGlyUaProValValGlyUaProGlyUaThrLeuGlyUaProGlyUa 1179  
Db 3740 TCGGCGACCTGTGAAGAACAGCCCGTATGGAACCTGAAAGAACTCTTGACACAGAA 3799  
Oy 1179 lAcysPheThrGlyGlyCysValGlnArgPheLysCysCysGlnIleAsnValGlyUaG 1199  
Db 3800 CTCTTTCACAGAAAGCTGTGTACAAAGATCAAGTGTTCACAAATCATATGTGGAAGAG 3859  
Oy 1199 lYArgGlyLysGlnThrPheAsnleuArgArgThrCysPheArgIleValGlyUaAsnAnt 1219  
Db 3860 GCAAGAGAAACAAATGGGGAACCTGGAAGAGACGTGTTCGGAATGATGTGAACCTAACT 3919  
Oy 1219 rPheGlyUaThrPheIleValPheMetIleLeuLeuSerSerGlyValAlaLeuAlaPheGlyUa 1239  
Db 3920 GGTGTGAGACCTGTGATTTTTCATGATTCCTCTTATGAGTGTGCTGTGGATTTGAA 3979  
Oy 1239 spIleTyrIleAspGlnArgLysThrIleLysThrMetLeuGlyUaIleAspLysValP 1259  
Db 3980 ATATATATATGATGACGGAAGAGCAATTAAGACATGTGGAATATGCTGCACAGGTTT 4039  
Oy 1259 heThrTyrIlePheIleLeuGlyUaMetLeuLysThrValAlaLysThrGlyUaIleThr 1279  
Db 4040 TCACCTTACATTTTATTTGGAAGAGCTTCTTAAATGGGTGCAATATGCTCATCAAAA-T 4098  
Oy 1279 yRPhetThrAsnAlaTyrCysThrLeuAspPheLeuIleValAlaPylSerLeuValSerI 1299  
Db 4099 ATTTTCACCAATGCCGTGGTGTGGCTGAGCTTCTTATGATGTTCATTTTCATTTGCGACGT 4158  
Oy 1299 eurThrAlaAsnAlaLeuGlyTyrSerGlyUaGlyAlaIleLysSerLeuArgThrLeu 1319  
Db 4159 TAACAGCAATAGCTTGGGTATCTAGAAAGCTTGAGCCATCAATCTCTCAGAGACATA 4218  
Oy 1319 rGAlaLeuArgProLeuArgAlaLeuSerArgPheGlyUaLysThrValValAlaAsn 1339  
Db 4219 GAGCTGTGAGACCTTAAAGACCTTATCTCATTTGGAAGGATGAGGTGTGTTGGAATG 4278  
Oy 1339 lAlaLeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheThrPL 1359  
Db 4279 CCGTTTATGAGCAATTCATTCATCATGAAATGTCTGTGCTTGTCTTATATCTGGC 4338  
Oy 1359 euIlePheSerIleMetGlyValAsnleuPheAlaGlyLysPheThrLysCysIleAsnT 1379  
Db 4339 TAAATTTAGCATCATGGGCGTAAATTTGTTTGTGCGCAATTCATACCACTATATTAACA 4398  
Oy 1379 hrThrThrGlyAspArgPheAspIleGlyUaPylAsnAsnIleThrAspCysLeuLysL 1399  
Db 4399 CCACAACTGTGACAGGTGTGATGACATCGAAGACGTGAATTAACATCATCTGATTCCTCAAAAC 4458  
Oy 1399 euIleGlyArgAsnGlyUaThrAlaArgTrpLysAsnValLysValAsnAsnAspAsnValG 1419  
Db 4459 TAAATGAAGAAGAAAGAGACTGCTCATGTAAGAAATGTGAAGTAACTTGTGTAATGTAG 4518  
Oy 1419 lYpHeGlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTyrPheAspIleMet 1439  
Db 4519 GATTGGGTATCTCTCTTGTCTCAAGTGTCCACATTCAGAGAGATGATATATATATGT 4578

Oy 1439 yRAlaAlaValAspSerArgAsnValGlyUaGlnProLysTyrGlyUaLysLeuTyrM 1459  
Db 4579 ATGCAAGCATGTGATTCAGAAATGTGAAATCCAGCCCAAGTATAGAAAGATCTGTACA 4638  
Oy 1459 eTyrLeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheI 1479  
Db 4639 TGTATCTTACTTGTGTATTTTTCATCATCTTGGGTCTCTTTCACCTTGAACCTGTATA 4698  
Oy 1479 lGlyValIleIleAspAsnPheAsnGlnGlyLysLysPheGlyGlyGlnAspIleP 1499  
Db 4699 TTGGTGTATGTGATATATTTCAACGACGAAAGAAAGTTGGAGGTACATCATCT 4738  
Oy 1499 heMetThrGlyUaGlnLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLysP 1519  
Db 4759 TTATGACAGAAAGAACAGAGAAATTCATATGCAATTAATAAATTAAGATCGAATAAAC 4818  
Oy 1519 rGlnLysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheValT 1539  
Db 4819 CGCAAAACCTATACCTCGACAGCAAAACAAATTCAGAGATGTCTTGTGACTTCGTAA 4878  
Oy 1539 hrArgGlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMet 1559  
Db 4879 CCAGCAAGTTTGTGACATTAAGCATCATGATTCATCTCATCTTAAACATGTGCAAAATGA 4938  
Oy 1559 eTValGlyUaThrAspAspLysSerGlyUaIleThrThrIleLeuSerArgIleAsnLeuV 1579  
Db 4939 TGTGTGAACAGATGACACAGAGTGAATATGTGACATCAATTTTGTACAGCATCAATCTGG 4998  
Oy 1579 aPheIleValLeuPheThrGlyGlyCysValLeuLysLeuIleSerLeuArgLysTyr 1599  
Db 4999 TGTTCATGTGCTATTTACTGGAGAGTGTGACAGAACTCATCTCTACGCCATATAT 5058  
Oy 1599 yRPhetThrIleGlyTyrAsnIlePheAspPheValValIleLeuSerIleValGlyM 1619  
Db 5059 ATTTTACCATGTGATGATATTTTGTATTTGTGTGTGATTCCTTCATCTGATGAGTA 5118  
Oy 1619 ePheLeuAlaGlyUaLeuIleGlyLysTyrPheValSerProThrLeuPheArgValIleA 1639  
Db 5119 TGTTCCTTGGCGAGCTGATAGAAAGATATTCGTGTCCCTTACCTGTGCGAGATATCC 5178  
Oy 1639 rGLeuAlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrL 1659  
Db 5179 GTCTGTGATGATGTGGCGAATTCCTAGCTGATCAAAAGAGCAAAAGGATCCGACAGC 5238  
Oy 1659 euLeuPheAlaLeuMetCetSerLeuProAlaLeuPheAsnIleGlyLeuLeuPheL 1679  
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Oy 1679 euValMetPheIleThrAlaIlePheGlyMetSerAsnPheAlaThrValLysArgGlyU 1699  
Db 5299 TAGTATGTGTCACTACGCCCATCTTGGAGTGTCCAACTGTGCTTAAAGAGGAG 5358  
Oy 1699 aGlyIleAspAspMetPheAsnPheGlyUaThrPheGlyAsnSerMetIleCysLeuPheG 1719  
Db 5359 TTGGATGTGATGACATGTTCACATTTGAGACCTTGGCAACAGCATGATCTGCCATATCC 5418  
Oy 5419 AAATTAACAACCTCTCTGCTGGATGATGATGCTGTGACCCATCTCAACAGTAAGCCAC 5478  
Oy 1739 rAspCysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsnP 1759  
Db 5479 CCGACTGTGACCTTAAATTAAGTTAACCTGTGAAGCTCAGTTAAAGGAACGTGGGAAC 5538  
Oy 1759 rSerValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValValAla 1779  
Db 5539 CATCTGTGGAATTTTCTTTTGTGACATCATATCATATATCTTCTGTGTGTGTGA 5598  
Oy 1779 snMetTyrIleAlaValIleLeuGlnAsnPheSerValAlaThrGlyUaSerAlaGlyU 1799  
Db 5599 ACATGTACATGCGCGTATCCGAGAACTCAGCTGTGCTACATCAAAAGATGAGAGC 5658



QY 1799 roleSerGIUAASPAPheglUmePheTyrGIUValTPGIULYSPheASPProAspA 1819  
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 QY 1819 laThrGIUmeTGIUphGIULYsUeSerGIUphleAlaAlaLeuGIUProFol 1839  
 DB 5719 CAACGTGCTGATGAGATTTGAAAAATATCTGAGTTGACGTGGCTTGAACGGCTC 5778  
 QY 1839 euSnuLeuProGIUProAspILYsUeGIUleuLeuAlaMetAPLeuPrometValSerg 1859  
 DB 5779 TCATCTGCGCAACCAAACTCCAGCTCATGCGCAAGATTGCCATGGTGTAGTG 5838  
 QY 1859 lYAspArgILeHsCYsLeuAspILeupheAlaPheThrLYsArgValleuGIULYsU 1879  
 DB 5839 GTACCGGATCCACTGCTTGTATCTTATTTGCTTTTACAAAGCGGCTTCTAGAGAGA 5898  
 QY 1879 erGIULYmeTAspAlaLeuArgILeGIUmeGIUArgPheMetAlaSerAspProS 1899  
 DB 5899 GTGGAGATGATGATGCTCTGCAATACAGATGAGAGAGATTCATGCTTCCATCTT 5958  
 QY 1899 erLYsValSerTYrGIUProIleThrThrLeuLYsArgLYsGIULYsUValSera 1919  
 DB 5959 CCAAGGTCTCTATCACGCCATCACTACTTAAAAACAAACAAAGAGAGATATCTG 6018  
 QY 1919 lAValILeIleGIUArgAlaTYrArgThrHisLeuLYsArgThrValLYsGIUAla 1939  
 DB 6019 CTGTCTATTATCACGGCTGTACAGCGCACTTTAAAGCGAACTGTAACCAACTT 6078  
 QY 1939 erPheThrTYrAsnLYsAsnLYsILeLYsGIULYsAlaAsnLeuLeuLYsGIUAspM 1959  
 DB 6079 CATTACGTCAATTAATAACAAATCAAGTGGGCTATCTCTTATTAAGAACACA 6138  
 QY 1959 etILeIleAspArgILeAsnGIUAsnSerILeThrGIULYsThrAspLeuThrMetSert 1979  
 DB 6139 TGATTAATTTGACAAATTAAGAAACTCTATTACAGAAAAACGATGACCATGTCCA 6198  
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 DB 6199 CTGACGCTTCTCCACTCTCTATGACCGGTGCAAAAGCCAAATTTGGAAAAACATGAGC 6258  
 QY 1999 lngULYsAspGIULYsAlaLYsGIULYs 2009  
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 AAD32846  
 ID AAD32846 standard; cDNA; 4362 BP.  
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 AC AAD32846;  
 XX  
 DT 01-JUL-2002 (first entry)  
 XX  
 DE Human ion channel cDNA #8.  
 XX  
 KW Human; novel human protein; NHP; voltage-gated sodium channel;  
 KW gene therapy; bioreactor; mental disorder; biological disorder;  
 KW gene; medical disorder; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key 1...4362 Location/Qualifiers  
 FT CDS  
 FT /tag= a  
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 PN WO200214498-A2.  
 PD 21-FEB-2002.  
 PF 15-ANG-2001; 2001WO-US25650.

XX  
 PR 16-ANG-2000; 2000US-2259689P.  
 XX  
 PA (LEXI-) LEXICON GENETICS INC.  
 XX  
 PI Turner CA, Mathur B, Mathur D;  
 XX  
 DR WPI: 2002-280757/32.  
 DR P-PDB; AAE20517.  
 XX  
 PT Novel polynucleotides encoding human sodium channel proteins,  
 PT particularly voltage-gated sodium channel proteins useful for drug  
 PT screening, diagnosis and in gene therapy of biological disorders -  
 PS Claim 1; Page 69-70; 83pp; English.  
 XX  
 CC The present sequence is a cDNA encoding novel human protein (NHP), ion  
 CC channel protein. NHP share structural similarity with mammalian sodium  
 CC channel proteins particularly voltage-gated sodium channel proteins.  
 CC NHP oligonucleotides are useful as hybridisation probes for screening  
 CC libraries and assessing gene expression patterns. Sequences derived  
 CC from regions adjacent to the intron/exon boundaries of NHP gene can be  
 CC used to design primers for use in amplification assays to detect  
 CC mutations within the exons, splice sites, introns that can be used in  
 CC diagnostics and pharmacogenomics. NHP nucleotide sequences are useful  
 CC for drug screening effective in the treatment of symptomatic or  
 CC phenotypic manifestations of perturbing the normal function of NHP in  
 CC the body, and nucleotide constructs encoding NHP products are useful to  
 CC genetically engineer host cells to express NHP products in vivo. These  
 CC delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion  
 CC protein to the body. Nucleotide construct encoding NHP products are  
 CC also useful in gene therapy for modulating NHP expression and to  
 CC produce genetically engineered host cells to express NHP products in  
 CC vivo. NHP nucleotide sequences may also be used as part of ribozyme  
 CC and/or triple helix sequences that are useful for NHP gene regulation.  
 CC The NHP polypeptides are useful for generating antibodies, as  
 CC reagents in diagnostic assays, for identifying other cellular gene  
 CC products related to NHP and as reagents in assays for screening for  
 CC compounds that are useful in the treatment of mental, biological or  
 CC medical disorders and diseases.  
 XX  
 SQ Sequence 4362 BP; 1300 A; 845 C; 995 G; 1219 T; 3 other:  
 Alignment Scores:  
 Pred. No.: 0 Length: 4362  
 Score: 1444.00 Matches: 1446  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 71.88% Indels: 0  
 DB: 24 Gaps: 0  
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 QY 41 LYsLYsAspAspAspGIUAsnGIULYProLYsProAsnSerAspLeuGIUAlaGIULYsAsn 60  
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 QY 61 LeuProPheIleTYrGIULYsAspILeProFroGIUmeValSergIUProLeuGIUAspLeu 80  
 DB 181 CTTCATATTATTATGAGAGCATTCCTCCAGAGATGGTGTCAAGAGCCCGAGAGACCTG 240  
 QY 81 AspProTYrTYrILeAsnLYsLYsThrPheILeValLeuAsnLYsGIULYsAlaIlePhe 100  
 DB 241 GACCCCTACTATATCAATTAAGAAACTTTATATGATTAATAAGGAGGAGGCATCTTC 300

[illegible]

|    |      |  |      |
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| QY | 461  | AlaAlaThrAlaThrAlaSerGlnHisSerArgIuprosSerAlaAlaGlyAyleSer       | 480  |
| Db | 1381 | GCAGCAACGGCACTGCTCCAGAACATTCCAGAGAGCCCACTGCACGACGAGCGCTCTCA      | 1444 |
| QY | 481  | AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg     | 500  |
| Db | 1441 | GACACCTCATCTGAAAGCCTTAAGTTGAGTTCCAAAGAGTGTATAGAAAGAAATCGG        | 150  |
| QY | 501  | ArgLysLysArgLysGlnLysGlnGlnSerGlyGlyGlnLysAspGluAspGluPhe        | 520  |
| Db | 1501 | AGGAAGAAAGAAAGAAAGAAAGAACAGCTGCTGTGGGAGAGAAAGATGAGATGAATTC       | 156  |
| QY | 521  | GlnLysSerGlnSerGluAspSerLysArgArgLysArgLysPheArgPheSerLysGlnLys  | 540  |
| Db | 1561 | CAAAATGTGAATCTGAGAGACGATCCAGAGGAAAGGATTTCCCTCTCCATTTGAAGGG       | 162  |
| QY | 541  | AsnArgLeuThrTyrGlnLysArgTyrSerSerProHisGlnSerLeuLeuSerLysArg     | 566  |
| Db | 1621 | AACCGATTGACATATGAAAAGAGTACTCCCTCCACACAGTCTTTGTTGAGCATCCGT        | 168  |
| QY | 561  | GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgLysArg     | 580  |
| Db | 1681 | GGCCTCCATTATTTCACCAAGCGCAAAATAGCAGAACAGCCTTTTCACCTTTAGAGGCGA     | 174  |
| QY | 581  | AlaLysAspValGlySerGlnAsnAspPheAlaAspArgLysHisSerThrPheGluAsp     | 600  |
| Db | 1741 | GCAAAAGATGTGGGATCTCGAAGACGACTTCGCAATGTATGACACACACCTTTGAGGAT      | 180  |
| QY | 601  | AsnGlnSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer     | 620  |
| Db | 1801 | AACGAGACCCGTAGATCTCTTTGTTGTGCCCGACGACACGAGAGACGCAACAGC           | 186  |
| QY | 621  | AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValPheProAlaAsnGlyLys     | 640  |
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| Db | 1921 | ATGCACACACACTGTGATGCAATGCTGTGCTTCCTGCTGTGGACCTTCAGTTGCTCT        | 198  |
| QY | 661  | ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp     | 680  |
| Db | 1981 | ACATGCGCTGTGGACACTTCTGCCAAGGTGATATAGATTAAAGCCAGCTACTGATGAC       | 20   |
| QY | 681  | AsnGlyThrThrGlnThrGlnMetArgLysArgArgSerSerPheHisValSer           | 700  |
| Db | 2041 | AATGGAACACACACTGAAACTGAAATGAGAAAGAAAGTCAAGTCTTCCACAGTTTCC        | 210  |
| QY | 701  | MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu     | 720  |
| Db | 2101 | ATGGACTTCTTGAAGATCTTCCCAAGGGAAGACGAAAGAAATATAGCCAGCATTTCTA       | 216  |
| QY | 721  | ThrAsnThrValGlnGlnLeuGlnLysSerArgGlnLysCysProProCysTyrTyrLys     | 744  |
| Db | 2161 | ACAAATACAGTATGAAGAACTTGAAAGATCCAGGCAAAATCCACACCTGTGGTATAAA       | 222  |
| QY | 741  | PheSerAsnIlePheLeuIleTyrPAspCysSerProTyrTyrLeuLysValHisVal       | 760  |
| Db | 2221 | TTTTCCAACTATCTTATATCGGGACATGCTTCCATATTTGGTATAAAGTGAACATGTT       | 228  |
| QY | 761  | ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrLysIleValLeu        | 786  |
| Db | 2281 | GTCAACACCTGGTGTATGATGAGCCCATTTGTAACCTGGCCACACCATCTGTATGTCTTA     | 234  |
| QY | 781  | AsnThrLeuPheMetAlaMetGlnLysIleArgProMetThrAspHisAspAsnAspValLeu  | 800  |
| Db | 2341 | ATATCTCTTTTATGTGCGCATGGAGACATATCAATGACGAGCACTTCAATAAATGTGCTT     | 240  |
| QY | 801  | ThrValGlyAsnLeuValPheThrGlyLysPheThrAlaGlnMetPheLeuLysIleIle     | 820  |
| Db | 2401 | ACAGTAGGAACCTGTTCACCTGAGATCTTTACAGCAGAAATCTTTCGTAAAAATATT        | 246  |
| QY | 821  | AlaMetAspProCysTyrTyrPheGlnGlnLysIleTyrPAsnIlePheAspGlyPheIleVal | 840  |

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 Db 3001 GCACCCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3060  
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 Db 4021 TTAGGACCAATTCATTCATCATCATCAATGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 4080  
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 Db 4261 GGGTATCTCTCTTGTCTTCAAGTTGCCACATTCAAAGATGATGATATATATGATGCA 4320  
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 Db 4321 GCAATTGATTCAGAAAT 4338  
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 ID AAD32847 standard; cDNA; 4179 BP.  
 XX AAD32847;  
 AC  
 XX 01-JUL-2002 (first entry)  
 DT  
 XX Human ion channel cDNA #9.  
 DE  
 XX Human: novel human protein; NHP; voltage-gated sodium channel;  
 KW gene therapy; bioelectronic; mental disorder; biological disorder;  
 KW gene; medical disorder; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..4179  
 FT /tag a

FT /product- "Human Ion channel protein #9"  
FT /transl\_except- (pos:2974...2976, aa:Xaa)  
FT /transl\_except- (pos:3199...3201, aa:Xaa)  
FT /note- "Xaa = any amino acid"  
XX  
XX W0200214498-A2.  
XX  
XX 21-FEB-2002.  
XX  
XX 15-AUG-2001; 2001WO-US25650.  
XX  
XX 16-AUG-2000; 2000US-225989P.  
XX  
XX (LEXI-) LEXICON GENETICS INC.  
XX  
XX Turner Ca, Mathur B, Mathur D;  
XX  
XX WPI; 2002-280757/32.  
XX  
XX P-PSDB; AAE20518.  
XX  
XX  
XX Novel polynucleotides encoding human sodium channel proteins,  
XX particularly voltage-gated sodium channel proteins useful for drug  
XX screening, diagnosis and in gene therapy of biological disorders  
XX  
XX  
XX Claim 1; Page 73-75; 83pp; English.  
XX  
XX The present sequence is a cDNA encoding novel human protein (NHP), ion  
XX channel protein. NHP share structural similarity with mammalian sodium  
XX channel proteins particularly voltage-gated sodium channel proteins.  
XX NHP oligonucleotides are useful as hybridisation probes for screening  
XX libraries and assessing gene expression patterns. Sequences derived  
XX from regions adjacent to the intron/exon boundaries of NHP gene can be  
XX used to design primers for use in amplification assays to detect  
XX mutations within the exons, splice sites, introns that can be used in  
XX diagnostics and pharmacogenomics. NHP nucleotide sequences are useful  
XX for drug screening effective in the treatment of symptomatic or  
XX phenotypic manifestations of perturbing the normal function of NHP in  
XX the body, and nucleotide constructs encoding NHP products are useful to  
XX genetically engineer host cells to express NHP products in vivo. These  
XX genetically engineered cells function as bioreactors in the body  
XX delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion  
XX protein to the body. Nucleotide construct encoding NHP products are  
XX also useful in gene therapy for modulating NHP expression and to  
XX produce genetically engineered host cells to express NHP products in  
XX vivo. NHP nucleotide sequences may also be used as part of ribozyme  
XX and/or triple helix sequences that are useful for NHP gene regulation.  
XX The NHP polypeptides are useful for generating antibodies, as  
XX reagents in diagnostic assays, for identifying other cellular gene  
XX products related to NHP and as reagents in assays for screening for  
XX compounds that are useful in the treatment of mental, biological or  
XX medical disorders and diseases.  
XX  
XX  
XX Sequence 4179 BP; 1239 A; 815 C; 958 G; 1164 T; 3 other;  
XX  
XX  
XX Alignment Scores:  
XX Pred. No.: 0 Length: 4179  
XX Score: 1382.00 Matches: 1384  
XX Percent Similarity: 100.00% Conservative: 0  
XX Best Local Similarity: 100.00% Mismatches: 0  
XX Query Match: 68.79% Indels: 0  
XX DB: 24 Gaps: 0  
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XX 21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluValAlaAlaGlyAsnProLysProasp 40  
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XX 61 TCTCTGGGGCTATTGAAAGAGCAATTCGACGAAAGGCAAAAGCAATCCCAACGACAGC 120  
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XX 41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60

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XX 241 GACCCCTACTATATCAATAAGAAACCTTTATAGATATGATTAAGGAGGCCATCTTC 300  
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XX 601 GCGTACGTCACAGAGATTGTGACCTGGCGAATGCTCGCATTAAGAATTCAGAGTT 660  
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XX 241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260  
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XX 721 ATCCAGTGTGGAAGAACTCTCAGATGATTAAGATCCGACGTGTTGCTGCGCTA 780  
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XX 261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280  
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XX 381 GluAspPheTyrPheLysLeuTyrGlnLeuThrPheLeuArgAlaAlaGlyLysThrMet 400  
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Db 1201 AFAATTTTGTGTCATTTTCTGGGCTCATTCACCTAAATAATTGATCGTGGCT 1260  
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Db 1261 GTGGTGGCCATGGCTGACGAGAACAGAAATCAGGCCACCTGGAGAGAACAGAACAGAA 1320  
QY 441 GlnAlaGluPheGlnGlnMetIleGlnGlnLeuLysGlnGlnGlnGlnAlaGlnGln 460  
Db 1321 GAGGCCGAATTTACAGCAGATGATGAAACGCTTAAAAAGCAGAACAGAGGAGCTCAGAC 1380  
QY 461 AlaAlaThrAlaThrAlaSerGlnLysSerArgLupProSerAlaAlaGluArgLeuSer 480  
Db 1381 GCAGCAACGGCAGCAGCTGCTCAGAAATCTCCAGAGAGCCAGTGAGAGCAGCAGCTCTCA 1440  
QY 481 AsnSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500  
Db 1441 GAGAGCTCACTAGAGGCTTAAAGTTGAGTTCCAGAGAGTCTTAAAGAAACAAATTCGG 1500  
QY 501 ArgLysLysArgLysGlnLysGlnLysGlnSerGlyGluGlnLupLysAspGluAspGluPhe 520  
Db 1501 AGGAGAGAAAGAAACAGAAAGAGCAGCTGTGGGAGAAAGAAAGATGAGATGAAATTC 1560  
QY 521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540  
Db 1561 CAAAAATCTGAATCTGAGCAGCAGCAGCAGCAGGAAAGCTTTGCTTCTCATTTGAAGG 1620  
QY 541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560  
Db 1621 AACCGATTGACATATGAAAAGAGTACTCTCCACACAGACTTTGTTGAGACATCCGT 1680  
QY 561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580  
Db 1681 GGCTCCCTATTTCACCAAGGCGAAATAGCAGAACAGACTTTTCAGCTTTAAGGGCGA 1740  
QY 581 AlaLysAspValGlySerGlnLysAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600  
Db 1741 GCAAGAGATGTGGGACTGTGAAGAGCAGCTTCGAGATGATAGCAGCAGCAGCTTTGAGAT 1800  
QY 601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620  
Db 1801 AACGAGAGCGGTAGAGATTCCTGTTGTTGCCCGCAGACAGAGAGAACCAACAGCAGC 1860  
QY 621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValPheProAlaAsnGlyLys 640  
Db 1861 AACCTGATGAGACAGAGTATGATCCCGAGCTGGCAGATGTTCCAGGAGATGGGAG 1920  
QY 641 MethIleSerThrValAspCysAsnGlyValValSerLeuValGlyLysProSerValPro 660  
Db 1921 ATGCACAGCAGCTGTGGATTCGATGGTGGTTCCTTGGTGGTGGACCTTCAGTTCCCT 1980  
QY 661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680  
Db 1981 ACATCCCTGTGTGACAGCTTCGCGAGAGGTATATATATATATATATATATATATATAT 2040  
QY 681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700  
Db 2041 AATGGAAACACAGCTGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAAT 2100  
QY 701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720  
Db 2101 ATGAGCTTTCTAGAGATCTCTCCAAAGCAGCAGCAGCAGTATAGCAGCAGCTCTCA 2160  
QY 721 ThrAsnThrValGluGluGlnGluGluSerArgGlnLysCysProProCysTyrPylLys 740  
Db 2161 ACAAAATACAGTACAGAACTTGAAGATCCAGGACAGAAATGAGCCACCTGTGTGTATAA 2220  
QY 741 PheSerAsnIlePheLeuIleTyrAspCysSerProTyrTyrPheLysValLysHisVal 760  
Db 2221 TTTTCCAAATATTTCTTAATCTGGAGCTGTCTCCATATTTGGTTAAAGGAAACATGTT 2280  
QY 761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780  
Db 2281 GTCACCTGGTGTGATGAGCCATTTGTTGACCTGGCCATCAGCATCTGTATTTGCTTA 2340

QY 781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnValLeu 800  
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QY 821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTyrAsnIlePheAspGlyPheIleVal 840  
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QY 841 ThrLeuSerLeuValGluGlnGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860  
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QY 861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTyrProThrLeuAsnMetLeuIle 880  
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QY 881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900  
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QY 901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920  
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QY 921 CysLysIleLeuAspSerCysGlnLeuProArgTyrPheHisMetAsnAspPhePheHisSer 940  
Db 2761 TGCAGAGTCGCGATGATGTCACCTCCAGCTGCGACATGATATACCTTTCCTCCATCC 2820  
QY 941 PheLeuIleValPheArgValLeuCysGlyGlyTyrIleGluThrMetTyrAspCysMet 960  
Db 2821 TTCCTGATGTGTTCGCGGCTGTGTGGGAGATGATAGAGCAGCATGTGGAGCTATAG 2880  
QY 961 GluValAlaGlyAlaMetCysLeuThrValPheMetCysValIleGlyAsn 980  
Db 2881 GAGGTGCTGGTCACCACTATGCTCTTACATGATGCTCATGATGCTGATGGAATC 2940  
QY 981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu\*\*\*SerSerPheSerAlaAspAsnLeu 1000  
Db 2941 CTAGTGTCTGTAATCTCTTCTGGCCTTGTGTGAGCTCATTTAGTGCAGCAACCTT 3000  
QY 1001 AlaAlaThrAspAspAsnGlnLysAsnLeuGlnIleAlaValAspArgMetHis 1020  
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QY 1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnLysLysAspSer 1060  
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QY 1061 CysMetSerAsnHisThr\*\*\*GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080  
Db 3181 TGTATGTCCATATATACARAGAAATTTGGAAAGATCTTACATCTTAAAGATGTAAT 3240  
QY 1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100  
Db 3241 GGAACCTACAAAGTGTATGAGTACAGCAGAGTGTGAAAAAATATATATATATATATAT 3300  
QY 1101 AspTyrMetSerPheIleAsnAspProSerLeuThrValThrValProIleAlaValGly 1120  
Db 3301 GATTACATGCTATCTTAACCAACCCAGCTTACGTGAGTACCAATGCTGTAGGA 3360  
QY 1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGln 1140  
Db 3361 GAATCTGACCTTGAATAATTTAAACACGAGAAAGATTTAGTAGTAAATCGGATCTGGAAGA 3420

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OY 1141 SerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGly 1160
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OY 1161 AlaProValGluGluGluGluProValValGluProGluGluThrLeuGluProGluValGly 1180
DB 3481 GGACCTGTGTAGAGAACAGCCCGTAGTGAAACCTGGAAGAAACCTTAAACAGAGAGCTTGT 3540
OY 1181 PheThrGluGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg 1200
DB 3541 TTCACGTGAAGGCTGTGTATCAAGATTCAGTGTTCATTAATGTGAGAGAGAGCAGA 3600
OY 1201 GlyLysGluThrPheAsnLeuArgArgArgPheArgIleValGluHisAsnTrpPhe 1220
DB 3601 GGAAAAACAATGATGGAACCTGAGAAAGAGAGCTGTTCCGAAATAGTGAACATACTGTTT 3660
OY 1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240
DB 3661 GAGACCTTCATGTTTTCATGATTCCTTAGTAGTGCGCTGCTGCAATTTGAAGATATA 3720
OY 1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr 1260
DB 3721 TATATTGATCAGCGAAGAGCATTAAGCATTTGGAATATCTGCAAGGTTTTCAC 3780
OY 1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTrpGlnThrTyrPhe 1280
DB 3781 TACATTTCATCTGTGAAATAGCTTAAATAGGTGCGCATAGGCTATCAACATATTTTC 3840
OY 1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300
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OY 1301 AlaAsnAlaLeuGluTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuAspAla 1320
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OY 1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIle 1360
DB 4021 TTAGGAGCAATTCATCCATCAATGAAATGTCCTTGTGTTGCTTATATCTGCTGCTAAT 4080
OY 1361 PheSerIleMetGlyValAsnLeuPheAlaGlyAspPheThrIleCysIleAsnThrThr 1380
DB 4081 TTCAGCATCTAGGCGCAAAATTTGTTGCGCAAAATCTACACATGATTAAACACCACA 4140
OY 1381 ThrGlyAspArg 1384
DB 4141 ACTGGTGACAGG 4152

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FT /transl_except- (pos:3199..3201, aa:Xaa)
FT /note- "Xaa = any amino acid"
PN WO200214498-A2.
PD 21-FEB-2002.
PE 15-AUG-2001; 2001WO-US25650.
PR 16-AUG-2000; 2000US-225989P.
PA (LEXI-) LEXICON GENETICS INC.
PI Turner CA, Mathur B, Mathur D;
PI WPI: 2002-280757/32.
DR P-PSDB; AAE20519.
DR
DR Novel polynucleotides encoding human sodium channel proteins,
XX particularly voltage-gated sodium channel proteins useful for drug
XX screening, diagnosis and in gene therapy of biological disorders
XX
XX Claim 1: Page 78-79; 83pp; English.
XX
XX The present sequence is a CDNA encoding novel human protein (NHP), Ion
XX channel protein. NHP share structural similarity with mammalian sodium
XX channel proteins particularly voltage-gated sodium channel proteins.
XX NHP oligonucleotides are useful as hybridisation probes for screening
XX libraries and assessing gene expression patterns. Sequences derived
XX from regions adjacent to the intron/exon boundaries of NHP gene can be
XX used to design primers for use in amplification assays to detect
XX mutations within the exons, splice sites, introns that can be used in
XX diagnostics and pharmacogenomics. NHP nucleotide sequences are useful
XX for drug screening effective in the treatment of symptomatic or
XX phenotypic manifestations of perturbing the normal function of NHP in
XX the body, and nucleotide constructs encoding NHP products are useful to
XX genetically engineer host cells to express NHP products in vivo. These
XX genetically engineered cells function as bioreactors in the body
XX delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion
XX protein to the body. Nucleotide construct encoding NHP products are
XX also useful in gene therapy for modulating NHP expression and to
XX produce genetically engineered host cells to express NHP products in
XX vivo. NHP nucleotide sequences may also be used as part of ribozyme
XX and/or triple helix sequences that are useful for NHP gene regulation.
XX The NHP polypeptides are useful for generating antibodies, as
XX reagents in diagnostic assays, for identifying other cellular gene
XX products related to NHP and as reagents in assays for screening for
XX compounds that are useful in the treatment of mental, biological or
XX medical disorders and diseases.
XX
XX SO Sequence 4197 BP; 1232 A; 821 C; 965 G; 1176 T; 3 other;
XX
XX Alignment Scores:
XX Pred. NO.: 0 Length: 4197
XX Score: 1332.00 Matches: 1334
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 66.30% Indels: 0
XX DB: 24 Gaps: 0
XX
XX US-09-930-871-12 (1-2009) x AAD32848 (1-4197)
OY 1 MetGluGlnPheValLeuValProProGluProAspSerPheAsnPhePheThrArgGlu 20
DB 1 ATGGAGCAAAACAGAGCTGTGACCAAGAGCTGACAGCTTCAACTTCTTACACAGAGAA 60
OY 21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
DB 61 TCTCTTCGGGCTATGTGAAGAACCGCATTCGAGAAAGCAAGAAATCCCAACACAGAC 120
OY 41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
DB 121 AAAAAAGATGACGACGAAATAGGCCCAAAACCAAAATAGTACTTGGAAGCTGGAAGAAC 180

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|    |      |   |      |
|----|------|---|------|
| Oy | 61   | LeutrophelleYrGlyAspIleProProGluMetValSerGluProLeuGlnAspLeu     | 80   |
| Db | 181  | CTTCACATTTATTTATGAGACATTTCTCCAGACATGTGTCCAGAGCCCTCGAGACCTGT     | 240  |
| Oy | 81   | AspProTyrTyrIleAsnLysThrPheIleValLeuAsnLysGlyValAlaIlePhe       | 100  |
| Db | 241  | GACCCCACRNRATCAATAAGAAACTTTTATATGTATTAAATMAAGGAAAGCCATCTTC      | 300  |
| Oy | 101  | ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle    | 120  |
| Db | 301  | CGGTACAGTGCCACCTGCGCTGTCATATTAACTTAACTCCCTCAACCTCTTAGAAAAATA    | 360  |
| Oy | 121  | AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr    | 140  |
| Db | 361  | GCTATTATAGATTGGTACATTCATTATATCCAGCATCTCAATTATATGACACTATTTTGACA  | 420  |
| Oy | 141  | AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluIuThr     | 160  |
| Db | 421  | NACGTGTGTTATGACAAAGAGATMACCCTCCGATTGGACAAAGAACTAAATACACC        | 480  |
| Oy | 161  | PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu    | 180  |
| Db | 481  | TTCCAGGAANAATATCTTTTGATTCATCTTAATAAAATTTTGCAAGGGAGTTCGTTTA      | 540  |
| Oy | 181  | GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe    | 200  |
| Db | 541  | GAACATTTTACTTCTTCCTTCGGGATCCATGGAATCGGCTCGATTTCACCTCATTTACATTT  | 600  |
| Oy | 201  | AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal    | 220  |
| Db | 601  | GCGTACGTCACAGAGTGTGGAGCTGGGCAATGTCGGCATTTGGAACTATCGAGATT        | 660  |
| Oy | 221  | LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyValLeu    | 240  |
| Db | 661  | CTCCGACGATGGAAGACGATTTTCAGTCATTTCCAGGCTTAAACCTTTGTGGAGCCCTG     | 720  |
| Oy | 241  | IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal    | 260  |
| Db | 721  | ATCCAGTCTGTGAAGAAGCTCTCAGATGTATATGATCTGACTGTGTGTCGTGAGCGTA      | 780  |
| Oy | 261  | PheAlaLeuIleGlyLeuGlnIleuPheMetGlyAsnLeuArgAsnLysValIleLeuTrp   | 280  |
| Db | 781  | TTTTCTCTTAATGGCGTCGACGCTGCATGGGCAACCTAGAAATAAAGTATACAAATGG      | 840  |
| Oy | 281  | ProProThrAsnAlaSerLeuGlnGluHisSerIleGlyAsnIleThrValAsnTyr       | 300  |
| Db | 841  | CTCTCCACACAACTGCTTCTTGAGAGAAACATAGTATGAAAAAATATATACCTGAAATAT    | 900  |
| Oy | 301  | AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp    | 320  |
| Db | 901  | AATGGTACACTTAATAATGAACCTGTCTTGAATTTGACTGGAGACATATATATCAAGAT     | 960  |
| Oy | 321  | SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyLysnSerSer   | 340  |
| Db | 961  | TCAAAGATATCATTAATTTCTCGAGAGGGTTTTTAAGATGACCTACTATGTGAAATATGCTCT | 1020 |
| Oy | 341  | AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr    | 360  |
| Db | 1021 | GATCGAGGCCAAATCTCCAGAGGGATATATGTGTGTAAGACGTGGTATGAAATCTCCAAATAT | 1080 |
| Oy | 361  | GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgMetLthr      | 380  |
| Db | 1081 | GGCTACACAAGCTTTGTATACCTTCAGATGGGCTTTTGTCTCTGTGTTCGACTATATGACT   | 1140 |
| Oy | 381  | GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet    | 400  |
| Db | 1141 | CAGACACTTCGGGAAATCTTTATCAACATGACATTCACGTGCTGGGGAACATGACATATG    | 1200 |
| Oy | 401  | IlePhePheValLeuValIlePheLeuGlySerPheThrLeuIleAsnLeuIleLeuAla    | 420  |
| Db | 1201 | ATATATTTTGTGTGGCATTTCTTGGGCTACTATTTCTACCTAATAAATTTGATCTCGGCT    | 1260 |

|    |      |  |      |
|----|------|--|------|
| Qy | 421  | ValAlaIaMetAlaIaTyrGluGluGluGlnAsnGlnAlaIaThrLeuGluGluAlaGluGlnIys | 440  |
| Db | 1261 | GTGGTGGCCATGGCCATCGAGGAACAGAAACAGGCCACCTTGGAAGAACCAACAGAA          | 1320 |
| Qy | 441  | GluAlaGluPheGlnGlnMetIleGluGlnLeuIleYsGlnGlnGluAlaIaGln            | 460  |
| Db | 1321 | GAGGCCAATTTCCAGCAGATGATTGAACACTTAAAAACACAGAGGCACCTACAG             | 1380 |
| Qy | 461  | AlaAlaThrAlaIaThrAlaSerGlnHisSerArgGluProSerAlaAlaIaIaYrLeuSer     | 480  |
| Db | 1381 | GCACCAACGGCAACTGCCCTCAGAACATTCACAGAGCCCAAGTCAGACAGCAGGCTTCA        | 1440 |
| Qy | 481  | AspSerSerSerGluAlaSerIysLeuSerSerIysSerAlaIysGluArgArgAsnArg       | 500  |
| Db | 1441 | GACAGCTCATCTGMAAGCCCTCAAGTTGAAGTTCACAGACAGTCACAGAAAGAAATCGG        | 1500 |
| Qy | 501  | ArgIysIysArgIysGlnIysGlnIysGlnIysGlnIysGlnIysAlaIysAspGluAspGluPhe | 520  |
| Db | 1501 | AGCAAGAAAGAAACAGAAACAGAACGACTCTGGTGGGAAGAAAGATAGAGGATTAATTC        | 1560 |
| Qy | 521  | GlnIysSerGluSerGluAspSerIleArgArgIysGlnIysPheArgPheSerIleGluIys    | 540  |
| Db | 1561 | CAAAATCTGAATCTGAGGACACACATCAGGAGGAAGTTTCGGCTCTCCATTAAGG            | 1620 |
| Qy | 541  | AsnArgLeuThrIyrGluIysArgIyrSerSerProHisGlnSerLeuSerIleArg          | 560  |
| Db | 1621 | AACCGATTGACATATGMAAGAGATCCTCCCTCCACACACATCTTTGTTGGACATCCGT         | 1680 |
| Qy | 561  | GlySerLeuPheSerProArgArgAsnSerArgIyrSerLeuPheSerPheArgGluArg       | 580  |
| Db | 1681 | GGCTCCCTATTTTCCACAGGCGAAATATGAGAAACAAGCCTTTACGCTTAGAGGGGGA         | 1740 |
| Qy | 581  | AlaIysAspValGlySerGluAsnAspPheAlaAspAspGlnHisSerThrPheGluAsp       | 600  |
| Db | 1741 | GCAAGAGATGGGAGATGTGAGAACGACTTCGCAAGATGAGACACAGCACCTTTAGAT          | 1800 |
| Qy | 601  | AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer       | 620  |
| Db | 1801 | AACGACAGCCGTAGAGATCTCTGTTGTCGCCCGACACGAGACAGACGACAAACAGC           | 1860 |
| Qy | 621  | AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValPheProAlaAsnIys          | 640  |
| Db | 1861 | AACCTGATCTAGACCACTAGATATCCCGGATGCTGGCAGTGTTCACAGATGGAGAG           | 1920 |
| Qy | 641  | MetHisSerThrValAspCysAsnGluValIaSerLeuValGlyIyrProSerValPro        | 660  |
| Db | 1921 | ATGCACAGCACTGGATGTCATGGTGCTGTTCTTGTTGGTGGACCTTCACTTCT              | 1980 |
| Qy | 661  | ThrSerProValGlyLeuLeuLeuProGluValIaIleAspIysProAlaThrAspAsp        | 680  |
| Db | 1981 | ACATCGCCTGTGGACAGCTTCTGCCAGAGGTATATGATTAAGCCACAGCTCATGATAC         | 2040 |
| Qy | 681  | AsnGlyThrThrProGluThrGluMetArgIysArgArgSerSerPheHisIaIaSer         | 700  |
| Db | 2041 | AATGAAACAACTGTAATCTGAAATGAGAAAGAAAGGTCAAGTCTTCCACTCTTCC            | 2100 |
| Qy | 701  | MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu       | 720  |
| Db | 2101 | ATGACATCTTACAGAGATCTCTCCCAAGGCAACGACGACATGATATGCCAGCATTCCTA        | 2160 |
| Qy | 721  | ThrAsnThrValGluGluLeuGluGluSerArgGlnIysCysProProCysIyrTrpIys       | 740  |
| Db | 2161 | ACAATATCACTAGACAGAACTTGAAGAATCCAGGCAAAATATGCCACCCGTTGGATATAA       | 2220 |
| Qy | 741  | PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuIysValHisIaIaIa       | 760  |
| Db | 2221 | TTTTCCAACTATTTCTTAATCTGGAGCTGTCTCCATATGGTTAAAGTGAACATCTT           | 2280 |
| Qy | 761  | ValAsnLeuValIaMetAspProPheValAspLeuAlaIaIeThrIleCysIleValLeu       | 780  |
| Db | 2281 | GTCACACTGGTGTGTGATGAGACCAATTTGTTGACCTGGCATCACCATCTGTATGTCTTA       | 2340 |
| Qy | 781  | AsnThrLeuPheMetAlaMetGlnIaIaIyrProMetThrAspHisPheAsnAsnValLeu      | 800  |

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DB 2341 AATACCTTTTCATGGCCAGGAGCACTATCCATGAGGACCACTTCATTAAGTGGCTT 2400
QY 801 ThrValGlyAsnLeuValPheThrGlyIlePheThrIleGluMetPheLeuValIle 820
DB 2401 ACAGTAGGAAGACCTGGTTTCACCTGGGATCTTACACAGCAAAATCTTCGAAATATAT 2460
QY 821 AlMetAspProTyrTyrTyrPheGlnGluIYrPasnIlePheAspGlyPheIleVal 840
DB 2461 GCCATGATCTTACTTACTTATTTCCAGAAAGCGGAAATATCTTGAAGGTTTATGTCG 2520
QY 841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860
DB 2521 ACCGTTAGCGTAGAACTTGGACCTGCCAATGTGGAAGATATCTGTTCCCTGCTCA 2580
QY 861 PheArgLeuLeuArgValPheValLeuAlaIleValSerTrpProThrLeuAsnMetLeuIle 880
DB 2581 TTTCGATTGCTGCGAGTTTCCAACTGGCAAAATCTTGGCCAAAGCTTAAATATCTATA 2640
QY 881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValIleAlaIleIle 900
DB 2641 AAGATCATGCGCAATTCCTCGGGGCTCTGGAAATTTAACCTCGTCTTGGCCATCTAC 2700
QY 901 ValPheIlePheAlaValAlaGlyMetGlnLeuPheGlyLysSerTyrTyrAspCysVal 920
DB 2701 GTCTTCATTTTGGCGTGGTGGCATGCAAGCTTTGGTAAAGCTTCAAAAGATTGTGTC 2760
QY 921 CysAlaIleAlaSerAspCysGlnLeuProArgTrpIleMetAsnAspPheHisSer 940
DB 2761 TGCAGATGCGCACTGATGTTCACATCCACGCTGGCAGCATGAATGACTTCTCCACATCC 2820
QY 941 PheLeuIleValPheArgValLeuGlyMetCysGlyIleTrpIleGluTrpMetTrpAspCysMet 960
DB 2821 TTCTCGATTGTGTTCGCCGTGCTGTGTGGGAGTGGATGAGACCATGTGGACCTGTG 2880
QY 961 GluValAlaGlyAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980
DB 2881 GAGGTGCTGTGTCAGGCACTGCTTACTTCTTCATGATGTCATGTCATGTCATGGAAC 2940
QY 981 LeuValIleLeuAsnLeuPheLeuAlaLeuLeu**SerSerPheSerAlaAspAsnLeu 1000
DB 2941 CTAGTGGTCCGATCTCTTCTGCGCTTCTGTTGACCTCATTTAGTGCAGACACTT 3000
QY 1001 AlaAlaThrAspAspAspAspGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020
DB 3001 GCACCCACTGATGATGAATGAATGAATATCTCCAAATGCTGTGGAATGAGTGCAC 3060
QY 1021 LysGlyValAlaIleValIleValArgLysIleTyrGluPheIleGlnIleSerPheIleArg 1040
DB 3061 AAAGGAGTAGCTTATGTGAAAGAAATATATGAAATTTATTCACAGCTCTTCTTATGAG 3120
QY 1041 LysGlnLysIleLeuAspGluIleLysPheLeuAspAspLeuAsnAsnLysLysAspSer 1060
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QY 1061 CysMetSerAsnHisThr**GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080
DB 3181 TGTATGTCACATCATACRCAAGAAATGGGAAAGTCTTGTGACTATCTTAAGATGTAAT 3240
QY 1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100
DB 3241 GGAACCTACAGTGGTATGAGAACTGGCAGCTGTGAAAAATACATTTATGATCAAAAGT 3300
QY 1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120
DB 3301 GATTACATGTCATCATCAACCAACCCAGCTCTACTGAGCTGATCAATGCTCTAGAGA 3360
QY 1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGlu 1140
DB 3361 GAATCTGACTTTGAAATTTAAACCGGAAACCTTATGATGAAATCGGACCTGGAAAGA 3420
QY 1141 SerLysGluLysLeuAsnGluSerSerSerSerSerGluLysSerThrValAspIleGly 1160

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DB 3421 ACCAAGAGAACTGAATGAAAGCAGTAGCTCATCAAGAGGTACCTGTGGACATCGCC 3480
QY 1161 AlaProValGluGluGlnProValValGluProGluGluTrpLeuGluProGluAlaCys 1180
DB 3481 GCACCTGTAGAAAGACAGCCCGTAGTGAACCTTAAGAACTCTTGAACCGAAAGCTTGT 3540
QY 1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluArg 1200
DB 3541 TTCATGAGGCTGTGATCAAAAGATCAAGTGTGTCAATCAATCAATGAGGAAGGAGAGA 3600
QY 1201 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAspTrpPhe 1220
DB 3601 GGAAGAAACATGTGTGAACCTGAGAGACGCTTCCGAATGATGGAACATTAAGCTGTT 3660
QY 1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240
DB 3661 GAGACCTTCATTTGTTTCATGATATCTCTTATGATGAGTGTGCTGTGGCATTTGAAGATATA 3720
QY 1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTrpAlaAspLysValPheThr 1260
DB 3721 TATATGATCGAGAAAGACATTAAGCATGTGTGGAATGTGTCACAAAGTTTCACT 3780
QY 1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyIleThrTyrPhe 1280
DB 3781 TACATTTTCATTCGAAATGCTCTTAAATGAGGTGGCATATGCTTCAAAACATATTTTC 3840
QY 1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300
DB 3841 ACCAATGCTGTGTGTGCTGTGACTTCTTAATGTGTGATGTTTATGTGCTGAGTTTACA 3900
QY 1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgTrpLeuArgAla 1320
DB 3901 GCAATGCTGTGTGTGCTGTGACTTCTTAATGTGTGATGTTTATGTGCTGAGTTTACA 3960
QY 1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArg 1334
DB 3961 CTGAGACCTCTTAAGACCTTATCTGATTTGAAGGATGAGG 4002

RESULT 9
ID AAD32839 standard; cDNA: 5997 BP.
AC AAD32839:
DE 01-JUL-2002 (first entry)
DE Human Ion channel cDNA #1.
KW Human; novel human protein; NRP; voltage-gated sodium channel;
KW gene therapy; bioreactor; mental disorder; biological disorder;
KW gene; medical disorder; ss.
OS Homo sapiens.
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FH Key 1..5997 Location/Qualifiers
FT CDS
FT /*tag= a
FT /product= "Human Ion channel protein #1"
FT /transl_except= (pos:2941..2943, aa:xaa)
FT /transl_except= (pos:3166..3168, aa:xaa)
FT /note= "Xaa - any amino acid"
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XX WO200214498-A2.
XX 21-FEB-2002.
XX 15-AUG-2001; 2001WO-US25650.
XX 16-AUG-2000; 2000US-225989P.
XX (LEXI-) LEXICON GENETICS INC.
XX PA
XX Turner CA, Mathur B, Mathur D;
PI

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Db 5788 AGTACAAATAAACAAATCAAGGTGGCTTAATCTTATTAAGACATGATA 5847  
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 Db 5848 ATTGACAGATATTAATGAAACTATATACAGAAAAAAGCTGACCTGCTCACTGCA 5907  
 QY 1981 AAlAcYpProSeTyrNspARyVALThrLysPProIleValGluLysHISgluIngu 2000  
 Db 5908 GCTTGCCACCTTCTATGACCGGGTGACAAAGCCAAATTGTGAAAAACATGAGCAAGA 5967  
 QY 2001 GIYLYSASPGLULYALALysGLYLYS 2009  
 Db 5968 GGCAGAGATGAAAAAGCCAAAGGAAA 5994

RESULT 10  
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 ID AAD32840 standard; cDNA; 5889 BP.  
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 AC AAD32840;  
 XX 01-JUL-2002 (first entry)  
 DE Human ion channel cDNA #2.  
 XX Human; novel human protein; NHP; voltage-gated sodium channel;  
 KN gene therapy; bio reactor; mental disorder; biological disorder;  
 KW gene; medical disorder; ss.  
 XX Homo sapiens.  
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 FH Location/Qualifiers  
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 FT CDS  
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 FT /product= "Human ion channel protein #2"  
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 FT /transl\_except= (pos:3165..3168, aa:xaa)  
 FT /note= "Xaa = any amino acid"  
 XX PN WO200214498-A2.  
 XX 21-FEB-2002.  
 PD 15-AUG-2001; 2001WO-US25650.  
 PF 16-AUG-2000; 2000US-225989P.  
 XX (LEXI-) LEXICON GENETICS INC.  
 PA Turner CA, Mathur B, Mathur D;  
 PI WPI: 2002-280757/32.  
 XX P-PSDB; AAE20511.  
 DR Novel polynucleotides encoding human sodium channel proteins,  
 PT particularly voltage-gated sodium channel proteins useful for drug  
 screening, diagnosis and in gene therapy of biological disorders -  
 XX Claim 1; Page 35-36; 83pp; English.

CC delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion  
 CC protein to the body. Nucleotide construct encoding NHP products are  
 CC also useful in gene therapy for modulating NHP expression and to  
 CC produce genetically engineered host cells to express NHP products in  
 CC vivo. NHP nucleotide sequences may also be used as part of ribozyme  
 CC and/or triple helix sequences that are useful for NHP gene regulation.  
 CC The NHP polypeptide sequences are useful for generating antibodies, as  
 CC reagents in diagnostic assays, for identifying other cellular gene  
 CC products related to NHP and as reagents in assays for screening for  
 CC compounds that are useful in the treatment of mental, biological or  
 CC medical disorders and diseases.

XX SQ Sequence 5889 BP; 1733 A; 1161 C; 1313 G; 1679 T; 3 other;  
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 Alignment Scores:  
 Pred. No.: 0 Length: 5889  
 Score: 1289.00 Matches: 1955  
 Percent Similarity: 99.14% Conservative: 0  
 Best Local Similarity: 99.14% Mismatches: 17  
 Query Match: 64.16% Indels: 17  
 Db: 24 Gaps: 0

US-09-930-871-12 (1-2009) x AAD32840 (1-5889)  
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 QY 21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAnProLysProAsp 40  
 Db 61 TCTCTTGGCGCTATGAAAGACGATGCGAAGAAAGCAAGAAATCCCAACCGACAG 120  
 QY 41 LysLysAspAspAspGluSngLysGlyProLysProAsnSerAspLeuLysGluLysAsn 60  
 Db 121 AAAAAGATGACAGCAAAATGCCCCAAGCCAAATAGACTGTGAAGCTGGAAGAAC 180  
 QY 61 LeuProPheIleTyrGlyLysPheProGluMetValSerGluProLeuGluAspLeu 80  
 Db 181 CTTCATTTATTTATGAGAGCATCTCCAGAGATGTTGTCAGAGGCCCTCGAGGACCTG 240  
 QY 81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100  
 Db 241 GACCCCTACTATATCAATTAAGAAACCTTATAGTATTAAGTAAGGAGGACATCTTC 300  
 QY 101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120  
 Db 301 CGGTTAGTGCCACCTGCGCCCTGATCAATTTAACTCCCTCAATCTCTTGAAGAAATA 360  
 QY 121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140  
 Db 361 GCTATTAAAGTTTGGTACATTCATTTATTCAGATCTCTAATTTATGCGACTATTGGA 420  
 QY 141 AsnCysValPheMetThrMetSerAsnProProAspTyrThrLysAsnValGluTyrThr 160  
 Db 421 AACTGTGTGTTATGACAAATGAGTAACTCCGATTGGCAAGAAATGTAAGATACACC 480  
 QY 161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180  
 Db 481 TTCACAGGAATATATCTTTGAAATCACTATTAATAAATTAATTCAGAGGGAATCTGTTA 540  
 QY 181 GluAspPheThrPheLeuArgAspProTyrAsnTyrLeuAspPheThrValIleThrPhe 200  
 Db 541 GAAGATTTTACTTCTCGGATTCATGCAATGGAATGCGCTGATTCATGCAATTAATTT 600  
 QY 201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220  
 Db 601 GCCTAGCTACAGAGTTTGGACCTGGGCAATGCTCGGCAATGAGAAACATTCAGAGTT 660  
 QY 221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240  
 Db 661 CTCGAGCATTAAGAGCATTTAGTCATTCAGGCTGAAACCAATGTGGAGGACCTG 720  
 QY 241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260

Db 721 ATCCAGCTGTCGAGCAAGCTCTCAGATGATATGATCCGACTGCTGTCTGACGCTA 780  
 Qy 261 PheAlaIeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280  
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 Db 841 CCTCCACCAATGCTCTCTGGAGAACATATATGAAAAAGATATTAACCTGTAATATAT 900  
 Qy 301 AsnGlyThrIleuIleAsnGlnThrValPheGlnPheAspTrpLysSerTrpIleGlnAsp 320  
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 Qy 341 AspAlaGlyGlnCysProGlnGlyTyrMetCysValLysAlaGlyArgAsnProAsnTrp 360  
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 Qy 401 IlePhePheValLeuValIlePheLeuGlySerPheTrpLeuIleAsnLeuIleLeuAla 420  
 Db 1201 ATATTTTGTGTGGTCATTTCTTGGCTCATCTCAATTAATTTGATCTGCT 1260  
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 Db 1381 GCAGCAAGCGCACTGCTCAGAACATTCAGAGAGCCAGTGCAGAGGAGGCTCTCA 1440  
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 Db 1441 GACAGCTCATCTGAAGCTCTTAAGTTAGTTCCAAAGCTGCTTAAGAAAGAAATCGG 1500  
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 Qy 561 GlySerLeuPheSerProArgArgAsnSerArgTrpHisSerLeuPheSerPheArgGlyArg 580  
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Db 1801 AACGAGAGCGGTAGAGATTCCTTGTGTGTGCCCCGAGACACAGGAGAGACGCAACAGC 1860  
 Qy 621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValPheProAlaAsnGlyLys 640  
 Db 1861 AACTGATGTCAGACAGATAGATCATCCCGGATGCTGGCAGGTGTCCAGCAATGGGAAAG 1920  
 Qy 641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660  
 Db 1921 ATGCACAGCACTGTGATGTCAATGGTGTGTTCTTGTGTGTGGTGGACCTTCAGTTCT 1980  
 Qy 661 ThrSerProValGlyGlnLeuLeuProGlnValIleIleAspLysProAlaThrAspAsp 680  
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|||||
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Db 5788 ACCTACATATAAACAATAATCAAAAGGTGGGCTTAATCTTCTTATATAAGAGACATGATA 5847
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RESULT 11
ABL39689
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AC
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XX 10-MAY-2002 (first entry)
DE Human sodium channel SCN1A encoding cDNA SEQ ID NO.1.
XX
XX Human sodium channel; SCN1A; chromosome 2q24; gene: ss;
KM familial hypercalcaemic periodic paralysis; motor endplate disease.
XX
OS Homo sapiens.
FH
FH Key Location/Qualifiers
FT CDS 15..6018
FT /tag= a
FT

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FT /product= "sodium channel SCN1A"
PN WO200196552-A1.
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XX 20-DEC-2001.
PD
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XX 12-JUN-2001; 2001WO-JP04956.
PF
XX 13-JUN-2000; 2000JP-0177540.
PR 13-JUN-2000; 2000JP-0177544.
XX
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX Kanazawa I, Goto J, Jeong S;
XX WPI; 2002-098066/13.
DR P-PDB; ABB06026.
XX
PT Human sodium channels SCN1A and SCN3A and encoded genes, useful in
PT studying physiological mechanism in which excitant cells participate
PT and causes of diseases and developing drugs for motor endplate disease
PT
XX
XX Claim 5; Page 20-40; 88pp; Japanese.
XX
XX The present invention describes human sodium channels SCN1A and SCN3A.
XX The present sequence encodes the human sodium channel SCN1A. SCN1A and
XX SCN3A have been located to the human chromosome 2 long arm, positions
XX 2q24 and 2q24-31 respectively. The sodium channel proteins are useful
XX in studying the physiological mechanism in which excitant cells
XX participate and cause human diseases, and in developing remedies for
XX e.g. familial hypercalcaemic periodic paralysis of extremities and
XX motor endplate disease.
XX
SO Sequence 8131 BP; 2453 A; 1530 C; 1719 G; 2422 T; 7 other;
Alignment Scores:
Pred. No.: 0 Length: 8131
Score: 947.00 Matches: 1988
Percent Similarity: 98.61% Conservative: 0
Best Local Similarity: 98.61% Mismatches: 21
Query Match: 47.14% Indels: 28
DB: 24 Gaps: 0
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Db 79 TCTCTTGGCGCTTGTGAACAGCCATTGCGAAGAAAGCAAGATCCCAACCAAGAC 138
QY 41 LysLysAspAspAspGluAsnGlyProIysProAsnSerAspLeuGluAlaGlyLysAsn 60
Db 139 AAAAAGATGACGACGAAATGCGCCAAAGCCAAATAGTACTGGAAGCTGGAAGAAAC 198
QY 61 LeuProPheIleTrpGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
Db 199 CTTCATTTATTTATGAGACATCTCTCCAGAGATGGTGTCAAGACCCCTGGAGGACCTG 258
QY 81 AspProTyrTrpIleAsnIysLysTrpPheIleValLeuAsnIysGlyLysAlaIlePhe 100
Db 259 GACCCCTACTATATCAATAAGAACTTTATGATGTGATATAAGAGAGGACCATCTTC 318
QY 101 ArgPheSerAlaThrSerAlaLeuTrpIleLeuThrProPheAsnProLeuArgLysIle 120
Db 319 CGGCTCAGTCCACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 378
QY 121 AlaIleLysIleLeuValIleSerLeuPheSerMetLeuIleMetGlyThrIleLeuThr 140
Db 379 GCTATTAGATTTTGTGTACTTCTATTATTCAGCATCTCAATTATGTGCACTATTGTGACA 438

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QY 161 PheThrGlyLeuThrPheGluSerLeuLeuLeuLeuLeuLeuLeuLeuLeu 180  
DB 499 TTCACAGAAATATATCTTTGAAATCACTTATAAAAATATGCAAGGAGATCTGTTA 558  
QY 181 GluAspPheThrPheLeuArgAspProThrAsnThrLeuAspPheThrValIleThrPhe 200  
DB 559 GAAGTTTACTCTTCCTGAGATCCATGAACTGCTGATTCATGCTCATTTCAATT 618  
QY 201 AlaThrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220  
DB 619 GCGATGTCACAGAGTTTGTGACCTGGCAATGCTCGGCAATGAGAAATTCAGAGTT 678  
QY 221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValAlaLeu 240  
DB 679 CTCGAGCATGGAAGACGATTCAGTTCAGGCTGAAACCATTCGTGGAGCCCTG 738  
QY 241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValIlePheCysLeuSerVal 260  
DB 739 ATCCAGTCTGGAAGAACCTCCAGATGATATGATCCGATGCTGTCTGTGAGCGTA 798  
QY 261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnThr 280  
DB 799 TTGCTCTAAATTTGGCTGACGCTGCTCATGGGCAACCTGAGAAATATGTTACAAATG 858  
QY 281 ProProThrAsnAlaSerLeuGluGluIleHisSerIleGluLysAsnIleThrValAsnThr 300  
DB 859 CCTCCACCAATGCTTCTCTGAGAGACATAGTATAGAAATATACCTGTAATAT 918  
QY 301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspThrPheLysSerThrIleGlnAsp 320  
DB 919 AATGTTACACTATATAAAGAACTGCTTGTGATGCTGAGAACTCATATATTTCAAGAT 978  
QY 321 SerArgThrIleSerPheLeuGluGluPheLeuAspAlaLeuLysCysGlyAsnSerSer 340  
DB 979 TCAGATATCATATATTTCTGAGGAGTTTATGATGCTCATATGAGAAATATGCTCT 1038  
QY 341 AspAlaGlyGlnCysProGluGluLysMetCysValLysAlaGlyLysAsnProAsnThr 360  
DB 1039 GATGAGGCAATGTCAGAGGATATATGCTGAAAGCTGATGAAATATCCCAATAT 1098  
QY 361 GlyThrSerPheAspThrPheSerThrAlaPheLeuSerLeuPheArgLeuMetThr 380  
DB 1099 GGCCTACACAAGCTTGATACCTTCAGTTGGCTTCTGCTGCTGCTGCTGCTGCT 1158  
QY 381 GlnAspPheThrGluAsnLeuThrGlnLeuThrLeuArgAlaAlaGlyLysThrIleMet 400  
DB 1159 CAGGACTCTGGGAAATCTTATATCACTGACATTAAGCTGCTGCTGCTGCTGCTGCT 1218  
QY 401 IlePhePheValLeuValIlePheLeuGlySerPheThrLeuIleAsnLeuIleLeuAla 420  
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QY 421 ValValAlaMetAlaThrGluGluGlnAsnGlnAlaThrLeuGluGluValGluGlnLys 440  
DB 1279 GGGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1338  
QY 441 GlnAlaGluPheGlnGluMetIleGluGlnLeuLysGlyGlnGluAlaAlaGlnGln 460  
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QY 461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480  
DB 1399 GAGAGCAAGGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1458  
QY 481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500  
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QY 501 ArgLysLysValArgGluGlnLysGluLysSerGlyGlyGluGluLysValAspGluPhe 520  
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QY 561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580  
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DB 1759 GCAAGAGATGAGGATCTGAGAAAGCTTCCGATATGATGAGACACAGCACTTTGAGAT 1818  
QY 601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyLysArgArgAsnSer 620  
DB 1819 AACGAGAGCGTGAAGATTTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1878  
QY 621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValPheProAlaAsnGlyLys 640  
DB 1879 AACCTGAGTACAGACAGTATGATCCGAGATCCGAGATGCTGCTGCTGCTGCTGCTGCT 1938  
QY 641 MetHisSerThrValAspCysAsnGlyValValIleSerLeuValGlyGlyProSerValPro 660  
DB 1939 ATGCACAGACAGTGTGATGCAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1998  
QY 661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680  
DB 1999 ACATGCGCTGTG--G--A--C--A--G--C--T--C--T--G--C--C--A--G-- 2026  
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QY 701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720  
DB 2086 ATGGAATCTTCTGAAAGATCTTCCAAAGGCAACAGCAATGATATCCAGCTTCTTA 2145  
QY 721 ThrAsnThrValGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 740  
DB 2146 ACATAATACGTAAGAACTTGAAGATCCAGGCAAGAAATGAGCAAGTCTTCCACGCTTCC 2205  
QY 741 PheSerAsnIlePheLeuIleThrAspCysSerProThrPheLysValLysHisVal 760  
DB 2206 TTTTCAACATATTT--CTCAATCTGGAGCTGCTCATATGCTGTTAAAGTGAACATCT 2264  
QY 760 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLe 780  
DB 2265 TGTCAACCTGCTGCTGATGAGCCATTTGTAACCTGCGCACACCATGTAATGCTCT 2324  
QY 780 AsnThrLeuPheMetAlaMetGluHisThrProMetThrAspHisPheAsnAsnValLe 800  
DB 2325 AATATCTTTTCAATGCGCATGAGGACATGATCATGAGGACATTTAAATATGCTGCT 2384  
QY 800 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820  
DB 2385 TACAGTAGAAGAACTGCTTTCACGAGATCTTACAGCAAGAAATGCTTCTGAAATATAT 2444  
QY 820 eAlaMetAspProThrThrThrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840  
DB 2445 TGGCATGAGATCTTATATATTTTCCAAAGGCTGGAATATCTTGAAGGCTTTATTTCT 2504  
QY 840 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860  
DB 2505 GACGCTTACCTGAGTGAAGCTTGAAGTCCGCAATGAGGATTTATCTGCTTCTCCGCTTC 2564  
QY 860 rPheArgLeuLeuArgValPheLysLeuAlaLysSerThrProThrLeuAsnMetLeuIle 880



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DB 2565 ATTTCGATTCCTCGAGATTTCAGTTGGCAAAATCTGGCCAACTTAATATGCTAAAT 2624
QY 880 elvsllellellyasnserfalgialaleuglyasnleuthrleuvalleualllel 900
DB 2625 AAAGATCATCGCAATTCCTGGGGGCTCGGAAATTAACCTCTCTGGGCATCAT 2684
QY 900 eValpheilephealavalaleuglymetglnleupheglylysertylsapcysva 920
DB 2685 CGCTTCATTTTGGCGGTGGGAGCATGAGCTCTTGGTAAAGCATCAAAAGATGTGT 2744
QY 920 lcyglylialasertapcysglnleupro---ArgTPHlsmetasnapphephei 939
DB 2745 CTCGAGATGCGCAGTATGTGTAACCTCCACACAGCTGGCAGATGATGATCTCTCCA 2804
QY 939 sserpheleullevalpheargvalleucysglylultrpilleglnlthmetrparpcy 959
DB 2805 CTCCTTCCTATGTTGTGTCGGGCTGTGTGGGAGTGAATGAGACCATGTGGGACTG 2864
QY 959 smetgluvalalaglyglnalamecysleuthrvalphemetmetvalmetalllegl 979
DB 2865 TATGGAGTGTCTGTGTAAACCATGTGCTTACTGTCTTATGATGTGTCATGGTGAATGG 2924
QY 979 yasnleuvalalleuasnleupheleualaleu---SerSerPheSerAlaAspa 999
DB 2925 AAACCTAGTGTGCTGTAATCTCTTCTGCGCTTCTCT- GAGCTCATTTAGTCAGACA 2983
QY 999 snleuualalatrparaspaspasnleumetasnleuglnillealvalaspargm 1019
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DB 3044 TGCACAAAGAGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 3103
QY 1039 learglysglnlyslleuasnplulleysproleuasppheuasnleuylsya 1059
DB 3104 TTAGGAAACAAAGATTTTGTATGATGATGATGATGATGATGATGATGATGATGATGATG 3163
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DB 3343 GTAGGAGAACTGACTTTGAAAATTTTAACACGAGAACCTTTAGTATGATGATGATGATG 3402
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QY 1198 uclayarglylyeglultrprrasnleuargarthrCysPhearglilevalgluHlSAs 1218
DB 3582 AGGCAGAGGAAACAAAGCTGTGAACTGTGAAAGAGAGCTGTTCCGAATATTTGAACCTAA 3641
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DB 3642 CTGGTTGAGACCTTCATTTTCATGATTCCTTAGTAGTGGTCTGGCATTTGA 3701
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DB 3762 TTTCACCTACATTTTCATTTTCGAAATGCTTCRAAATGGGTGGCAGATATGATCAAC 3821
QY 1278 rlyrPheThrAsnAlatrPcystrrpleuasppheleullevalaspyalserleuylse 1298
DB 3822 ATATTCACCAAGAGCCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 3881
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QY 1338 nalaleuLeuglyAlalatrProserlilemetasnvalleuvalcysleullepethr 1358
DB 4002 TGCCCTTTAGGAGCAATTCATCCATCATGAAATGTCTGTGTGTGTGTGTGTGTGTGTGT 4061
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DB 4242 AGGATTTGGGTATCTCTCTTCTTCAAGTTCACACTTTCAAAGATGATGATGATGATGAT 4301
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DB 4302 GTRAGCAGAGCTGATTCAGAAATGTGGAATCCAGCAATGATGATGATGATGATGATGAT 4361
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QY 1478 eilleglyvalilleleasppasnpheasnnglnlysllysllyPhegllyglina 1498
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QY 1558 tMetvalglulthrAspaspInserglultryfvalalthrThrilleuSerarglileasne 1578
DB 4662 GATGTGTGAAACAGATGACAGAGTGAATATGTGACTACATTTTGTGACGCTCAATCT 4721
QY 1578 uvalPheillevalleuPheThrGlyglucysvalleuyllyleuulleSerleuarghlystry 1598
DB 4722 GGTGTATGTGTGTATTTACTGAGAGTGTGTAAGTCACTCAAACTCATCTCTACGCCATTA 4781

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|    |      |   |      |
|----|------|---|------|
| QY | 1598 | RTYRPHETHTLIEGLYTPRASNILPEHASPHEVAIVALLIEUSERTIEVAGI            | 1618 |
| Db | 4782 | TTATATTTACCATGGATGAGAAATATTTTGATTTGTGGTGTGCATCTCTCCATGTGAGG     | 4841 |
| QY | 1618 | YMETPHEVALAAGLIEULIEGLIUDYSTYRZHEVALSERPROTHIRPEUPHEATGVALI     | 1638 |
| Db | 4842 | TATGTTCTTGCCGACACTATAGAAAAGATTTGGTGTGCCCTACCGCTTCCGAGGAT        | 4901 |
| QY | 1638 | EATGLEUALAATGILEGIYARGTIELEUARGLEULIELYSGIYALAIYSGIYIIEARGTH    | 1658 |
| Db | 4902 | CCGCTCTTGCTAGAGATTGGCCGGAATCCAGTCTGTGATCAAGAGACAAAGGGGATCCGCAC  | 4961 |
| QY | 1658 | RIEULIEUPHALALEUMETSERLEUPROBLALEUPHASNILIEGIYLEULIEULIUPH      | 1678 |
| Db | 4962 | GGTGGCTTGGTTGATATGATGTCCTTCGCGTGGTTGTTAAACATCGGCCCTCCATCTCT     | 5021 |
| QY | 1678 | ELEUVALMETPHEIETRYALAILPEHEGLYMETSERANPHEALTRYALVLYSARGI        | 1698 |
| Db | 5022 | CCATGTCATGTTATCTAGCCATCTTGGAGATGTCCAACTTGGCTATGTATAAGAGGA       | 5081 |
| QY | 1698 | UVALGIYIEASPASPMEPEHASNHEGLIUNRPEHEGLYASNSERMETILECYSLEUPH      | 1718 |
| Db | 5082 | AGTTGGGATCGAGACATGTGTCACATTGTGAGACCTTTGGCAACAGCATGCTCGTAT       | 5141 |
| QY | 1718 | EGLNILEHTHTHSERIAGLYTPRASPGLYLEULUALAPROILEUASNSELYSPR          | 1738 |
| Db | 5142 | CCAAATTTACAACCTCTGCTGGCGTGGAGATTGGTACACCCCATTCCTCAACAGATAAGCC   | 5201 |
| QY | 1738 | OPROASPCCYASPRIOASNLYVALASNPROLYSERVALYLYSGIYASPCYSGIYAS        | 1758 |
| Db | 5202 | ACCCGATGTGACCCCTPATTAAGTTAACCTGTGAAGCTCAGTTAAGGAGACTGTGGGAA     | 5261 |
| QY | 1758 | NPROSEVALIGIYLPEPHEPHEVALSERTRYILLEIIELESERPEHEUALVALVA         | 1778 |
| Db | 5262 | CCCATCTGTTGGAAATTTCTTTTGTCTAGTTACATCATCATCATCTCTCGGTGTGTGGCT    | 5321 |
| QY | 1778 | IASNMETTRYTIALAVALILEUENGLUASNBPHESEVALAATHRGIUGIUNSERIAGI      | 1798 |
| Db | 5322 | GAACATGTACATCGCGGTCTCCTGTGAGAACTTCAGTGTGCTACTGTAAGAAAGTGGCAGA   | 5381 |
| QY | 1798 | UPROLESERCIUNASPSPHEGLIUNETHETRYGIUVALTPROGLYSPHEASPROAS        | 1818 |
| Db | 5382 | GCCCTGAGAGAGATGACTTGTAGATGTTCTATGAGGTTGGGAGAAAGTTGATCCCGA       | 5441 |
| QY | 1818 | PALATHGILPHMEHGLIUPHEGLIYUSLEUSERGINPHEALIAALAIENGLIUPROPR      | 1838 |
| Db | 5442 | TGCACATCAATTCATGGAATTTGAAAAATTAATCTCAAGTTGCAAGCTGGCGCTTGAACGCC  | 5501 |
| QY | 1838 | OLEUASNLEUPROGLINPROASNLYSLEUNILEUULEALAMETASPLEUPROMETVALSE    | 1858 |
| Db | 5502 | TCTCAATCTGCCCAACAACCAACCAACTCCAGCTCATGTCGATGAGTTGGCCCATGTTGAG   | 5561 |
| QY | 1858 | RGLYASPARGLIEHISCYSLEUASPILLEUPHEALAPHEHTRYLSARGVALLIEUGLYI     | 1878 |
| Db | 5562 | TGGTGACCGGATCCACTGTCCTTATATCTTATTTGGCTTTTACAAAGCCGGGTTCTAGAGAGA | 5621 |
| QY | 1878 | USERCILYGLIMETASPALALEUARGIIEGLINMETGIUGIUNARGPHEMETALASERASPR  | 1898 |
| Db | 5622 | GAGTGGAGAAATGAGATGCTCTTCAGAAATACAGATGAGAAAGGCAATTCAGGCTTCCAAACC | 5681 |
| QY | 1898 | OSERLYVALSERTRYGLINPROLIEHTHTHTRILEUYSATGLYSGINGLIUNGLIVALSE    | 1918 |
| Db | 5682 | TTTCCAAAGTCTCCTATACGCAATCTACTACTTTTAAACGAAAAACAAGAGAAATGTC      | 5741 |
| QY | 1918 | FALAVALLIEGLEINARGIATRYARGTHGISLEULEUYSARGTHVALYSGINAL          | 1938 |
| Db | 5742 | TGCTGTATATTACAGGCTCTTACAGAGCCACCTTTAAAGCAACTGTAAAAACAAGC        | 5801 |
| QY | 1938 | ASERPHETHTTRYASNLYSASNLYSILEYSGIYGIYALASNLEULEULIELYSGIUNAS     | 1958 |
| Db | 5802 | TTTCCTTAGCTACATATTAACAAATCAAAAGGTGGGCTATCTCTTATTAATAAGAGA       | 5861 |

|           |  |  |      |
|-----------|--|--|------|
| Oy        | 1958   | pmetlleleaspargileangluanserl ethergiulystrhaplethrmetse         | 1978 |
| Dd        | 5862   | CATGTAATTTCAGACAAATAAATGAAAACTCATTACAGAAAAAAACTGATCGACATGTC      | 5921 |
| Oy        | 1978   | ITThralaaIacyspproserferyasparyalThrlyspProilevalGIuLySHIsGI     | 1998 |
| Dd        | 5922   | CACGCACACTGTGTCCACCTTCTCTATGACC GG GTGACAAAGCCAATTTGGAAAAAACATGA | 5981 |
| Oy        | 1998   | ugIngluGIuLySaspGIuLySaLaLyGIuLyLS                               | 2009 |
| Dd        | 5982   | GCAAGAGGCCAAAGATGAAAAAGCCAAAGGGAAA                               | 6015 |
| RESULT 12 |  |  |      |
| AAD32841  |  |  |      |
| ID        | AAD32841   | standard; cDNA; 4329 BP.   |      |
| XX        |  |  |      |
| AC        | AAD32841;  |  |      |
| DE        |  |  |      |
| XX        | 01-JUL-2002  | (first entry)  |      |
| XX        |  |  |      |
| DE        |  | Human Ion channel cDNA #3.                                       |      |
| XX        |  |  |      |
| KW        |  | Human; novel human protein; NHP; voltage-gated sodium channel;   |      |
| KW        |  | gene therapy; bioreactor; mental disorder; biological disorder;  |      |
| KX        |  | gene; medical disorder; ss.                                      |      |
| XX        |  |  |      |
| OS        |  | Homo sapiens.  |      |
| XX        |  |  |      |
| FH        |  |  |      |
| FT        | Key  | Location/Qualifiers  |      |
| FT        | CDS  | 1..4329  |      |
| FT        |  | /tag= a  |      |
| FT        |  | /product= "Human Ion channel protein #3"                         |      |
| FT        |  | /transl_except= (pos:2941..2943, aa:Xaa)                         |      |
| FT        |  | /transl_except= (pos:3165..3168, aa:Xaa)                         |      |
| FT        |  | /note= "Xaa = any amino acid"                                    |      |
| XX        |  |  |      |
| PN        | WO200214498-A2.  |  |      |
| PD        | 21-FEB-2002.   |  |      |
| XX        |  |  |      |
| PF        | 15-AUG-2001; 2001WO-US2650.  |  |      |
| XX        |  |  |      |
| PR        | 16-AUG-2000; 2000US-225989P.   |  |      |
| PA        | (LEXI-) LEXICON GENETICS INC.  |  |      |
| PI        | Turner CA, Mathur B, Mathur D;   |  |      |
| XX        |  |  |      |
| DR        | WPI: 2002-280757/32.   |  |      |
| DR        | P-PsDB; AAE20512.  |  |      |
| PT        |  |  |      |
| PT        |  |  |      |
| PS        |  |  |      |
| XX        | Claim 1; Page 41-42; 83pp; English.                                      |  |      |
| XX        |  |  |      |
| CC        | The present sequence is a cDNA encoding novel human protein (NHP), ion   |  |      |
| CC        | channel protein. NHP share structural similarity with mammalian sodium   |  |      |
| CC        | channel proteins particularly voltage-gated sodium channel proteins.     |  |      |
| CC        | NHP oligonucleotides are useful as hybridisation probes for screening    |  |      |
| CC        | libraries and assessing gene expression patterns. Sequences derived      |  |      |
| CC        | from regions adjacent to the intron/exon boundaries of NHP gene can be   |  |      |
| CC        | used to design primers for use in amplification assays to detect         |  |      |
| CC        | mutations within the exons, splice sites, introns that can be used in    |  |      |
| CC        | diagnostics and pharmacogenomics. NHP nucleotide sequences are useful    |  |      |
| CC        | for drug screening effective of perturbing the normal function of NHP in |  |      |
| CC        | phenotypic manifestations of perturbing the normal function of NHP in    |  |      |
| CC        | the body, and nucleotide constructs encoding NHP products are useful to  |  |      |
| CC        | genetically engineer host cells to express NHP products in vivo. These   |  |      |
| CC        | genetically engineered cells function as bioreactors in the body         |  |      |
| CC        | delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion  |  |      |
| CC        | protein to the body. Nucleotide construct encoding NHP products are      |  |      |

CC also useful in gene therapy for modulating NHP expression and to  
 CC produce genetically engineered host cells to express NHP products in  
 CC vivo. NHP nucleotide sequences may also be used as part of ribozyme  
 CC and/or triple helix sequences that are useful for NHP gene regulation.  
 CC The NHP polypeptides are useful for generating antibodies, as  
 CC reagents in diagnostic assays, for identifying other cellular gene  
 CC products related to NHP and as reagents in assays for screening for  
 CC compounds that are useful in the treatment of mental, biological or  
 CC medical disorders and diseases.

XX Sequence 4329 BP; 1287 A; 840 C; 988 G; 1211 T; 3 other;

# Alignment Scores:

| Pred. No.:             | 0      | Length:       | 4329 |
|------------------------|--------|---------------|------|
| Score:                 | 763.00 | Matches:      | 1429 |
| Percent Similarity:    | 96.82% | Conservative: | 0    |
| Best Local Similarity: | 96.82% | Mismatches:   | 17   |
| Query Match:           | 37.98% | Indels:       | 17   |
| DB:                    | 24     | Gaps:         | 0    |

US-09-930-871-12 (1-2009) x AAD32841 (1-4329)

QY 1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhenThrArgGlu 20  
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 QY 21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40  
 DB 61 TCTCTTGGCGGTATTTGAAAGACCATTCGAGAAAGCAAGAAATCCCAACAGAC 120  
 QY 41 LysLysAspAspAspGlnGlnGlyProLysProAsnSerAspLeuAlaGlyLysAsn 60  
 DB 121 AAAAAAGATGACAGCAAAAATGGCCAAAGCCAAATAGTACTTGGAAAGTGAAGAAC 180  
 QY 61 LeuProPheIleTyrGlyAspIleProGluMetValSerGluProLeuGluAsnLeu 80  
 DB 181 CTTCATTTATTTATGAGAGCATCTCTCCAGAGATGCTGTCAGAGCCCTCGAGAGACTG 240  
 QY 81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100  
 DB 241 GACCCCTACTATATCAATTAAGAAACTTTATAGTATTCGAAATGAAGGACCATCTTC 300  
 QY 101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120  
 DB 301 CGGTTAGTGCACCTCTGCTGACATTTAACTCCCTCAATCCTCTTACGAAATAA 360  
 QY 121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140  
 DB 361 GCATTAAGATTTTGGTACATTCATTTATTCAGACATGCTAATTTATGACACTATTTGACA 420  
 QY 141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160  
 DB 421 AACTGTGTGTTTATGACAAATGAGTAACCTCCGATTGGACAAAGATGAAATACAC 480  
 QY 161 PheThrGlyIleTyrThrPheGluSerIleLysIleIleLeuArgGlyPheCysLeu 180  
 DB 481 TTCACAGGATATATACCTTTGATATCTTAATAAAATTAATGCAAGGAGATCTGTTA 540  
 QY 181 GluAspPheThrPheLeuArgAspProTyrPasnTrpLeuAspPheThrValIleThrPhe 200  
 DB 541 GAAGATTTTACTTCTCTGGGATCCATGGAAGTGGCTGATTTTCACTGATTAATTT 600  
 QY 201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220  
 DB 601 GGTGAGTACAGAGATTTGTGACCTGGCAATGCTCGGCATTTGAGAACATTCAGAGTT 660  
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 DB 661 CTCGAGACATGGAAGAGATTCAGTCAATTCAGGCTGAAACCAATTTGGAGAGCCCTG 720  
 QY 241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260  
 DB 721 ATCCATCTGTGTAAGAGCTCTCAGATGTAATATCTCTGACTGTGTCTGTGACGCTA 780

QY 261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280  
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 QY 381 GlnAspPheTrpGlnAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400  
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 QY 421 ValValAlaMetAlaTyrGluGlnGluGlnAsnGlnAlaThrLeuGlnGluAlaGlnLys 440  
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 DB 1621 AACCATGACATATGAAAGAGATCTCTCCACACAGCTTTGTTGACATCCCT 1680  
 QY 561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheArgGlyArg 580  
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 QY 601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620  
 DB 1801 AACGAGCGGTAGAGATTCCTTGTGTTGCTCCCGACGACAGGAGAGAGAGAGCAACAGC 1860

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661 ThrSerProValGlyIleLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680  
1981 ACATGCGCTGTGG--G--A--C--A--G--C--T--T--C--T--G--C--C--A--G--G-- 2008  
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2188 TTTTCCAAATATCTTAAATGCGGACCTGCTCCATATGTTGTTAAATGAAACATGAT 2247  
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2548 TTTGCAATGCTGCGAGTTTCAAGTGGCAAAATCTTGGCCAAAGTAAATATGCTAAATA 2607  
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 Db 4288 GCAGTGTATTCAGAAAT 4305  
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 AC AAD32842;  
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 DT 01-JUL-2002 (first entry)  
 XX  
 DE Human ion channel cDNA #4.  
 XX  
 KW Human; novel human protein; NHP; voltage-gated sodium channel;  
 KM gene therapy; bioreactor; mental disorder; biological disorder;  
 KW gene; medical disorder; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
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 FT /product- "Human ion channel protein #4"  
 FT /transl\_except- (pos:2941..2943, aa:xa)aa  
 FT /transl\_except- (pos:3166..3168, aa:xa)aa  
 FT /note- "Xaa - any amino acid"  
 XX  
 PN MO200214498-A2.  
 XX  
 PD 21-FEB-2002.  
 XX  
 PF 15-AUG-2001; 2001MO-US25650.  
 XX  
 PR 16-AUG-2000; 2000US-225989P.  
 XX  
 PA (LEXI-) LEXICON GENETICS INC.  
 XX  
 PI Turner CA, Mathur B, Mathur D;  
 XX  
 DR WPI; 2002-280757/32.  
 DR P-PSDB; AAE20513.  
 XX  
 PT Novel polynucleotides encoding human sodium channel proteins,  
 PT particularly voltage-gated sodium channel proteins useful for drug  
 PT screening, diagnosis and in gene therapy of biological disorders  
 XX  
 PS Claim 1; Page 46-47; 83pp; English.  
 XX  
 CC The present sequence is a cDNA encoding novel human protein (NHP), ion  
 CC channel protein. NHP share structural similarity with mammalian sodium  
 CC channel proteins particularly voltage-gated sodium channel proteins.  
 CC NHP oligonucleotides are useful as hybridisation probes for screening  
 CC libraries and assessing gene expression patterns. Sequences derived  
 CC from regions adjacent to the intron/exon boundaries of NHP gene can be

CC used to design primers for use in amplification assays to detect  
 CC mutations within the exons, splice sites, introns that can be used in  
 CC diagnostics and pharmacogenomics. NHP nucleotide sequences are useful  
 CC for drug screening effective in the treatment of symptomatic or  
 CC phenotypic manifestations of perturbing the normal function of NHP in  
 CC the body, and nucleotide constructs encoding NHP products are useful to  
 CC genetically engineer host cells to express NHP products in vivo. These  
 CC genetically engineered cells function as bioreactors in the body  
 CC delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion  
 CC protein to the body. Nucleotide construct encoding NHP products are  
 CC also useful in gene therapy for modulating NHP expression and to  
 CC produce genetically engineered host cells to express NHP products in  
 CC vivo. NHP nucleotide sequences may also be used as part of ribozyme  
 CC and/or tripeptide sequences that are useful for NHP gene regulation.  
 CC The NHP polypeptides are useful for generating antibodies, as  
 CC reagents in diagnostic assays, for identifying other cellular gene  
 CC products related to NHP and as reagents in assays for screening for  
 CC compounds that are useful in the treatment of mental, biological or  
 CC medical disorders and diseases.  
 XX  
 SQ Sequence 4146 BP; 1226 A; 810 C; 951 G; 1156 T; 3 other;  
 Alignment Scores:  
 Pred. No.: 0 Length: 4146  
 Score: 701.00 Matches: 1367  
 Percent Similarity: 98.77% Conservative: 0  
 Best Local Similarity: 98.77% Mismatches: 17  
 Query Match: 34.89% Indels: 17  
 DB: 24 Gaps: 0  
 US-09-930-871-12 (1-2009) x AAD32842 (1-4146)  
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 Qy 21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluValAsnValAsnProLysProAsp 40  
 Db 61 TCTCTGGCGCTATTGAAAGCCGATTCACAGAAAGGCAAGATCCCAACCAAC 120  
 Qy 41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60  
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Db 721 ATCCAGTCTGAGAAAGACTCTCAGATGTAATGATCTGAGCTGTCTGCTGAGCGTA 780  
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Db 1741 GCAAGAGATGTGGATCTGAGAGACAGCTTCGAGATGATGACACAGACACCTTGAAGAT 1800  
Qy 601 AsnGlnSerArgArgAspSerLeuPheValProArgArgHisGlyGlnArgArgAsnSer 620  
Db 1801 AACGAGACCCGAGAGATCTCTTGTGTGGCCACACACAGGAGAGAGAGCAACAGC 1860  
Qy 621 AsnLeuSerGlnThrSerArgSerArgMetLeuAlaValPheProAlaAsnLys 640  
Db 1861 AACCTGAGTCAGACCAAGGATGATCCGAGAGCTGGCAGTCTTCCAGCGATGGAGAG 1920  
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Db 1981 ACATCGCTGTG--G--A--C--A--G--C--T--T--C--T--G--C--C--A--G-- 2008  
Qy 681 AsnGlyThrThrThrGlnThrGlnMetArgLysArgArgSerSerSerPheHisValSer 700  
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Qy 701 MetAspPheLeuGlnAspProSerGlnArgGlnAlaMetSerIleAlaSerIleLeu 720  
Db 2068 ATGACTTTCTTGAAGATCTTCCCAAGGACACAGCAATGATATGACCGCATTTCTA 2127  
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Db 2128 ACAATATACAGTGAAGAACTTGAAGATCCAGACAGCAAGAAATGCCACCGTGGATATAA 2187  
Qy 741 PheSerAsnIlePheLeuIleTrpAspCysSerProTrpTrpLeuLysValHisVal 760  
Db 2188 TTTTCAACATATTTCTTATCTGAGGAGCTGTTCTCATATGTTGTTAAAGTGAACATGT 2247  
Qy 761 ValAsnLeuValIleMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780  
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Qy 881 LysIleIleGlyAsnSerValGlyValAlaLeuGlnAsnLeuThrLeuValLeuAlaIleIle 900  
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Qy 921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPheHisSer 940  
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QY 941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluTrpMetTrpPaspCysMet 960
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QY 961 GluValAlaLeuGlnAlaMetCysLeuThrValPheMetCysValMetValIleGlyAsn 980
DB 2848 GAGGTGCTGCTCAAGCAAGTGTCTTACGTCTCATGATGGTCATGATGGTGGAAAC 2907
QY 981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu**SerSerPheSerAlaAspAsnLeu 1000
DB 2908 CTAGTGCTCTGGAATCTCTTTCGCTTGTGAGTCATCTTATGTGAGACACACTT 2967
QY 1001 AlaAlaThrAspAspAspAsnGluMetCysAsnLeuGlnIleAlaValAspArgMetHis 1020
DB 2968 GCAGCCCATGATGATGATTAATGAAATATCTCCAAATTTGCTGTGATGATGATGCAC 3027
QY 1021 LysGlyValAlaValValValValValValValValValValValValValValVal 1040
DB 3028 AAAGAGTACCTTATGTGAAAGAAAGAAATATATGAAATTTATTCACAGCTCTTATTAG 3087
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DB 3148 TGTATGTCATATCATACACACAGAAATGGAAAGATCTGACATCTTAAAGATGTAAT 3207
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QY 1141 SerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGly 1160
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QY 1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240
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QY 1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaIleGlyTrpGlnThrPhe 1280
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QY 1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300
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QY 1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValAlaValAsnAlaLeu 1340
DB 3928 CTGAGACCTCTTAAGAGCTTATCTCGATTTGAAAGGATGAGGCTGTGTGAAAGCCCTT 3987
QY 1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpIle 1360
DB 3988 TTGAGACCATTCATCCTCATCATGAAATGTGCTTGTGTGTGTGTGTGTGTGTGTGTGT 4047
QY 1361 PheSerIleMetGlyValAlaLeuPheAlaGlyLysPheThrLysCysIleAsnThrThr 1380
DB 4048 TTCAGCATCATGGGCGTAAATTTGTTGTGTGCGCAAAATTCACACGTATTAACACACA 4107
QY 1381 ThrGlyAspArg 1384
DB 4108 ACTGTGTACAGG 4119

RESULT 14
AAD32843
ID AAD32843 standard; cDNA; 4164 BP.
XX
AC AAD32843;
XX
DT 01-JUL-2002 (first entry)
XX
DE Human Ion channel cDNA #5.
XX
KW Human; novel human protein; NHP; voltage-gated sodium channel;
KW gene therapy; bioelectro; mental disorder; biological disorder;
KW gene; medical disorder; ss.
XX
OS Homo sapiens.
XX
FH
FT 1..4164
FT CDS
FT
FT /tag- a
FT /product- "Human Ion channel protein #5"
FT /transl_except- (pos:2941..2943, aa:Xaa)
FT /transl_except- (pos:3166..3168, aa:Xaa)
FT /note- "Xaa = any amino acid"
XX
PN MO200214498-A2.
XX
PD 21-FEB-2002.
XX
PF 15-AUG-2001; 2001MO-US25650.
XX
PR 16-AUG-2000; 2000US-225989P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Turner CA, Mathur B, Mathur D;
XX
PT Novel polynucleotides encoding human sodium channel proteins,
XX particularly voltage-gated sodium channel proteins useful for drug
XX screening, diagnosis and in gene therapy of biological disorders
XX
PS Claim 1; Page 51-52; 83pp; English.
XX
CC The present sequence is a cDNA encoding novel human protein (NHP), ion
CC channel protein. NHP share structural similarity with mammalian sodium
CC channel proteins particularly voltage-gated sodium channel proteins.
CC NHP oligonucleotides are useful as hybridisation probes for screening
CC libraries and assessing gene expression patterns. Sequences derived
CC from regions adjacent to the intron/exon boundaries of NHP gene can be
CC used to design primers for use in amplification assays to detect
CC mutations within the exons, splice sites, introns that can be used in

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CC diagnostics and pharmacogenomics. NHP nucleotide sequences are useful  
 CC for drug screening effective in the treatment of symptomatic or  
 CC phenotypic manifestations of perturbing the normal function of NHP in  
 CC the body, and nucleotide constructs encoding NHP products are useful to  
 CC genetically engineer host cells to express NHP products in vivo. These  
 CC genetically engineered cells function as bioreactors in the body  
 CC delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion  
 CC protein to the body. Nucleotide construct encoding NHP products are  
 CC also useful in gene therapy for modulating NHP expression and to  
 CC produce genetically engineered host cells to express NHP products in  
 CC vivo. NHP nucleotide sequences may also be used as part of ribozyme  
 CC and/or triple helix sequences that are useful for NHP gene regulation.  
 CC The NHP polypeptides are useful for generating antibodies, as  
 CC reagents in diagnostic assays, for identifying other cellular gene  
 CC products related to NHP and as reagents in assays for screening for  
 CC compounds that are useful in the treatment of mental, biological or  
 CC medical disorders and diseases.

Sequence 4164 BP; 1219 A; 816 C; 958 G; 1168 T; 3 other;

# Alignment Scores:

Pred. No.: 0 Length: 4164  
 Score: 670.00 Matches: 1317  
 Percent Similarity: 98.73% Conservative: 0  
 Best Local Similarity: 98.73% Mismatches: 17  
 Query Match: 33.35% Indels: 17  
 DB: 24 Gaps: 0

US-09-930-871-12 (1-2009) x AAD32843 (1-4164)

OY 1 MetGUGInThrValLeuValProProGlyProAspSerPheAsnPhetherArgGlu 20  
 DB 1 ATGGAGCAACAGTGGCTTTACCCACGAGCTGACAGCTTCACTTCTTCACAGAGA 60  
 OY 21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40  
 DB 61 TCTCTGGCGGTATGAAAGACGATTCGAGAAAGCAAGAAATCCCAACACAGAC 120  
 OY 41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluLysAsn 60  
 DB 121 AAAAAAGATGACGAGAAATGAGCCCAAGCAAAATGAGACTGGAGCTGGAAAGAAC 180  
 OY 61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80  
 DB 181 CTTCCATTTATTTATGAGACATCTCTCCAGAGATGCTGACAGGCCCTGGAGACCTG 240  
 OY 81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100  
 DB 241 GACCCCTACTATATCAATTAAGAAACTTTATGATGAAATGAAGGAGGCACTCTTC 300  
 OY 101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120  
 DB 301 CGGTTACAGGCCACCTCCCTCCGTACATTTAACTCCCTTCATCTCTTAGGAAATA 360  
 OY 121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140  
 DB 361 GCTATTAGATTTTGGTAAATTCATTTATTCAGATCTCAATTTATGGCAGCTATTGGACA 420  
 OY 141 AsnCysValPheMetThrMetSerAsnProProAspTyrThrLysAsnValGluTyrThr 160  
 DB 421 AACTGCTGTTATGACATGAGTAACCTCCGATTGGACAAAGATGAAATACAC 480  
 OY 161 PheThyGlyIleTyrThrPheGluSerLeuIleLysIleLeuAlaArgGlyPheCysLeu 180  
 DB 481 TTCACAGGAGATATATCTTTGATCACTATTAATAAATTAATGCAAGGGGATCTGTTTA 540  
 OY 181 GluAspPheThrPheLeuArgAspProTyrPasnTyrPheAspPheThrValIleThrPhe 200  
 DB 541 GAAGATTTTACTTCTCTGGGATCCATGGAAGCTGCTGATTTCACTGTCATTAATTT 600  
 OY 201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220  
 DB 601 GGCTACGTACAGAGATTGTGGAGCTGGCAATGCTCGGCAATTGAGAACATTCAGAGTT 660

OY 221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240  
 DB 661 CTTCCAGAGATTAACAGATTTTCACTGATTCAGAGCTGAAACATATGTTGGAGCCCTG 720  
 OY 241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260  
 DB 721 ATCCAGTCTGTGAAAGAGCTTCAGATGTAATGAATCACTGCTGCTGTCTGAGCGTA 780  
 OY 261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnThr 280  
 DB 781 TTTTGCTTAATGGGCTGAGCTGCTGATGAGGCAACCTGAGGAAATTAATGATACAAAG 840  
 OY 281 ProProThrAsnAlaSerSerLeuGluHisSerIleGluLysAsnIleThrValAsnTyr 300  
 DB 841 CTTCCACCAATAGCTTCTCTGAGAGACATATATGAAATAATTAATCTGTAATTA 900  
 OY 301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTyrPheLysSerTyrIleGlnAsp 320  
 DB 901 AATGGAGACTATATAATGAACCTGCTTGAATTTGACTGGAACATATATCAAGAT 960  
 OY 321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340  
 DB 961 TCAGATATCATATTAATTTCTCTGAGAGGTTTTTATGATGCACTATGTTGGAATAGCTCT 1020  
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 OY 361 GlyTyrThrSerPheAspThrPheSerTyrAlaPheLeuSerLeuPheArgLeuMetThr 380  
 DB 1081 GGCTACACAGGCTTGAATATCTTCACTGATGGCTTTTGTCTCTGTTGAGCAATAGACT 1140  
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 DB 1141 CAGGACTCTGGGAAATCTTATATCAACATTAACGTCGCTGGGAAACGTAACAG 1200  
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 DB 1201 ATATTTTGTGTGGTCAATTTCTTGGGCTCATTTCTACCTTAATTAATTTGATCCGGCT 1260  
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 DB 1381 GCAGCAACGGCACTCTCTCAGAACATTTCCAGAGACCCAGTGCACAGGAGGCTCTCA 1440  
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QY 1201 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe 1220  
DB 3568 GGAAGAAAGATGGTGAACCTGGAAGAGACGTGTTCGAAAGATTTGAACATACATGCTGT 3627  
QY 1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyValAlaValAlaPheGluAspIle 1240  
DB 3628 GAGACCTTCATGTGTTTCAATGATCTCTCTTATGTGTGTGCTGCGCATTTGAAGATATA 3687  
QY 1241 TyrIleAspGlnArgLysTrpIleLysThrMetLeuGluTrpAlaAspLysValPheThr 1260  
DB 3688 TATATGATCAGCAAGAAAGCATTAAGACATGTGGAATATGCTGCAAGGTTTCACT 3747  
QY 1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaIleGlyTrpGlnThrTrpPhe 1280  
DB 3748 TACATTTTCAATTCGAAAGCTTCTTAATATGGGTGCAATGTGCTTCAACATATATTC 3807  
QY 1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300  
DB 3808 ACCAATGCCGTGGTGTGCTGAGACTTCTTAATGTGTATGTATGATGATGATGATGATTA 3867  
QY 1301 AlaAsnAlaLeuGlyTrpSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320

```

Db      3866 GGAATTCCTTGGGTACACAGAACTTGAGGCATCAAAATCTCTCAGGACACTAAGAGCT 3927
OY      1321 leuargproleuargalaleusearqphnegluglymetarg 1334
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Db      3928 CTGAGACCCTCTTAAGAGCCCTTATCTCATTTGAAGGATGAG 3969
RESULT 15
AKA02861/C
ID      AAK02861 standard; DNA; 1992 BP.
XX      AAK02861;
AC
AD
AE      05-NOV-2001 (first entry)
AF
AG
AH
AI
AJ
AK      Human brain expressed single exon probe SEQ ID NO: 2852.
AL
AM
AN
AO
AP
AQ
AR      Homo sapiens.
AS      MO200157275-AZ.
AT
AU
AV
AW
AX      30-JAN-2001; 2001WO-US000667.
AY
AZ
BA      04-FEB-2000; 2000US-0180312.
BB      26-MAY-2000; 2000US-0207456.
BC      30-JUN-2000; 2000US-0608408.
BD      03-AUG-2000; 2000US-0632366.
BE      21-SEP-2000; 2000US-0234687.
BF      27-SEP-2000; 2000US-0236359.
BG      04-OCT-2000; 2000GB-0024263.
BH
BI
BJ
BK      (MOLE-) MOLECULAR DYNAMICS INC.
BL
BM      Penn SG, Hanzel DK, Chen W, Rank DR;
BN      WPI: 2001-483446/52.
BO
BP      Single exon nucleic acid probes for analyzing gene expression in human
BQ      brains -
BR
BS      Example 4; SEQ ID NO: 2852; 650bp + Sequence Listing; English.
BT
BU
BV
BW
BX
BY
BZ
CA      The present invention provides a number of single exon nucleic acid
CB      probes which are derived from genomic sequences expressed in the human
CC      brain. They can be used to measure gene expression in brain cell samples,
CD      which may enable the diagnosis and improved treatment of nervous system
CE      diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CF      epilepsy and cancers. The present sequence is one of the probes of the
CG      invention.
CH
CI
CJ
CK
CL
CM
CN
CO
CP
CQ
CR
CS
CT
CU
CV
CW
CX
CY
CZ
DA      Sequence 1992 BP; 589 A; 399 C; 384 G; 620 T; 0 other;
DB
DC
DD
DE
DF
DG
DH
DI
DJ
DK
DL
DM
DN
DO
DP
DQ
DR
DS
DT
DU
DV
DW
DX
DY
EZ
FA      Alignment Scores:
FB      Pred. No.: 0 Length: 1992
FC      Score: 392.00 Matches: 392
FD      Percent Similarity: 100.00% Conservative: 0
FE      Best Local Similarity: 100.00% Mismatches: 0
FF      Query Match: 19.51% Indels: 0
FG      DB: 22 Gaps: 0
FH
FI
FJ
FK
FL
FM
FN
FO
FP
FQ
FR
FS
FT
FU
FV
FW
FX
FY
FZ
GA      -US-09-930-871-12 (1-2009) x AAK02861 (1-1992)
GB
GD
GE      1618 GlyMetPheLeuAlaIleuIleGIuLysTYRPhEValSerProHrLeuPheArgVal 1637
GF      1445 GGATGATTCTTCGCCGAGCGATGATAAAGAATTTGCTGTGTCCTTACCTGTTCGAGTG 1386
GH      1638 IleargLeuAlaIleuIleGIuLysTYRPhEValSerProHrLeuPheArgVal 1657

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|----|------|---|------|
| Db | 1385 | ATCCGTTGCTCTGGAATTTGGCCGAATCTACGTCGTCATCAAGGACAAAGGAGATCCGC     | 1326 |
| Qy | 1658 | ThrlEudPheAlaLeuMetSerLeuProAlaLeuPheAsnIleGlyLeuLeu            | 1677 |
| Db | 1325 | ACGGTCTCTTCTGTTGATGAGATGCCCTCTCTGCTGTGTTTACATGGGCTCTCATCC       | 1266 |
| Qy | 1678 | PheLeuValMetPheIleTyrAlaIlePheGlyMetSerAspPheAlaTyrValLysArg    | 1697 |
| Db | 1265 | TTCTCATCTCATGTCATCTACAGCCACTTTGGAGATGTCACACTTTGGCTCATGTTAAGGG   | 1206 |
| Qy | 1698 | GluValAlaGlyIleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeu | 1717 |
| Db | 1205 | GAAATGGAGATTCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCGCCTA    | 1146 |
| Qy | 1718 | PheGlnIleThrThrSerAlaGlyTyrPaspGlyLeuLeuAlaProIleLeuAsnSerLys   | 1737 |
| Db | 1145 | TTCCAAATTTCAACACTCTGCTGGCTGGAGTGGTCTGACACCATTCCTCAACAGTAAAG     | 1086 |
| Qy | 1738 | ProProAspProLysAspProAsnLysValAsnProGlySerSerValLysGlyAspProGly | 1757 |
| Db | 1085 | CCACCCGACGTGACCTTAATTAAGTTAACCCCTGGAGAGCTCAGTTAAGGAGACCTGTGG    | 1026 |
| Qy | 1758 | AsnProSerValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValAla    | 1777 |
| Db | 1025 | AACCATCTGTGGAAATTTCTTTTGTGCATGATCATCATATCTCTCTGGTGTG            | 966  |
| Qy | 1778 | ValAsnMetTyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluuSerAla      | 1797 |
| Db | 965  | GTGAACATGATACATCGGGGATCATCCAGGAACCTTCAGTGTGCTACGAAAGATGCA       | 906  |
| Qy | 1798 | GluProLeuSerGluAspAspPheGluMetPheTyrGluValTyrGluLysPheAspPro    | 1817 |
| Db | 905  | GAGCTCTGAGTGGATGTGACTTTGAGATGTTCTTACGAGTGTGGAGAGACTTATGCC       | 846  |
| Qy | 1818 | AspAlaThrGlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaIleuGluPro      | 1837 |
| Db | 845  | GATCCAACTCATGTCATGAAATTTGAAAAATTAATTCACATGTTGCAGCTGGCTTACCG     | 786  |
| Qy | 1838 | ProLeuAsnLeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetVal    | 1857 |
| Db | 785  | CTCTCAATCTGCCACAAACCAACCAACTCCAGCTCATTTGCCATGATTTGCCCATGGTG     | 726  |
| Qy | 1858 | SerGlyAspArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGly    | 1877 |
| Db | 725  | AGTGGTGACCGATCCACTGCTCTGTGATCTTATTTGCTTTTACAAAGCGGGTCTACAGA     | 666  |
| Qy | 1878 | GluSerGlyuMetAspAlaLeuArgIleGlnMetGluGluuArgPheMetLysSerAsn     | 1897 |
| Db | 665  | GAGAGTGGAGAGATGAGTGTCTACGAATTCACATGGAAGAGCGATTCATGGCTTCCAT      | 606  |
| Qy | 1898 | ProSerLysValSerTyrGlnProIleThrThrLeuLysArgLysGlnGluVal          | 1917 |
| Db | 605  | CTTCCAAAGCTCTCTATCAGCCATCATCTACTTCTTAAACGAAAAAACAAGAGAGTA       | 546  |
| Qy | 1918 | SerAlaValIleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGln    | 1937 |
| Db | 545  | TCTGTGTCATTATTCAGCGGCTTACAGACGCCACCTTTAAAGCAACTATAAACAA         | 486  |
| Qy | 1938 | AlaSerPheThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuLysGlu       | 1957 |
| Db | 485  | GCTTCCTTTACGTCAATTAATAAACAATTAAGAGGGGGGCTTAATCTTTTAAAGAA        | 426  |
| Qy | 1958 | AspMetIleIleAspArgIleAsnGluAsnSerIleThrGluLysThrAspLeuThrMet    | 1977 |
| Db | 425  | GACATGATTAATGACAAATTAATGAAAACTATTAATCAGAAAAAACTATCTGACATG       | 366  |
| Db | 365  | TTCATGTGAGCTGTCCACCTCTCTATGACCGGGGTACAAAGCCATTTGTGAAAAACAT      | 306  |
| Qy | 1998 | GluGlnGluGlyLysAspGluLysAlaLysGlyLys                            | 2009 |
| Db | 305  | GAGCAAGAAAGGCAAGATGAAAAAGCCAAAGGGGAAA                           | 270  |

Thu Apr 24 07:57:12 2003

us-09-930-871-12.olgop2n.rng

Page 44

Search completed: April 23, 2003, 05:07:08  
Job time : 909 secs

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GenCore version 5.1.4-p5.4578  
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OM nucleic - nucleic search, using sw model

Run on: April 22, 2003, 14:05:09 ; Search time 127 Seconds  
(Without alignments)  
14561.109 Million cell updates/sec

Title: US-09-930-871-11

Perfect score: 6030  
Sequence: 1 atgagcaaacagtcgtt.....aaaagccaaggaataa 6030

Scoring table: OLIGO-MDC  
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 862724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
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5: /cgn2\_6/ptodata/1/1na/PTUS.COMB.seq.\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID                | Description       |
|------------|-------|-------------|--------|-------------------|-------------------|
| 1          | 104   | 1.7         | 930    | US-08-605-284B-1  | Sequence 1, Appl  |
| 2          | 104   | 1.7         | 930    | US-08-605-284B-2  | Sequence 2, Appl  |
| 3          | 104   | 1.7         | 930    | US-08-605-284B-21 | Sequence 21, Appl |
| 4          | 79    | 1.3         | 6371   | US-08-836-325-13  | Sequence 13, Appl |
| 5          | 79    | 1.3         | 6404   | US-08-836-325-14  | Sequence 14, Appl |
| 6          | 53    | 0.9         | 3303   | US-08-836-325-1   | Sequence 1, Appl  |
| 7          | 44    | 0.7         | 3033   | US-08-836-325-9   | Sequence 9, Appl  |
| 8          | 44    | 0.7         | 6452   | US-08-836-325-1   | Sequence 1, Appl  |
| 9          | 29    | 0.5         | 5977   | US-09-024-020B-1  | Sequence 1, Appl  |
| 10         | 29    | 0.5         | 6007   | US-09-024-020B-2  | Sequence 2, Appl  |
| 11         | 29    | 0.5         | 6007   | US-09-024-020B-7  | Sequence 7, Appl  |
| 12         | 29    | 0.5         | 6556   | US-09-024-020B-3  | Sequence 3, Appl  |
| 13         | 29    | 0.5         | 6556   | US-09-024-020B-7  | Sequence 7, Appl  |
| 14         | 29    | 0.5         | 6556   | US-09-024-020B-5  | Sequence 5, Appl  |
| 15         | 29    | 0.5         | 6556   | US-09-024-020B-43 | Sequence 43, Appl |
| 16         | 29    | 0.5         | 6556   | US-09-024-020B-8  | Sequence 8, Appl  |
| 17         | 29    | 0.5         | 6826   | US-09-024-020B-8  | Sequence 8, Appl  |
| 18         | 29    | 0.5         | 6826   | US-09-024-020B-3  | Sequence 3, Appl  |
| 19         | 29    | 0.5         | 6826   | US-09-024-020B-3  | Sequence 3, Appl  |
| 20         | 26    | 0.4         | 6315   | US-08-808-793-2   | Sequence 2, Appl  |
| 21         | 26    | 0.4         | 6315   | US-08-772-512A-2  | Sequence 2, Appl  |
| 22         | 26    | 0.4         | 6318   | US-08-808-793-1   | Sequence 1, Appl  |
| 23         | 26    | 0.4         | 6318   | US-08-772-512A-1  | Sequence 1, Appl  |
| 24         | 22    | 0.4         | 696    | US-09-024-020B-5  | Sequence 5, Appl  |
| 25         | 22    | 0.4         | 696    | US-09-024-020B-5  | Sequence 5, Appl  |
| 26         | 20    | 0.3         | 702    | US-08-843-417-3   | Sequence 3, Appl  |
| 27         | 20    | 0.3         | 2508   | US-07-959-943-10  | Sequence 10, Appl |

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|----|----|-----|------|---------------------|---------------------|
| 28 | 20 | 0.3 | 2573 | US-08-669-656A-3    | Sequence 3, Appl    |
| 29 | 20 | 0.3 | 6344 | US-08-843-417-1     | Sequence 1, Appl    |
| 30 | 20 | 0.3 | 6524 | US-08-669-656A-1    | Sequence 1, Appl    |
| 31 | 20 | 0.3 | 6527 | US-08-669-656A-7    | Sequence 7, Appl    |
| 32 | 20 | 0.3 | 7052 | US-08-669-656A-5    | Sequence 5, Appl    |
| 33 | 19 | 0.3 | 944  | US-08-786-606-4     | Sequence 4, Appl    |
| 34 | 19 | 0.3 | 987  | US-08-786-606-4     | Sequence 4, Appl    |
| 35 | 19 | 0.3 | 1032 | US-08-843-417-3     | Sequence 3, Appl    |
| 36 | 19 | 0.3 | 1112 | US-08-933-750C-97   | Sequence 97, Appl   |
| 37 | 19 | 0.3 | 1112 | US-09-234-613-97    | Sequence 97, Appl   |
| 38 | 19 | 0.3 | 1120 | US-08-188-582-8     | Sequence 8, Appl    |
| 39 | 19 | 0.3 | 1120 | US-08-646-715-8     | Sequence 8, Appl    |
| 40 | 19 | 0.3 | 1314 | US-09-134-001C-1070 | Sequence 1070, Appl |
| 41 | 19 | 0.3 | 5874 | US-08-843-417-3     | Sequence 3, Appl    |
| 42 | 19 | 0.3 | 8252 | US-08-046-585-15    | Sequence 15, Appl   |
| 43 | 19 | 0.3 | 8252 | US-08-393-703-15    | Sequence 15, Appl   |
| 44 | 19 | 0.3 | 8252 | PCT-US93-11721-15   | Sequence 15, Appl   |
| 45 | 18 | 0.3 | 189  | US-08-248-474-68    | Sequence 68, Appl   |

## ALIGNMENTS

RESULT 1  
US-08-605-284B-1  
Sequence 1, Application US/08605284B  
Patent No. 6060271

GENERAL INFORMATION:

APPLICANT: WALEWSKI, JOSE L.

APPLICANT: REGIO-PINTO, ESPERANZA

TITLE OF INVENTION: VOLTAGE GATED SODIUM CHANNELS FROM

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESSES:

ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP

STREET: CLINTON SQUARE, P.O. BOX 1051

CITY: ROCHESTER

STATE: NEW YORK

COUNTRY: USA

ZIP: 14603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/605,284B

FILING DATE: 09-FEB-1996

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: BRAMAN, SUSAN J.

REGISTRATION NUMBER: 34,103

REFERENCE/DOCKET NUMBER: 19603/800 (CRF D-1705)

TELECOMMUNICATION INFORMATION:

TELEPHONE: 716-263-1636

TELEFAX: 716-263-1600

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 930 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-08-605-284B-1

Query Match 1.7%; Score 104; DB 3; Length 930;

Best Local Similarity 100.0%; Pred. No. 1.1e-39; Indels 0; Gaps 0;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4924 AGAATGGCGGAATCCAGCTGATCAAGGAGGAGGATCCGACGCTCTTT 4993

487 AGGATGGCGGAATCCAGCTGATCAAGGAGGAGGATCCGACGCTCTTT 546



QY 4984 GCTTGTGATGATGCTCCTCTGCTGCTTGTATACATCGGCTCCT 5027  
|||||  
DB 547 GCTTGTGATGATGCTCCTCTGCTGCTTGTATACATCGGCTCCT 590

## RESULT 2

US-08-605-284B-2  
; Sequence 2, Application US/08605284B  
; Patent No. 6060271  
; GENERAL INFORMATION:  
; APPLICANT: WALEWSKI, JOSE L.  
; APPLICANT: RECIO-PINTO, ESPERANZA  
; TITLE OF INVENTION: VOLTAGE GATED SODIUM CHANNELS FROM  
; TITLE OF INVENTION: HUMAN PERIPHERAL NERVE  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP  
; STREET: CLINTON SQUARE, P.O. BOX 1051  
; CITY: ROCHESTER  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 14603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/605,284B  
; FILING DATE: 09-FEB-1996  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BRAMAN, SUSAN J.  
; REGISTRATION NUMBER: 34,103  
; REFERENCE/DOCKET NUMBER: 19603/800 (CRF D-1705)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 716-263-1636  
; TELEFAX: 716-263-1600  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 930 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-605-284B-2

Query Match 1.7%; Score 104; DB 3; Length 930;  
Best Local Similarity 100.0%; Pred. No. 1.1e-39;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4924 AGGATGGCCGATCTACGTCTGATCAAGAGCAAGGAGATCCGACGCTGCTTT 4983  
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DB 487 AGGATGGCCGATCTACGTCTGATCAAGAGCAAGGAGATCCGACGCTGCTTT 546

QY 4984 GCTTGTGATGATGCTCCTCTGCTGCTTGTATACATCGGCTCCT 5027  
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DB 547 GCTTGTGATGATGCTCCTCTGCTGCTTGTATACATCGGCTCCT 590

## RESULT 3

US-08-605-284B-21  
; Sequence 21, Application US/08605284B  
; Patent No. 6060271  
; GENERAL INFORMATION:  
; APPLICANT: WALEWSKI, JOSE L.  
; APPLICANT: RECIO-PINTO, ESPERANZA  
; TITLE OF INVENTION: VOLTAGE GATED SODIUM CHANNELS FROM  
; TITLE OF INVENTION: HUMAN PERIPHERAL NERVE  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP  
; STREET: CLINTON SQUARE, P.O. BOX 1051

CITY: ROCHESTER  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 14603

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/605,284B  
FILING DATE: 09-FEB-1996  
CLASSIFICATION: 424

## ATTORNEY/AGENT INFORMATION:

NAME: BRAMAN, SUSAN J.  
REGISTRATION NUMBER: 34,103  
REFERENCE/DOCKET NUMBER: 19603/800 (CRF D-1705)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 716-263-1636  
TELEFAX: 716-263-1600

## INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:  
LENGTH: 930 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-605-284B-21

Query Match 1.7%; Score 104; DB 3; Length 930;  
Best Local Similarity 100.0%; Pred. No. 1.1e-39;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4924 AGGATGGCCGATCTACGTCTGATCAAGAGCAAGGAGATCCGACGCTGCTTT 4983  
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DB 487 AGGATGGCCGATCTACGTCTGATCAAGAGCAAGGAGATCCGACGCTGCTTT 546

QY 4984 GCTTGTGATGATGCTCCTCTGCTGCTTGTATACATCGGCTCCT 5027  
|||||  
DB 547 GCTTGTGATGATGCTCCTCTGCTGCTTGTATACATCGGCTCCT 590

## RESULT 4

US-08-836-325-13  
; Sequence 13, Application US/08836325  
; Patent No. 6110672  
; GENERAL INFORMATION:  
; APPLICANT: Mandel, Gail  
; APPLICANT: Halegoua, Simon  
; APPLICANT: Borden, Laurence A.  
; TITLE OF INVENTION: Peripheral Nervous System Specific  
; TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,  
; TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational  
; TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 New York Ave., N. W., Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/836,325  
; FILING DATE: 2-MAY-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/14251  
FILING DATE: 02-NOV-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/482,401  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/334,029  
FILING DATE: 02-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ludwig, Steven R.  
REGISTRATION NUMBER: 36,203  
REFERENCE/DOCKET NUMBER: 0917.0240002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6371 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: DNA (genomic)  
US-08-836-325-13

Query Match 1.3%; Score 79; DB 3; Length 6371;  
Best Local Similarity 100.0%; Pred. No. 9.5e-28;  
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4949 TCAAAGAGCAAAAGGGATCGCAGCTGCTTGGCTTGATGATGTCCTTCGCGT 5008  
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DB 4886 TCAAAGAGCAAAAGGGATCGCAGCTGCTTGGCTTGATGATGTCCTTCGCGT 4945  
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QY 5009 TGTTAACATCGGCTCCT 5027  
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DB 4946 TGTTAACATCGGCTCCT 4964  
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RESULT 5  
US-08-836-325-14  
Sequence 14, Application US/08836325  
Patent No. 6110672  
GENERAL INFORMATION:  
APPLICANT: Mandel, Gall  
APPLICANT: Halegoua, Simon  
APPLICANT: Borden, Laurence A.  
TITLE OF INVENTION: Peripheral Nervous System Specific  
TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,  
TITLE OF INVENTION: X-Ray Diffraction, Computer Molecular Modeling, Rational  
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 New York Ave., N. W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/836,325  
FILING DATE: 2-MAY-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/14251  
FILING DATE: 02-NOV-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/482,401  
FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/334,029  
FILING DATE: 02-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ludwig, Steven R.  
REGISTRATION NUMBER: 36,203  
REFERENCE/DOCKET NUMBER: 0917.0240002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6404 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: DNA (genomic)  
US-08-836-325-14

Query Match 1.3%; Score 79; DB 3; Length 6404;  
Best Local Similarity 100.0%; Pred. No. 9.5e-28;  
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4949 TCAAAGAGCAAAAGGGATCGCAGCTGCTTGGCTTGATGATGTCCTTCGCGT 5008  
|||||  
DB 4919 TCAAAGAGCAAAAGGGATCGCAGCTGCTTGGCTTGATGATGTCCTTCGCGT 4978  
|||||

QY 5009 TGTTAACATCGGCTCCT 5027  
|||||  
DB 4979 TGTTAACATCGGCTCCT 4997  
|||||

RESULT 6  
US-08-605-284B-3  
Sequence 3, Application US/08605284B  
Patent No. 6060271  
GENERAL INFORMATION:  
APPLICANT: WALEWSKI, JOSE L.  
APPLICANT: RECIO-PINTO, ESPERANZA  
TITLE OF INVENTION: VOLTAGE GATED SODIUM CHANNELS FROM  
TITLE OF INVENTION: HUMAN PERIPHERAL NERVE  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP  
STREET: CLINTON SQUARE, P.O. BOX 1051  
CITY: ROCHESTER  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 14603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/605,284B  
FILING DATE: 09-FEB-1996  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: BRAMAN, SUSAN J.  
REGISTRATION NUMBER: 34,103  
REFERENCE/DOCKET NUMBER: 19603/800 (CRF D-1705)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 716-263-1600  
TELEFAX: 716-263-1636  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 930 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-605-284B-3



Sequence 1, Application US/090240208  
Patent No. 6030810  
GENERAL INFORMATION:  
APPLICANT: DELGADO, STEPHEN G.  
APPLICANT: DIETRICH, PAUL S.  
APPLICANT: FISH, LINDA M.  
APPLICANT: HERMAN, RONALD C.  
APPLICANT: SANGAMESWARAN, LAKSHMI  
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE  
SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: JANET PAULINE CLARK  
STREET: 3401 HILLVIEW AVENUE, MS A2-250  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94304-1397  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/024,0208  
FILING DATE: 16-FEB-1998  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/039,447  
FILING DATE: 26-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: CLARK, JANET P.  
REGISTRATION NUMBER: 34,799  
REFERENCE/DOCKET NUMBER: R0020B-REG  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 852-3097  
TELEFAX: (650) 855-5322  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5977 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-024-0208-1

Query Match 0.5%; Score 29; DB 3; Length 5977;  
Best Local Similarity 100.0%; Pred. No. 0.00063;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 610 ACAGAGTTGTGGACCTGGGCAATGTC 638  
DB 643 ACAGAGTTGTGGACCTGGGCAATGTC 671  
|||||

RESULT 10  
US-09-425-043-1  
Sequence 1, Application US/09425043  
Patent No. 6335172  
GENERAL INFORMATION:  
APPLICANT: DELGADO, STEPHEN G.  
APPLICANT: DIETRICH, PAUL S.  
APPLICANT: FISH, LINDA M.  
APPLICANT: HERMAN, RONALD C.  
APPLICANT: SANGAMESWARAN, LAKSHMI  
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE  
SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: JANET PAULINE CLARK  
STREET: 3401 HILLVIEW AVENUE, MS A2-250  
CITY: PALO ALTO  
STATE: CA

COUNTRY: U.S.A.  
ZIP: 94304-1397  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/425,043  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/024,020  
FILING DATE: 16-FEB-1998  
APPLICATION NUMBER: US 60/039,447  
FILING DATE: 26-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: CLARK, JANET P.  
REGISTRATION NUMBER: 34,799  
REFERENCE/DOCKET NUMBER: R0020B-REG  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 852-3097  
TELEFAX: (650) 855-5322  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5977 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-425-043-1

Query Match 0.5%; Score 29; DB 4; Length 5977;  
Best Local Similarity 100.0%; Pred. No. 0.00063;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 610 ACAGAGTTGTGGACCTGGGCAATGTC 638  
DB 643 ACAGAGTTGTGGACCTGGGCAATGTC 671  
|||||

RESULT 11  
US-09-024-0208-2  
Sequence 2, Application US/090240208  
Patent No. 6030810  
GENERAL INFORMATION:  
APPLICANT: DELGADO, STEPHEN G.  
APPLICANT: DIETRICH, PAUL S.  
APPLICANT: FISH, LINDA M.  
APPLICANT: HERMAN, RONALD C.  
APPLICANT: SANGAMESWARAN, LAKSHMI  
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE  
SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: JANET PAULINE CLARK  
STREET: 3401 HILLVIEW AVENUE, MS A2-250  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94304-1397  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/024,0208  
FILING DATE: 16-FEB-1998  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/039,447  
FILING DATE: 26-FEB-1997

ATTORNEY/AGENT INFORMATION:  
NAME: CLARK, JANET P.  
REGISTRATION NUMBER: 34,799  
REFERENCE/DOCKET NUMBER: R0020B-REG  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 852-3097  
TELEFAX: (650) 855-5322  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6007 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-024-020B-2

Query Match  
Best Local Similarity 100.0%; Pred. No. 0.00063;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 610 ACAGAGTTGTGGACCTGGGCATGTCTC 638  
Db 643 ACAGAGTTGTGGACCTGGGCATGTCTC 671  
|||||

RESULT 12  
US-09-425-043-2  
Sequence 2, Application US/09425043  
Patent No. 6335172

GENERAL INFORMATION:  
APPLICANT: DELGADO, STEPHEN G.  
APPLICANT: DIETRICH, PAUL S.  
APPLICANT: FISH, LINDA M.  
APPLICANT: HERMAN, RONALD C.  
APPLICANT: SANGAMESWARAN, LAKSHMI  
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE  
TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: JANET PAULINE CLARK  
STREET: 3401 HILLVIEW AVENUE, MS A2-250  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94304-1397

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/425,043  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/024,020  
FILING DATE: 16-FEB-1998  
APPLICATION NUMBER: US 60/039,447  
FILING DATE: 26-FEB-1997

ATTORNEY/AGENT INFORMATION:  
NAME: CLARK, JANET P.  
REGISTRATION NUMBER: 34,799  
REFERENCE/DOCKET NUMBER: R0020B-REG  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 852-3097  
TELEFAX: (650) 855-5322  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6007 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)

US-09-425-043-2

Query Match  
Best Local Similarity 100.0%; Pred. No. 0.00063;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 610 ACAGAGTTGTGGACCTGGGCATGTCTC 638  
Db 643 ACAGAGTTGTGGACCTGGGCATGTCTC 671  
|||||

RESULT 13  
US-09-024-020B-7  
Sequence 7, Application US/09024020B  
Patent No. 6030810

GENERAL INFORMATION:  
APPLICANT: DELGADO, STEPHEN G.  
APPLICANT: DIETRICH, PAUL S.  
APPLICANT: FISH, LINDA M.  
APPLICANT: HERMAN, RONALD C.  
APPLICANT: SANGAMESWARAN, LAKSHMI  
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE  
TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: JANET PAULINE CLARK  
STREET: 3401 HILLVIEW AVENUE, MS A2-250  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94304-1397

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/024,020B  
FILING DATE: 16-FEB-1998  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/039,447  
FILING DATE: 26-FEB-1997

ATTORNEY/AGENT INFORMATION:  
NAME: CLARK, JANET P.  
REGISTRATION NUMBER: 34,799  
REFERENCE/DOCKET NUMBER: R0020B-REG  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 852-3097  
TELEFAX: (650) 855-5322  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6556 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-024-020B-7

Query Match  
Best Local Similarity 100.0%; Pred. No. 0.00063;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 610 ACAGAGTTGTGGACCTGGGCATGTCTC 638  
Db 790 ACAGAGTTGTGGACCTGGGCATGTCTC 818  
|||||

RESULT 14  
US-09-425-043-7  
Sequence 7, Application US/09425043  
Patent No. 6335172

GENERAL INFORMATION:

APPLICANT: DELGADO, STEPHEN G.  
 APPLICANT: DIETRICH, PAUL S.  
 APPLICANT: FISH, LINDA M.  
 APPLICANT: HERMAN, RONALD C.  
 APPLICANT: SANGAMESWARAN, LAKSHMI  
 TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE  
 TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF  
 NUMBER OF SEQUENCES: 43  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: JANET PAULINE CLARK  
 STREET: 3401 HILLVIEW AVENUE, MS A2-250  
 CITY: PALO ALTO  
 STATE: CA  
 COUNTRY: U.S.A.  
 ZIP: 94304-1397  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/425,043  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 09/024,020  
 FILING DATE: 16-FEB-1998  
 APPLICATION NUMBER: US 60/039,447  
 FILING DATE: 26-FEB-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: CLARK, JANET P.  
 REGISTRATION NUMBER: 34,799  
 REFERENCE/DOCKET NUMBER: R0020B-REG  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (650) 852-3097  
 TELEFAX: (650) 855-5322  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6556 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 US-09-425-043-7

Query Match 0.5%; Score 29; DB 4; Length 6556;  
 Best Local Similarity 100.0%; Pred. No. 0.00063;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 610 ACAGAGTTGTGGACCTGGGCAATGTC 638  
 DB 790 ACAGAGTTGTGGACCTGGGCAATGTC 818

RESULT 15  
 US-09-024-020B-43  
 Sequence 43; Application US/09024020B  
 Patent No. 6030810  
 GENERAL INFORMATION:  
 APPLICANT: DELGADO, STEPHEN G.  
 APPLICANT: DIETRICH, PAUL S.  
 APPLICANT: FISH, LINDA M.  
 APPLICANT: HERMAN, RONALD C.  
 APPLICANT: SANGAMESWARAN, LAKSHMI  
 TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE  
 TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF  
 NUMBER OF SEQUENCES: 43  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: JANET PAULINE CLARK  
 STREET: 3401 HILLVIEW AVENUE, MS A2-250  
 CITY: PALO ALTO  
 STATE: CA  
 COUNTRY: U.S.A.

ZIP: 94304-1397  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/024,020B  
 FILING DATE: 16-FEB-1998  
 CLASSIFICATION: 536  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/039,447  
 FILING DATE: 26-FEB-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: CLARK, JANET P.  
 REGISTRATION NUMBER: 34,799  
 REFERENCE/DOCKET NUMBER: R0020B-REG  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (650) 852-3097  
 TELEFAX: (650) 855-5322  
 INFORMATION FOR SEQ ID NO: 43:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6586 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 US-09-024-020B-43

Query Match 0.5%; Score 29; DB 3; Length 6586;  
 Best Local Similarity 100.0%; Pred. No. 0.00063;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 610 ACAGAGTTGTGGACCTGGGCAATGTC 638  
 DB 790 ACAGAGTTGTGGACCTGGGCAATGTC 818

Search completed: April 22, 2003, 18:38:43  
 Job time: 178 secs





|    |      |   |      |
|----|------|---|------|
| QY | 241  | GAOCCGACATATATACAAATAGAAAACCTTTTATATAGTTATGAATAAAGGGAAGCCATCTC  | 300  |
| Db | 241  | GAOCCGACATATATACAAATAGAAAACCTTTTATATAGTTATGAATAAAGGGAAGCCATCTTC | 300  |
| QY | 301  | CGGTTCAGTCCACACCTCTGCCCCTGTACATTTTAACTCCCTTCATCTCTTAAGSAAATA    | 360  |
| Db | 301  | CGGTTCAGTCCACACCTCTGCCCCTGTACATTTTAACTCCCTTCATCTCTTAAGSAAATA    | 360  |
| QY | 361  | GCATTTAAGATTTTGGTACATTATATATCAGACATGCTAAATATGTGCACATTTTGTACA    | 420  |
| Db | 361  | GCATTTAAGATTTTGGTACATTTATTTATTCAGACATGCTAAATATGTGCACATTTTGTACA  | 420  |
| QY | 421  | AACGTGTGTTTATGACAAATGAGTAACCCCTCCGATGTGACAAAGATATGATATACAC      | 480  |
| Db | 421  | AACGTGTGTTTATGACAAATGAGTAACCCCTCCGATGTGACAAAGATATGATATACAC      | 480  |
| QY | 481  | TTTCACAGGAATATATACATTGTTGAATACATTATATATAAATTTATTGCAAGGGGATTCGT  | 540  |
| Db | 481  | TTTCACAGGAATATATACATTGTTGAATACATTATATATAAATTTATTGCAAGGGGATTCGT  | 540  |
| QY | 541  | GAAGATTTTACTTCCCTCGGGATTCATGGAATGGAATGGAATGGAATGGAATGGAATGGAAT  | 600  |
| Db | 541  | GAAGATTTTACTTCCCTCGGGATTCATGGAATGGAATGGAATGGAATGGAATGGAATGGAAT  | 600  |
| QY | 601  | GCGTACGTACAGAGTTTGTGACCTGTGGCAATGTCTCGGCAATTGAGAACATTCAGAGTT    | 660  |
| Db | 601  | GCGTACGTACAGAGTTTGTGACCTGTGGCAATGTCTCGGCAATTGAGAACATTCAGAGTT    | 660  |
| QY | 661  | CTCCGACATTTGAAGACGATTTTACATGCTATTCACAGGCTTAAACCATTTGTGGAGCCCTG  | 720  |
| Db | 661  | CTCCGACATTTGAAGACGATTTTACATGCTATTCACAGGCTTAAACCATTTGTGGAGCCCTG  | 720  |
| QY | 721  | ATCCAGCTCTGGAAGAGCTCTCAGATGTATATGATCCTGACTGTCTGTCTGAGCCTA       | 780  |
| Db | 721  | ATCCAGCTCTGGAAGAGCTCTCAGATGTATATGATCCTGACTGTCTGTCTGAGCCTA       | 780  |
| QY | 781  | TTTGTCTTAAATTTGGGCTGTGACGCTGTTCATGTGGCACTGTGAGAAATATATATACATGG  | 840  |
| Db | 781  | TTTGTCTTAAATTTGGGCTGTGACGCTGTTCATGTGGCACTGTGAGAAATATATATACATGG  | 840  |
| QY | 841  | CCCTCCACACATGCTCTCTTGGAGAAACATATGATATGAAAGATATATATATATATATAT    | 900  |
| Db | 841  | CCCTCCACACATGCTCTCTTGGAGAAACATATGATATGAAAGATATATATATATATATATAT  | 900  |
| QY | 901  | ATATGATACATTTAATTAATGAACCTGTCTTGAATTTGACTGAGAGTCAATATATTCAGAT   | 960  |
| Db | 901  | ATATGATACATTTAATTAATGAACCTGTCTTGAATTTGACTGAGAGTCAATATATTCAGAT   | 960  |
| QY | 961  | TCAAGATATATATTTTCCGAGAGGTTTTTATGATGCACTATATATATATATATATATAT     | 1020 |
| Db | 961  | TCAAGATATATATTTTCCGAGAGGTTTTTATGATGCACTATATATATATATATATATATAT   | 1020 |
| QY | 1021 | GATGACAGCCAAATGTCCAGAGGATATATATGTGTGAAGCTGTGATAGAAATCCCAATAT    | 1080 |
| Db | 1021 | GATGACAGCCAAATGTCCAGAGGATATATATGTGTGAAGCTGTGATAGAAATCCCAATAT    | 1080 |
| QY | 1081 | GGCTACACAAAGCTTTGATACCTTCACTGTGGGCTTTTGTCTGTCTGTTCGACTAATGACT   | 1140 |
| Db | 1081 | GGCTACACAAAGCTTTGATACCTTCACTGTGGGCTTTTGTCTGTCTGTTCGACTAATGACT   | 1140 |
| QY | 1141 | CAGAGCTTCGGGAAATCTTTATCACTGACATTCAGGCTGTGGGAAACGATACATG         | 1200 |
| Db | 1141 | CAGAGCTTCGGGAAATCTTTATCACTGACATTCAGGCTGTGGGAAACGATACATG         | 1200 |
| QY | 1201 | ATATTTTGTGTGTGCTATTTTCTTGGGCTCATCTACCTATATATATATATATATATAT      | 1260 |
| Db | 1201 | ATATTTTGTGTGTGCTATTTTCTTGGGCTCATCTACCTATATATATATATATATATATAT    | 1260 |
| QY | 1261 | GTGTGGCCATGGCTCTACAGAGAAACGATACAGGCACTTGTGAAGAAACGACACAA        | 1320 |
| Db | 1261 | GTGTGGCCATGGCTCTACAGAGAAACGATACAGGCACTTGTGAAGAAACGACACAA        | 1320 |

|    |      |  |      |
|----|------|--|------|
| OY | 1321 | GAGGGCGAATTTTACACAGATGTTTGAACAGCTTTAAAAAGCAACAGSAGGCGCTCAGAG   | 1380 |
| OY | 1321 | GAGGGCGAATTTTACACAGATGTTTGAACAGCTTTAAAAAGCAACAGSAGGCGCTCAGAG   | 1380 |
| OY | 1381 | GCAGCAGCGCAACCTCGCCTCAGAACATTCACAGAGAGCCAGTGCAGCAGCGCAGCTCTCA  | 1440 |
| DB | 1381 | GCAGCAGCGCAACCTCGCCTCAGAACATTCACAGAGAGCCAGTGCAGCAGCGCAGCTCTCA  | 1440 |
| OY | 1441 | GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAAGAGTGCCTAAGGAAAGAAATCGG    | 1500 |
| DB | 1441 | GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAAGAGTGCCTAAGGAAAGAAATCGG    | 1500 |
| OY | 1501 | AGGAAGAAAGAAACAGAAAAGAGCAGTCTGGTGGGGAAGAAAGATAGAGATGAATTC      | 1560 |
| DB | 1501 | AGGAAGAAAGAAACAGAAAAGAGCAGTCTGGTGGGGAAGAAAGATAGAGATGAATTC      | 1560 |
| OY | 1561 | CAAAAATCTGAATCTGAGSAGACAGCATCAGSAGSAGAAAGGTTTTGCGTCTCCATTGAAGG | 1620 |
| DB | 1561 | CAAAAATCTGAATCTGAGSAGACAGCATCAGSAGSAGAAAGGTTTTGCGTCTCCATTGAAGG | 1620 |
| OY | 1621 | AACCGATTGACATATGAAAAGAGTACTCTCCACACACAGTCTTTGTGAGATCCGT        | 1680 |
| DB | 1621 | AACCGATTGACATATGAAAAGAGTACTCTCCACACACAGTCTTTGTGAGATCCGT        | 1680 |
| OY | 1681 | GGCTCCGATTTTTCACCAAGGGGAATGCAAAACACCAAGTCTTTGAGAGGGGA          | 1740 |
| DB | 1681 | GGCTCCGATTTTTCACCAAGGGGAATGCAAAACACCAAGTCTTTGAGAGGGGA          | 1740 |
| OY | 1741 | GCAAAAGATGTGGATCTGAGAACGATCTGAGATGATGAGACACAGCACTTTAGAT        | 1800 |
| DB | 1741 | GCAAAAGATGTGGATCTGAGAACGATCTGAGATGATGAGACACAGCACTTTAGAT        | 1800 |
| OY | 1801 | AACGAGACCCGTAGAGATTCCTGTTGTGCCCGACAGACAGSAGAGAGACGCAACAGC      | 1860 |
| DB | 1801 | AACGAGACCCGTAGAGATTCCTGTTGTGCCCGACAGACAGSAGAGAGACGCAACAGC      | 1860 |
| OY | 1861 | AACCTGACTCAGACCCAGTAGTCAATCCCGGAGTGTGCGAGTGTTCACGCAATGGGAAG    | 1920 |
| DB | 1861 | AACCTGACTCAGACCCAGTAGTCAATCCCGGAGTGTGCGAGTGTTCACGCAATGGGAAG    | 1920 |
| OY | 1921 | ATGCACAGCACTGTGATGTGCAATGSGTGTGTTCTTGTTGGTGTGCACTTCACTTCT      | 1980 |
| DB | 1921 | ATGCACAGCACTGTGATGTGCAATGSGTGTGTTCTTGTTGGTGTGCACTTCACTTCT      | 1980 |
| OY | 1981 | ACATGCGCTGTGGACAGCTTCTGCCAAGSGTAGAATAGATAGAACCCAGCTACTATGAC    | 2040 |
| DB | 1981 | ACATGCGCTGTGGACAGCTTCTGCCAAGSGTAGAATAGATAGAACCCAGCTACTATGAC    | 2040 |
| OY | 2041 | AATGGAACAACACACGGAACCTGAATGAGAAAGAAAGSTCAAGTTCTTCCAGCTTCC      | 2100 |
| DB | 2041 | AATGGAACAACACACGGAACCTGAATGAGAAAGAAAGSTCAAGTTCTTCCAGCTTCC      | 2100 |
| OY | 2101 | ATGGAATCTCTGAGAGATCTCTCCCAAGAGCAACAGAAATAGATAGCCAGCTTCTCA      | 2160 |
| DB | 2101 | ATGGAATCTCTGAGAGATCTCTCCCAAGAGCAACAGAAATAGATAGCCAGCTTCTCA      | 2160 |
| OY | 2161 | ACAAATACAGTAGAAGAACTTGAAATCCAGSAGAAATGCCAACCCTGTTGATATAA       | 2220 |
| DB | 2161 | ACAAATACAGTAGAAGAACTTGAAATCCAGSAGAAATGCCAACCCTGTTGATATAA       | 2220 |
| OY | 2221 | TTTTTCCAAATATTTCTTAATCTGGGAGCTGTCTCCATATTTGGTTAAAGTGAACATGTT   | 2280 |
| DB | 2221 | TTTTTCCAAATATTTCTTAATCTGGGAGCTGTCTCCATATTTGGTTAAAGTGAACATGTT   | 2280 |
| OY | 2281 | GTCACACGTTGTATATGAGCCCATTTTGTATCTGGCGCATACCATCTGATATGTCTTA     | 2340 |
| DB | 2281 | GTCACACGTTGTATATGAGCCCATTTTGTATCTGGCGCATACCATCTGATATGTCTTA     | 2340 |
| OY | 2341 | AATACTCTTTTCATGGCCATGGAGCATATCCAAATGAGCGACATTTAAATATGTGTT      | 2400 |
| DB | 2341 | AATACTCTTTTCATGGCCATGGAGCATATCCAAATGAGCGACATTTAAATATGTGTT      | 2400 |
| OY | 2401 | ACAGTAGAACAATCTGGTTTCACTGGGATCTTTACAGCAGAAATGTTCTGAAAATTTT     | 2460 |

|   |   |      |   |      |
|---|---|------|---|------|
| D | b | 2401 | ACAGTAGGAACCTTGGTTTTCTACTGGGATCTTACAGCAAAATCTTCTGAAATATAT     | 2460 |
| Q | y | 2461 | GCATGATCCTTACTATTATTTCCAAAGAGCGTGAATATCTTTGACGGTTTTATTGTG     | 2520 |
| D | b | 2461 | GCATGATCCTTACTATTATTTCCAAAGAGCGTGAATATCTTTGACGGTTTTATTGTG     | 2520 |
| Q | y | 2521 | ACGTTAGCGCTGGTAGAAGCTTGGACCTGGCCAAATGAGGATATATCTGTTCTCCGTCA   | 2580 |
| D | b | 2521 | ACGTTAGCGCTGGTAGAAGCTTGGACCTGGCCAAATGAGGATATATCTGTTCTCCGTCA   | 2580 |
| Q | y | 2581 | TTTTCGATTCGTGGAGAGTTTCAAGTTGGGAAAATCTTGGCCAACTTTAAATATGCTAATA | 2640 |
| D | b | 2581 | TTTTCGATTCGTGGAGAGTTTCAAGTTGGGAAAATCTTGGCCAACTTTAAATATGCTAATA | 2640 |
| Q | y | 2641 | AAATCATCGGCAATTCCTGGGGGGCTCTGGGAAATTTAAACCTCGTCTGGCCATATC     | 2700 |
| D | b | 2641 | AAATCATCGGCAATTCCTGGGGGGCTCTGGGAAATTTAAACCTCGTCTGGCCATATC     | 2700 |
| Q | y | 2701 | GTCCTCATTTTTGCGCGTGGTGGCAGTCTTTGGTAAAAAGCTAACAAAGATGTCTC      | 2760 |
| D | b | 2701 | GTCCTCATTTTTGCGCGTGGTGGCAGTCTTTGGTAAAAAGCTAACAAAGATGTCTC      | 2760 |
| Q | y | 2761 | TGCAAGATCGCAGTGTATTTCTCAACTCCACGCTGGCAATGAAGATCTCTTCCACTCC    | 2820 |
| D | b | 2761 | TGCAAGATCGCAGTGTATTTCTCAACTCCACGCTGGCAATGAAGATCTCTTCCACTCC    | 2820 |
| Q | y | 2821 | TTCCGTGATTTGTTCCTCCGCTGCTGTGTGGGAGTGGATAGAGACCATGTGGAGCTATG   | 2880 |
| D | b | 2821 | TTCCGTGATTTGTTCCTCCGCTGCTGTGTGGGAGTGGATAGAGACCATGTGGAGCTATG   | 2880 |
| Q | y | 2881 | GAGGTGCTGTCTCAAGCCATGTGCTTACTGTCTCTATGATGTCTATGTGTTGGAAC      | 2940 |
| D | b | 2881 | GAGGTGCTGTCTCAAGCCATGTGCTTACTGTCTCTATGATGTCTATGTGTTGGAAC      | 2940 |
| Q | y | 2941 | CTAATGGTCCGAATCTCTTCTGGGCTGTMTAGTCAATTAAGTCAACAACCTT          | 3000 |
| D | b | 2941 | CTAATGGTCCGAATCTCTTCTGGGCTGTMTAGTCAATTAAGTCAACAACCTT          | 3000 |
| Q | y | 3001 | GCAGCCACTGATGATGATTAATGAATGAATATCTCCAAATTCGTGTGATAGATGAC      | 3060 |
| D | b | 3001 | GCAGCCACTGATGATGATTAATGAATGAATATCTCCAAATTCGTGTGATAGATGAC      | 3060 |
| Q | y | 3061 | AAAGAGTAGCTTATGTGAAAAAGAAAAATATATGAATTTATCACAAGCTCTTCAATPAG   | 3120 |
| D | b | 3061 | AAAGAGTAGCTTATGTGAAAAAGAAAAATATATGAATTTATCACAAGCTCTTCAATPAG   | 3120 |
| Q | y | 3121 | AAACAAAAGATTTAGTATGAATTAACCACTGATGATCTAAACAAGAAACACAGT        | 3180 |
| D | b | 3121 | AAACAAAAGATTTAGTATGAATTAACCACTGATGATCTAAACAAGAAACACAGT        | 3180 |
| Q | y | 3181 | TGTATGTCCATTCATACARCAAGAAATGGGAAAGATCTTGACATCTTTAAAGATPAAAT   | 3240 |
| D | b | 3181 | TGTATGTCCATTCATACARCAAGAAATGGGAAAGATCTTGACATCTTTAAAGATPAAAT   | 3240 |
| Q | y | 3241 | GGAACTACAACTGGTATAGGAAGTGGCAGCAGTGTGAAAAAATACATTAATGATGAAGT   | 3300 |
| D | b | 3241 | GGAACTACAACTGGTATAGGAAGTGGCAGCAGTGTGAAAAAATACATTAATGATGAAGT   | 3300 |
| Q | y | 3301 | GATTACATGTCTATTCATTAACACCCACGCTTACTGCTGATCAGTACCAATTCCTGTAGGA | 3360 |
| D | b | 3301 | GATTACATGTCTATTCATTAACACCCACGCTTACTGCTGATCAGTACCAATTCCTGTAGGA | 3360 |
| Q | y | 3361 | GAATGTGACTTTGAAAAATTTAAACAGGAAGACTTTTAGTATGATGAAGAA           | 3420 |
| D | b | 3361 | GAATGTGACTTTGAAAAATTTAAACAGGAAGACTTTTAGTATGATGAAGAA           | 3420 |
| Q | y | 3421 | AGCAAAAGAACTGAATGGAAGCAGTAGCTCATCAGAGTAGCACTGTGGACATCGGC      | 3480 |
| D | b | 3421 | AGCAAAAGAACTGAATGGAAGCAGTAGCTCATCAGAGTAGCACTGTGGACATCGGC      | 3480 |
| Q | y | 3481 | GCACCTGAGAAAGACAGCCCGTAGTGTGAACCTGAAAGAACTTTGAAACCAAGAGCTGT   | 3540 |

|   |      |   |      |
|---|------|---|------|
| D | 3481 | GCACCTTGAGAAAGACAGCCCGTAGTGGAAACCTGGAAGAAACCTTGAACACGAAGCTTGT | 3540 |
| Q | 3541 | TTCACTAAGAGCGTGTGTACCAAGATTCCAAGTGTGTCCAATCAATGTGGAAAGACGAGA  | 3600 |
| D | 3541 | TTCACTAAGAGCGTGTGTACCAAGATTCCAAGTGTGTCCAATCAATGTGGAAAGACGAGA  | 3600 |
| Q | 3601 | GGAAACAATAGTGGGAACCGAAGAGAGCGTGTCCGAATAGTGGAAACATCAACGCGTTT   | 3660 |
| D | 3601 | GGAAACAATAGTGGGAACCGAAGAGAGCGTGTGTCCGAATAGTGGAAACATCAACGCGTTT | 3660 |
| Q | 3661 | GAGACCTTCATTTGTTTTCATGATTCCTTAGTAGTGGTGGCTGGCAATTTGAAGATATA   | 3720 |
| D | 3661 | GAGACCTTCATTTGTTTTCATGATTCCTTAGTAGTGGTGGCTGGCAATTTGAAGATATA   | 3720 |
| Q | 3721 | TATATGATGACGGAAGACGATTTAAGACAGTGTGGAAATATGTCAGACAGGTTTCACT    | 3780 |
| D | 3721 | TATATGATGACGGAAGACGATTTAAGACAGTGTGGAAATATGTCAGACAGGTTTCACT    | 3780 |
| Q | 3781 | TACATTTCAATTCGGAAGATGCTTCAAAAATGGGTGGCATATGGCATCAAAACATATTC   | 3840 |
| D | 3781 | TACATTTCAATTCGGAAGATGCTTCAAAAATGGGTGGCATATGGCATCAAAACATATTC   | 3840 |
| Q | 3841 | ACCAATGCGCTGGTGGTGGCGACTTCCTTAATGTTGATGATTCATTGGTCAGTTTAA     | 3900 |
| D | 3841 | ACCAATGCGCTGGTGGTGGCGACTTCCTTAATGTTGATGATTCATTGGTCAGTTTAA     | 3900 |
| Q | 3901 | GCAAAATGCGTGGGTACTCAGAACTTGGAGCCATCAAAATCTCGACACACTAAGACT     | 3960 |
| D | 3901 | GCAAAATGCGTGGGTACTCAGAACTTGGAGCCATCAAAATCTCGACAGCACATAAGACT   | 3960 |
| Q | 3961 | CTGAGACCTCTAAGGCTTAATCTCCATTTGAAGGGAATGAGGTGGTGTGAATGCCCTT    | 4020 |
| D | 3961 | CTGAGACCTCTAAGGCTTAATCTCCATTTGAAGGGAATGAGGTGGTGTGAATGCCCTT    | 4020 |
| Q | 4021 | TTAGAGCAATTCATCATCATCAGTAATGTCTCTGTGTCTTAATATTCGCGCTAAT       | 4080 |
| D | 4021 | TTAGAGCAATTCATCATCATCAGTAATGTCTCTGTGTCTTAATATTCGCGCTAAT       | 4080 |
| Q | 4081 | TTCAACATCATGGCGTAAATTTGTGTCTGTCGCAAAATCTACCACTGATTAACACACA    | 4140 |
| D | 4081 | TTCAACATCATGGCGTAAATTTGTGTCTGTCGCAAAATCTACCACTGATTAACACACA    | 4140 |
| Q | 4141 | ACTGGTACAGGTTTGACATCAGGAAGCTGAATATATCATATCAGATTTGCCATAATA     | 4200 |
| D | 4141 | ACTGGTACAGGTTTGACATCAGGAAGCTGAATATATCATATCAGATTTGCCATAATA     | 4200 |
| Q | 4201 | GAAAGAATAGACTGCTGCATGGAAGAAATGTGAAGTAAACTTGGATATGTAGAGATT     | 4260 |
| D | 4201 | GAAAGAATAGACTGCTGCATGGAAGAAATGTGAAGTAAACTTGGATATGTAGAGATT     | 4260 |
| Q | 4261 | GGGTATCTCTTTTGTCTCAAGTTGCCAATTCMAAGATGATGATTAATGTATGCA        | 4320 |
| D | 4261 | GGGTATCTCTTTTGTCTCAAGTTGCCAATTCMAAGATGATGATTAATGTATGCA        | 4320 |
| Q | 4321 | GCAGTGTATTCAGAAATGTGGAACTCCACCTCAAGTATGAAGAAAGTCTGTACATGAT    | 4380 |
| D | 4321 | GCAGTGTATTCAGAAATGTGGAACTCCACCTCAAGTATGAAGAAAGTCTGTACATGAT    | 4380 |
| Q | 4381 | CTTTACTTGTATTTTTCATCATCTTGGGTCTCTCTCACTGAACTGTTATTTGTT        | 4440 |
| D | 4381 | CTTTACTTGTATTTTTCATCATCTTGGGTCTCTCTCACTGAACTGTTATTTGTT        | 4440 |
| Q | 4441 | GTCATCATAGATTAATTTTCAACACAGCAAGAAAGTTTGGAGTCAACACATCTTTATG    | 4500 |
| D | 4441 | GTCATCATAGATTAATTTTCAACACAGCAAGAAAGTTTGGAGTCAACACATCTTTATG    | 4500 |
| Q | 4501 | ACAGAGAACAAGAAATACTATATATGCAATGAAAAAATTAGATCGAAAAACCGCA       | 4560 |
| D | 4501 | ACAGAGAACAAGAAATACTATATATGCAATGAAAAAATTAGATCGAAAAACCGCA       | 4560 |
| Q | 4561 | AAGCCTATACCTGCACAGGAACAAATTTCAAGGAATGGTCTTTACACTTCTATACAGA    | 4620 |
| D | 4561 | AAGCCTATACCTGCACAGGAACAAATTTCAAGGAATGGTCTTTACACTTCTATACAGA    | 4620 |

QY 4621 CAAGTTTTCATTAAGCATCATGATTCATCTGTCTTACATGTCACATGATGATG 4680  
 |||||  
 Db 4621 CAAGTTTTCATTAAGCATCATGATTCATCTGTCTTACATGTCACATGATGATG 4680  
 QY 4681 GAAACAGATGACAGAGATGATGATGATGATGATGATGATGATGATGATGATG 4740  
 |||||  
 Db 4681 GAAACAGATGACAGAGATGATGATGATGATGATGATGATGATGATGATGATG 4740  
 QY 4741 ATTGTCTATTACTGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 4800  
 |||||  
 Db 4741 ATTGTCTATTACTGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 4800  
 QY 4801 ACCATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4860  
 |||||  
 Db 4801 ACCATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4860  
 QY 4861 CTTCGCGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4920  
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 Db 4861 CTTCGCGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4920  
 QY 4921 GCTAGAGTTGGCGGATCTCTACCTGATGATGATGATGATGATGATGATGATGATG 4980  
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 Db 4921 GCTAGAGTTGGCGGATCTCTACCTGATGATGATGATGATGATGATGATGATGATG 4980  
 QY 4981 TTTGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5040  
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 Db 4981 TTTGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5040  
 QY 5041 ATGTTTCATGACCCATCTTTGGGATGATGATGATGATGATGATGATGATGATGATG 5100  
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 Db 5041 ATGTTTCATGACCCATCTTTGGGATGATGATGATGATGATGATGATGATGATGATG 5100  
 QY 5101 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5160  
 |||||  
 Db 5101 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5160  
 QY 5161 ACAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5220  
 |||||  
 Db 5161 ACAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5220  
 QY 5221 TGTGACCTGATTAAGTAACTGATGATGATGATGATGATGATGATGATGATGATG 5280  
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 Db 5221 TGTGACCTGATTAAGTAACTGATGATGATGATGATGATGATGATGATGATGATG 5280  
 QY 5281 GTTGGAAATTTCTTTTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 5340  
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 Db 5281 GTTGGAAATTTCTTTTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 5340  
 QY 5341 TACATGCGGCTGATCTCTGAGGATGATGATGATGATGATGATGATGATGATGATGATG 5400  
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 Db 5341 TACATGCGGCTGATCTCTGAGGATGATGATGATGATGATGATGATGATGATGATGATG 5400  
 QY 5401 AGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5460  
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 Db 5401 AGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5460  
 QY 5461 CAGTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5520  
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 Db 5461 CAGTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5520  
 QY 5521 CTGCGCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 5580  
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 Db 5521 CTGCGCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 5580  
 QY 5581 CGGATCCACTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5640  
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 Db 5581 CGGATCCACTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5640  
 QY 5641 GAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5700  
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 Db 5641 GAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5700

QY 5701 GTCTCTATCAGCCAAATCACTACTACTTTAAAGAAACAAAGAGAGATGCTGCTC 5760  
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 Db 5701 GTCTCTATCAGCCAAATCACTACTACTTTAAAGAAACAAAGAGAGATGCTGCTC 5760  
 QY 5761 ATTATTCAGGCTGCTTACAGAGCCACCTTTTAAAGGAACTGTAAACAGCTTCCTT 5820  
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 Db 5761 ATTATTCAGGCTGCTTACAGAGCCACCTTTTAAAGGAACTGTAAACAGCTTCCTT 5820  
 QY 5821 ACCTACATTAATAAACAAGAGAGGCTGATCTTCTTTTAAAGAGACATGATA 5880  
 |||||  
 Db 5821 ACCTACATTAATAAACAAGAGAGGCTGATCTTCTTTTAAAGAGACATGATA 5880  
 QY 5881 ATTGACAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5940  
 |||||  
 Db 5881 ATTGACAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5940  
 QY 5941 GCTTGTCCACCTTCTATGACCGGGTGACAAAGCCAAATTTGTGAAAAACATGAGCAAGAA 6000  
 |||||  
 Db 5941 GCTTGTCCACCTTCTATGACCGGGTGACAAAGCCAAATTTGTGAAAAACATGAGCAAGAA 6000  
 QY 6001 GGCAGAGATGAAAAAGCCAAAGGAAATTA 6030  
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 Db 6001 GGCAGAGATGAAAAAGCCAAAGGAAATTA 6030

RESULT 2  
 US-09-930-871-13  
 ; Sequence 13, Application US/09930871  
 ; Patent No. US20020076780A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Turner, C. Alexander Jr.  
 ; APPLICANT: Mathur, Daniel  
 ; APPLICANT: Mathur, Brian  
 ; TITLE OF INVENTION: No. US20020076780A1 Human Ion Channel Proteins and Polynucle  
 ; FILE REFERENCE: LEX-0216-USA  
 ; CURRENT APPLICATION NUMBER: US/09/930,871  
 ; CURRENT FILING DATE: 2001-08-14  
 ; PRIOR APPLICATION NUMBER: US 60/225,989  
 ; PRIOR FILING DATE: 2000-08-16  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 13  
 ; LENGTH: 5922  
 ; TYPE: DNA  
 ; ORGANISM: homo sapiens  
 ; US-09-930-871-13

Query Match 98.1%; Score 5917; DB 10; Length 5922;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 5917; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGCAAAACACTGCTGTGACACAGACCTGACAGCTTCACTTCCACAGAGAA 60  
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 Db 1 ATGAGCAAAACACTGCTGTGACACAGACCTGACAGCTTCACTTCCACAGAGAA 60  
 QY 61 TCTCTTGGCGCTATTGAAAGACGCTATTGCAAGAAAAAGGCAAGATCCCAACAGAC 120  
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 Db 61 TCTCTTGGCGCTATTGAAAGACGCTATTGCAAGAAAAAGGCAAGATCCCAACAGAC 120  
 QY 121 AAAAAAGATGACAGCAAAAAATGCGCCAAAGCCAAATAGTACTTGGAAAGTGGAAAGAC 180  
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 Db 121 AAAAAAGATGACAGCAAAAAATGCGCCAAAGCCAAATAGTACTTGGAAAGTGGAAAGAC 180  
 QY 181 CTTCATTTATTTATGAGAGCATCTCCAGAGATGATGATGATGATGATGATGATGATGATG 240  
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 Db 181 CTTCATTTATTTATGAGAGCATCTCCAGAGATGATGATGATGATGATGATGATGATGATG 240  
 QY 241 GACCCCTACTATATCAATAAGAACTTTATATGATGATGATGATGATGATGATGATGATG 300  
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 Db 241 GACCCCTACTATATCAATAAGAACTTTATATGATGATGATGATGATGATGATGATGATG 300  
 QY 301 CGGTTCAGTCCACCTCTGCGCTGTGATCTTTTAACTCCCTCAATCCTTAAAGAAATA 360

Db 301 CGGTTCAGTCCACCTCTGCGCTGATCTTTAACTCCCTCAATCTCTTAGAATAATA 360  
 QY 361 GCATTTAGATTTTGTGACATCATTTATGACATGCTATTTATGTCACATTTTGA 420  
 Db 361 GCTATTAGATTTTGTGACATCATTTATGACATGCTATTTATGTCACATTTTGA 420  
 QY 421 AACTGTGTATTGACAAATAGATTAACCTCTGATTTGACAAAGAAATGTGAATAC 480  
 Db 421 AACTGTGTATTGACAAATAGATTAACCTCTGATTTGACAAAGAAATGTGAATAC 480  
 QY 481 TTACAGGAATATATATCTTTGAATCACTTATATAAATATGCAAGGGATCTGT 540  
 Db 481 TTACAGGAATATATATCTTTGAATCACTTATATAAATATGCAAGGGATCTGT 540  
 QY 541 GAAGATTTTCTTCTCCGGAATCCATGGAACCTGGCTCATTTCACTGTCATTA 600  
 Db 541 GAAGATTTTCTTCTCCGGAATCCATGGAACCTGGCTCATTTCACTGTCATTA 600  
 QY 601 GCGTACGTCACAGAGTTGTGACCTGGCAATGTCGCGCATTTGAGAACATTCAG 660  
 Db 601 GCGTACGTCACAGAGTTGTGACCTGGCAATGTCGCGCATTTGAGAACATTCAG 660  
 QY 661 CTCGAGCATTTGAAGCATTTCAATCATTCCAGGCTGAAAACCATTTGGAGCC 720  
 Db 661 CTCGAGCATTTGAAGCATTTCAATCATTCCAGGCTGAAAACCATTTGGAGCC 720  
 QY 721 ATCCAGCTGTGAAGAGCTCTCAGATGTAATGATCTGACTGCTGTCTGAGGTA 780  
 Db 721 ATCCAGCTGTGAAGAGCTCTCAGATGTAATGATCTGACTGCTGTCTGAGGTA 780  
 QY 781 TTGCTCTAATTTGGGCTGACAGCTGTTGATGGCAACCTGAGGAATTAATGAT 840  
 Db 781 TTGCTCTAATTTGGGCTGACAGCTGTTGATGGCAACCTGAGGAATTAATGAT 840  
 QY 841 CCGTCCACCAATGCTCTTGGAGGAACATATATAGAAAAGAAATATACGTGA 900  
 Db 841 CCGTCCACCAATGCTCTTGGAGGAACATATATAGAAAAGAAATATACGTGA 900  
 QY 901 AATGCTACATTTAATATGAACCTGTGATTTGAGTTACACGGAATATATCAAG 960  
 Db 901 AATGCTACATTTAATATGAACCTGTGATTTGAGTTACACGGAATATATCAAG 960  
 QY 961 TCAAGATATCATTTATCTCTGAGAGGTTTATGATGACATCAATATGGAATAG 1020  
 Db 961 TCAAGATATCATTTATCTCTGAGAGGTTTATGATGACATCAATATGGAATAG 1020  
 QY 1021 GATGACAGCCAAATGTCAGAGGATATATGTTGTAAGCTGTGTAGAAATCC 1080  
 Db 1021 GATGACAGCCAAATGTCAGAGGATATATGTTGTAAGCTGTGTAGAAATCC 1080  
 QY 1081 GCGTACACAAGCTTTGATACCTCAAGTTGGGCTTTTTCCTGTTTCCAGTA 1140  
 Db 1081 GCGTACACAAGCTTTGATACCTCAAGTTGGGCTTTTTCCTGTTTCCAGTA 1140  
 QY 1141 CAGGACTTGGGAAAATCTTTATCAACGACATGACATGCTGTGTGGAAGAA 1200  
 Db 1141 CAGGACTTGGGAAAATCTTTATCAACGACATGACATGCTGTGTGGAAGAA 1200  
 QY 1201 AATATTTTGTGTGATCTTTCTTGGGCTCATTTCACTAATTAATTTGAT 1260  
 Db 1201 AATATTTTGTGTGATCTTTCTTGGGCTCATTTCACTAATTAATTTGAT 1260  
 QY 1261 GTGTGTGCTATGCTTACGAGGAACAGAAATCAGGCCACTTGGAAAGAG 1320  
 Db 1261 GTGTGTGCTATGCTTACGAGGAACAGAAATCAGGCCACTTGGAAAGAG 1320  
 QY 1321 GAGGCGCAATTTAGCAGATGATTAACACATTAATAAGCAACGAGGAGCT 1380  
 Db 1321 GAGGCGCAATTTAGCAGATGATTAACACATTAATAAGCAACGAGGAGCT 1380  
 QY 1381 GCAGCAACGGCAATGCTCTGAGAACATTTCCAGAGAGCCAGTGAGGAGGCTCT 1440  
 Db 1381 GCAGCAACGGCAATGCTCTGAGAACATTTCCAGAGAGCCAGTGAGGAGGCTCT 1440  
 Db 1441 GACAGCTCATCTGAGAGCTCTTAAGTTAGTTCCAAAGTGCTTAAGAAAGAA 1500  
 QY 1501 AGGAAGAAAGAAAGAAAGAAAGAGACAGTCTGTTGGGGAAGAAAGATGAG 1560  
 Db 1501 AGGAAGAAAGAAAGAAAGAAAGAGACAGTCTGTTGGGGAAGAAAGATGAG 1560  
 QY 1561 CAAAATCTGATCTGAGACAGCATCAGAGAGAAAGTTTGGCTTCCATTTGA 1620  
 Db 1561 CAAAATCTGATCTGAGACAGCATCAGAGAGAAAGTTTGGCTTCCATTTGA 1620  
 QY 1621 AACGATTTGACATTTGAAAAGAGTACTCTCCCAACACAGTCTTGTGAGAT 1680  
 Db 1621 AACGATTTGACATTTGAAAAGAGTACTCTCCCAACACAGTCTTGTGAGAT 1680  
 QY 1681 GCGTCCCTAATTTTCCAGAGGCGAAATAGCAACAAGCTTTTCACTTTAGAG 1740  
 Db 1681 GCGTCCCTAATTTTCCAGAGGCGAAATAGCAACAAGCTTTTCACTTTAGAG 1740  
 QY 1741 GCAAGAGATGAGGATCTGAGAACGACTTGCAGATGATGACACACACCTTTGAG 1800  
 Db 1741 GCAAGAGATGAGGATCTGAGAACGACTTGCAGATGATGACACACACCTTTGAG 1800  
 QY 1801 AACGAGACCGGTAGATTTCTTTTGTGTCGCCGACGACAGAGAGAGACACAG 1860  
 Db 1801 AACGAGACCGGTAGATTTCTTTTGTGTCGCCGACGACAGAGAGAGACACAG 1860  
 QY 1861 AACCTGATCAGACCATAGGTCATCCCGATGCTGGCAGTGTCCAGGAATGGAG 1920  
 Db 1861 AACCTGATCAGACCATAGGTCATCCCGATGCTGGCAGTGTCCAGGAATGGAG 1920  
 QY 1921 ATGCAAGACAGCTGTGATGCAATGTTGTTGCTTGGTGTGAGACCTTCAGT 1980  
 Db 1921 ATGCAAGACAGCTGTGATGCAATGTTGTTGCTTGGTGTGAGACCTTCAGT 1980  
 QY 1981 ACATCGGCTGTGGACAGCTTTCGCAAGAGTGTATATAGAACAGCTACGATGAC 2040  
 Db 1981 ACATCGGCTGTGGACAGCTTTCGCAAGAGTGTATATAGAACAGCTACGATGAC 2040  
 QY 2041 AATGAAACAACCACTGAAACGAAATGAGAAAGAAAGGTCAGTCTTCCAG 2100  
 Db 2041 AATGAAACAACCACTGAAACGAAATGAGAAAGAAAGGTCAGTCTTCCAG 2100  
 QY 2101 ATGACATTTCTAGAAATCTCTCCCAAGGCAAGCAATGATATAGCAGATCT 2160  
 Db 2101 ATGACATTTCTAGAAATCTCTCCCAAGGCAAGCAATGATATAGCAGATCT 2160  
 QY 2161 ACAATATCAGTAGAAGAACTTGAAGAAATCCAGGAGAAATGCCCTGTGTAT 2220  
 Db 2161 ACAATATCAGTAGAAGAACTTGAAGAAATCCAGGAGAAATGCCCTGTGTAT 2220  
 QY 2221 TTTTCAACATATTTCTTAATCTGGAGCTGTTTCCATATGTTTAAAGTGA 2280  
 Db 2221 TTTTCAACATATTTCTTAATCTGGAGCTGTTTCCATATGTTTAAAGTGA 2280  
 QY 2281 GTCAACCTGTGTGATGAGACCAATTTGTTGAGCTGTCATCACATCTGAT 2340  
 Db 2281 GTCAACCTGTGTGATGAGACCAATTTGTTGAGCTGTCATCACATCTGAT 2340  
 QY 2341 AATATCTTTTCAATGCGCAATGAGACATATCCATGACGACATTTCAAT 2400  
 Db 2341 AATATCTTTTCAATGCGCAATGAGACATATCCATGACGACATTTCAAT 2400  
 QY 2401 ACAGTAGAAGAACTTGTTCACAGGATCTTACAGCAAGAAATGTTTGA 2460  
 Db 2401 ACAGTAGAAGAACTTGTTCACAGGATCTTACAGCAAGAAATGTTTGA 2460  
 QY 2461 GCCATGATCTTACTATTTTCAAGAGGCTGAAATCTTTGACAGGTTTAT 2520  
 Db 2461 GCCATGATCTTACTATTTTCAAGAGGCTGAAATCTTTGACAGGTTTAT 2520



|    |      |  |      |
|----|------|--|------|
| QY | 2521 | ACGCTTACCGCTGGTAGAAGCTTGGACCTCGCCAAATGTGGGAAGATATCTGTCCTCGCTCA | 2580 |
| Db | 2521 | ACGCTTACCGCTGGTAGAAGCTTGGACCTCGCCAAATGTGGGAAGATATCTGTCCTCGCTCA | 2580 |
| QY | 2581 | TTTCGATGCGCGAGCTTTCAAGTTGGCAAAATCTTGCCCAAGCTTAATATGCTAATA      | 2640 |
| Db | 2581 | TTTCGATGCGCGAGCTTTCAAGTTGGCAAAATCTTGCCCAAGCTTAATATGCTAATA      | 2640 |
| QY | 2641 | AAGATCATCGGCATTTCCGCTGGGGGCTCTGGGAAATTTAAACCTGCTTGCCCAATCATC   | 2700 |
| Db | 2641 | AAGATCATCGGCATTTCCGCTGGGGGCTCTGGGAAATTTAAACCTGCTTGCCCAATCATC   | 2700 |
| QY | 2701 | GCTTCATTTTTGCGCGTGGGACATGACGCTTTGTGTAAAAGCTAACAAAGATGTGTCTC    | 2760 |
| Db | 2701 | GCTTCATTTTTGCGCGTGGGACATGACGCTTTGTGTAAAAGCTAACAAAGATGTGTCTC    | 2760 |
| QY | 2761 | TGCAAGATCCGCAGTGTATTTGTCAATCCACGCTGGCACATGATAGACTTCTCCACTCC    | 2820 |
| Db | 2761 | TGCAAGATCCGCAGTGTATTTGTCAATCCACGCTGGCACATGATAGACTTCTCCACTCC    | 2820 |
| QY | 2821 | TTCCGATGTGTGTCGCCGCTGGCTGTGGGGAGTGGATAGACACATGTGGGACTGTATG     | 2880 |
| Db | 2821 | TTCCGATGTGTGTCGCCGCTGGCTGTGGGGAGTGGATAGACACATGTGGGACTGTATG     | 2880 |
| QY | 2881 | GAGGTGCTGTGTCACGCGCATGCTCCTTACTGTGCTTCATGATGTCATGTCGATTTGAAAC  | 2940 |
| Db | 2881 | GAGGTGCTGTGTCACGCGCATGCTCCTTACTGTGCTTCATGATGTCATGTCGATTTGAAAC  | 2940 |
| QY | 2941 | CTAGTGTCTGGAATCTCTTTCTGGCCTTGTCTTGTAGCTCATTTTATGTGCAGACAACCTT  | 3000 |
| Db | 2941 | CTAGTGTCTGGAATCTCTTTCTGGCCTTGTCTTGTAGCTCATTTTATGTGCAGACAACCTT  | 3000 |
| QY | 3001 | GCAGCCACTGATGTGATTAATGAAATGAATTAATCCCAAATGGCTGGGATAGGATGCAC    | 3060 |
| Db | 3001 | GCAGCCACTGATGTGATTAATGAAATGAATTAATCCCAAATGGCTGGGATAGGATGCAC    | 3060 |
| QY | 3061 | AAAGAGTAGCTTATGTGAAAGAAAAATATGATTAATTAATCAACAGCTCCTTCATTAGG    | 3120 |
| Db | 3061 | AAAGAGTAGCTTATGTGAAAGAAAAATATGATTAATTAATCAACAGCTCCTTCATTAGG    | 3120 |
| QY | 3121 | AAACAAAAGATTTTAACTGAAATTTAAACCACTTGATGATCTTAACACAGAAAAGACAGT   | 3180 |
| Db | 3121 | AAACAAAAGATTTTAACTGAAATTTAAACCACTTGATGATCTTAACACAGAAAAGACAGT   | 3180 |
| QY | 3181 | TGTATGTCCATCATATCARGAAGAAATTTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT | 3240 |
| Db | 3181 | TGTATGTCCATCATATCARGAAGAAATTTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT | 3240 |
| QY | 3241 | GGAACCTCAAGTGTGTATAGCAACTGTGCACACAGTGTGTAAGAAATACATATTGATGAAGT | 3300 |
| Db | 3241 | GGAACCTCAAGTGTGTATAGCAACTGTGCACACAGTGTGTAAGAAATACATATTGATGAAGT | 3300 |
| QY | 3301 | GATTACATGTCATTCATATAACCAACCCCACTCTTACTGTGACTGTAGCAAAATGCTGTAGA | 3360 |
| Db | 3301 | GATTACATGTCATTCATATAACCAACCCCACTCTTACTGTGACTGTAGCAAAATGCTGTAGA | 3360 |
| QY | 3361 | GAATCTGACTTTGAAAATTTTAAACACGGAAGCTTTATTAATGATGGGATCTGTGAAGAA   | 3420 |
| Db | 3361 | GAATCTGACTTTGAAAATTTTAAACACGGAAGCTTTATTAATGATGGGATCTGTGAAGAA   | 3420 |
| QY | 3421 | AGCAAAAGAGAACTGATGAAGCAAGCTACTCATAGAAAGGTAGCACTGTGGACATCGGC    | 3480 |
| Db | 3421 | AGCAAAAGAGAACTGATGAAGCAAGCTACTCATAGAAAGGTAGCACTGTGGACATCGGC    | 3480 |
| QY | 3481 | GCACCTGTAGAGAACAGCCCGTAGTGGAACTGTGAAGAACTCTTGAACCGAAGCTGTGT    | 3540 |
| Db | 3481 | GCACCTGTAGAGAACAGCCCGTAGTGGAACTGTGAAGAACTCTTGAACCGAAGCTGTGT    | 3540 |
| QY | 3541 | TTTCACTGAAGCGCTGTACAAAGATTTCAAGTGTCTTCAAAATCTGTGGGAAGAGCGACA   | 3600 |
| Db | 3541 | TTTCACTGAAGCGCTGTACAAAGATTTCAAGTGTCTTCAAAATCTGTGGGAAGAGCGACA   | 3600 |

|    |      |               |                                     |  |            |        |      |
|----|------|---------------|-------------------------------------|--|------------|--------|------|
| QY | 3601 | GGAAACAACTG   | GTGGAACCTG                          | GAGAGACGCTGTTTCCGAATAGT                | GAAACAACTG | GTGTTT | 3660 |
| Db | 3601 | GGAAAAACAATG  | GTGGAACCTG                          | GAGAGAGACGCTGTTTCCGAATAGT              | GAAACAACTG | GTGTTT | 3660 |
| QY | 3661 | GAGACCTTCATG  | TGTTTTCATG                          | ATTCCTCTAGTAGAGGGGCTCTGGCATTTAAACATATA |            |        | 3720 |
| Db | 3661 | GAGACCTTCATG  | TGTTTTCATG                          | ATTCCTCTAGTAGAGGGGCTCTGGCATTTAAACATATA |            |        | 3720 |
| QY | 3721 | TATATGTATG    | ACGCAAAAGAGATTTA                    | GACGATTTGGAATATGCTACAAAGGTTTTCCT       |            |        | 3780 |
| Db | 3721 | TATATGTATG    | ACGCAAAAGAGATTTA                    | GACGATTTGGAATATGCTACAAAGGTTTTCCT       |            |        | 3780 |
| QY | 3781 | TACATTTTCATTC | TGCGAAATGCTCTTAATATGGGTGGCATATG     | GGCATCAAAACATATTTCC                    |            |        | 3840 |
| Db | 3781 | TACATTTTCATTC | TGCGAAATGCTCTTAATATGGGTGGCATATG     | GGCATCAAAACATATTTCC                    |            |        | 3840 |
| QY | 3841 | ACCAATGCGTGG  | GTGTTTGGGCTGGACCTCTTAATGTGATG       | TTTCATGTTGCTACGTTTAA                   |            |        | 3900 |
| Db | 3841 | ACCAATGCGTGG  | GTGTTTGGGCTGGACCTCTTAATGTGATG       | TTTCATGTTGCTACGTTTAA                   |            |        | 3900 |
| QY | 3901 | GCAATGCGCTGG  | GTGTTTACTCAGAACTTGGAGCATCAAAATCTCTG | AGGACATAGACT                           |            |        | 3960 |
| Db | 3901 | GCAATGCGCTGG  | GTGTTTACTCAGAACTTGGAGCATCAAAATCTCTG | AGGACATAGACT                           |            |        | 3960 |
| QY | 3961 | CTGAGACCTCTTA | GAGCCTTATCTCGATTTGAAGGATGAGG        | TGGTGTGATGCTCCCTT                      |            |        | 4020 |
| Db | 3961 | CTGAGACCTCTTA | GAGCCTTATCTCGATTTGAAGGATGAGG        | TGGTGTGATGCTCCCTT                      |            |        | 4020 |
| QY | 4021 | TTAGAGCAATTC  | ATCCATCATGATATG                     | TGCTCTGTTGTCTTATATCTG                  | GCTAATTT   |        | 4080 |
| Db | 4021 | TTAGAGCAATTC  | ATCCATCATGATATG                     | TGCTCTGTTGTCTTATATCTG                  | GCTAATTT   |        | 4080 |
| QY | 4081 | TTACAGCATCATG | GGCGGTAATTTGTGCGGGCAATTTAC          | ACATGATTAACCCACA                       |            |        | 4140 |
| Db | 4081 | TTACAGCATCATG | GGCGGTAATTTGTGCGGGCAATTTAC          | ACATGATTAACCCACA                       |            |        | 4140 |
| QY | 4141 | ACTGGTACAG    | GTGTTGACATCGAAGACGTGAATATCATATCTG   | ATGCTTAAACTATA                         |            |        | 4200 |
| Db | 4141 | ACTGGTACAG    | GTGTTGACATCGAAGACGTGAATATCATATCTG   | ATGCTTAAACTATA                         |            |        | 4200 |
| QY | 4201 | GAAAGAAATG    | AGACTGCTGCATG                       | GAAGAAATGTGAAGTAACTTTGATTAATGTAG       | ATTT       |        | 4260 |
| Db | 4201 | GAAAGAAATG    | AGACTGCTGCATG                       | GAAGAAATGTGAAGTAACTTTGATTAATGTAG       | ATTT       |        | 4260 |
| QY | 4261 | GGGATATCTCTT  | GGCTTCAAGTTGGCAATTC                 | CAAGATGGAATGATATATG                    | ATGATGCA   |        | 4320 |
| Db | 4261 | GGGATATCTCTT  | GGCTTCAAGTTGGCAATTC                 | CAAGATGGAATGATATATG                    | ATGATGCA   |        | 4320 |
| QY | 4321 | GCACTTATTC    | ACGAATATGTGAACCTCCAGCTAAGTATG       | AGAAGATCTG                             | ATCATGAT   |        | 4380 |
| Db | 4321 | GCACTTATTC    | ACGAATATGTGAACCTCCAGCTAAGTATG       | AGAAGATCTG                             | ATCATGAT   |        | 4380 |
| QY | 4381 | CTTACTTGTAT   | TTTTCATCATCTTTGGGCTCTTCC            | ACCTGAAACCTGTATTTGGT                   |            |        | 4440 |
| Db | 4381 | CTTACTTGTAT   | TTTTCATCATCTTTGGGCTCTTCC            | ACCTGAAACCTGTATTTGGT                   |            |        | 4440 |
| QY | 4441 | GTCATCTAG     | CTATATTTCAACCGGCAAGAAAGATTTG        | GAAGGTCAGACATCTTTATG                   |            |        | 4500 |
| Db | 4441 | GTCATCTAG     | CTATATTTCAACCGGCAAGAAAGATTTG        | GAAGGTCAGACATCTTTATG                   |            |        | 4500 |
| QY | 4501 | ACAGAAACAG    | AAGAATACTTAATGCAATGA                | AAAAATTTAGATCGAAAAACCCGAA              |            |        | 4560 |
| Db | 4501 | ACAGAAACAG    | AAGAATACTTAATGCAATGA                | AAAAATTTAGATCGAAAAACCCGAA              |            |        | 4560 |
| QY | 4561 | AAGCCTATAC    | CTGACAGGAAACAAATTTCAAGAAATG         | GTCTTGACTTGTAACAGA                     |            |        | 4620 |
| Db | 4561 | AAGCCTATAC    | CTGACAGGAAACAAATTTCAAGAAATG         | GTCTTGACTTGTAACAGA                     |            |        | 4620 |
| QY | 4621 | CAAGTTTTC     | ACATTAAGCATATGATTC                  | CAATCTGTTTAACATG                       | GTGACATATG | GTG    | 4680 |
| Db | 4621 | CAAGTTTTC     | ACATTAAGCATATGATTC                  | CAATCTGTTTAACATG                       | GTGACATATG | GTG    | 4680 |
| QY | 4681 | GAAACAGATAC   | CAGAGTGAATATG                       | TGATACATTTTGTACG                       | GATCAATCTG | GTG    | 4740 |



|    |      |   |      |
|----|------|---|------|
| Db | 4681 | GAAGAGATACAGAGTGAATATGAGCTACACTTTGTGCAGGATCAATCTGTGCTC      | 4740 |
| OY | 4741 | ATTGTGCTATTACTGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTT   | 4800 |
| Db | 4741 | ATTGTGCTATTACTGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTT   | 4800 |
| OY | 4801 | ACCAATTGAGGAATATTTTATTTGATTTGGGTGTGCATCTCTCATGTGTGATATTT    | 4860 |
| Db | 4801 | ACCAATTGAGGAATATTTTATTTGATTTGGGTGTGCATCTCTCATGTGTGATATTT    | 4860 |
| OY | 4861 | CTTGCCAGCTGATATAAAAGATTATTCGTGTCCCTTACCCTGTTCGAGTATCCGTCT   | 4920 |
| Db | 4861 | CTTGCCAGCTGATATAAAAGATTATTCGTGTCCCTTACCCTGTTCGAGTATCCGTCT   | 4920 |
| OY | 4921 | GCTAGATTGGCGAAATCCTAGCTGTGATCAAAAGAGCAAAAGGGATCCGACGCTGTC   | 4980 |
| Db | 4921 | GCTAGATTGGCGAAATCCTAGCTGTGATCAAAAGAGCAAAAGGGATCCGACGCTGTC   | 4980 |
| OY | 4981 | TTTCTCTGATGATGTCCCTCTCTGTGGTGTTTAACTACGTGGCTCTCTCTTCTCTGTC  | 5040 |
| Db | 4981 | TTTCTCTGATGATGTCCCTCTCTGTGGTGTTTAACTACGTGGCTCTCTCTTCTCTGTC  | 5040 |
| OY | 5041 | ATGTTCATCAACGCATCTTTGGAGTGTCCAACTTGTGCTATGTATAAGGAAGTTGGG   | 5100 |
| Db | 5041 | ATGTTCATCAACGCATCTTTGGAGTGTCCAACTTGTGCTATGTATAAGGAAGTTGGG   | 5100 |
| OY | 5101 | ATCGATGACATGTTCAACTTTTGAGACCTTTGGCAACAGATGATCTGCTATTCGAAT   | 5160 |
| Db | 5101 | ATCGATGACATGTTCAACTTTTGAGACCTTTGGCAACAGATGATCTGCTATTCGAAT   | 5160 |
| OY | 5161 | ACAACCTCTGTGTGGTGGATGGATGTGTCTAGACACCATCTCTCACATGAACACCGAC  | 5220 |
| Db | 5161 | ACAACCTCTGTGTGGTGGATGGATGTGTCTAGACACCATCTCTCACATGAACACCGAC  | 5220 |
| OY | 5221 | TGTACCCCTAATAAGTTAACCTGTGAAGCTCAGTTAAGGGAGATGTGGGAACCATCT   | 5280 |
| Db | 5221 | TGTACCCCTAATAAGTTAACCTGTGAAGCTCAGTTAAGGGAGATGTGGGAACCATCT   | 5280 |
| OY | 5281 | GTTGGAATTTTCTTTTGTCACTGTACATCATCATCTCTCTGTGTGGTGTGAACATG    | 5340 |
| Db | 5281 | GTTGGAATTTTCTTTTGTCACTGTACATCATCATCTCTCTGTGTGGTGTGAACATG    | 5340 |
| OY | 5341 | TACATCGCGGTCACTCTGAGAACTTCACTGTTGCTACTGAAAGAAAGTGCAGAGCTGTG | 5400 |
| Db | 5341 | TACATCGCGGTCACTCTGAGAACTTCACTGTTGCTACTGAAAGAAAGTGCAGAGCTGTG | 5400 |
| OY | 5401 | AGTGAAGTACTTTGAGATGTCTCTAGAGGTTTGGGAAATTTGATCCCGATGCAACT    | 5460 |
| Db | 5401 | AGTGAAGTACTTTGAGATGTCTCTAGAGGTTTGGGAAATTTGATCCCGATGCAACT    | 5460 |
| OY | 5461 | CAGTTCATGGAATTTGAAAAATTATCCATGATTGTGCGAGCTGTGAACCCGCTCTCAT  | 5520 |
| Db | 5461 | CAGTTCATGGAATTTGAAAAATTATCCATGATTGTGCGAGCTGTGAACCCGCTCTCAT  | 5520 |
| OY | 5521 | CTGCGACAACCAAACTCCAGCTCATTTGCCATGATTTGCCATGGTGAAGTGTGAC     | 5580 |
| Db | 5521 | CTGCGACAACCAAACTCCAGCTCATTTGCCATGATTTGCCATGGTGAAGTGTGAC     | 5580 |
| OY | 5581 | CGGATCCACTGTCTTGTATCTTATTGTCTTTTACAAACGGGGTCTGTGGAAGTGTGA   | 5640 |
| Db | 5581 | CGGATCCACTGTCTTGTATCTTATTGTCTTTTACAAACGGGGTCTGTGGAAGTGTGA   | 5640 |
| OY | 5641 | GAGATGATGTGCTACGAATACAGATGGAAGAGCGATGTATGSGTCCAACTCTCCAAAG  | 5700 |
| Db | 5641 | GAGATGATGTGCTACGAATACAGATGGAAGAGCGATGTATGSGTCCAACTCTCCAAAG  | 5700 |
| OY | 5701 | GTCCTCATCAGCCATCACTACTACTTTAAACGAAAAACAAGAGAGTATCTGCTGTC    | 5760 |
| Db | 5701 | GTCCTCATCAGCCATCACTACTACTTTAAACGAAAAACAAGAGAGTATCTGCTGTC    | 5760 |
| OY | 5761 | ATTATTCAGGTGTTACAGAGCCACTTTTAAAGCAACTGTAAAAACAGCTTCTTT      | 5820 |

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Db      5761 ATTATTCAGCCGCTTACAGAGCCACCTTTTAAAGCGAATGTAAACACCTTCCTT 5820
QY      5821 ACGTACAAATATAAAACAAATTCAAAGGTGGGGCTAATCTTATATATAAAACATGATA 5880
Db      5821 ACGTACAAATATAAAACAAATTCAAAGGTGGGGCTAATCTTATATATAAAACATGATA 5880
QY      5881 ATTGACAGAAATATATGAATACTATTTACAGAAAAA 5917
Db      5881 ATTGACAGAAATATATGAATACTATTTACAGAAAAA 5917

RESULT 3
US-09-930-871-15
; Sequence 15, Application US/09930871
; Patent No. US20020076780A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Daniel
; APPLICANT: Mathur, Brian
; TITLE OF INVENTION: No. US20020076780A1el Human Ion Channel Proteins and Polynucle
; FILE REFERENCE: Lex-0216-USA
; CURRENT APPLICATION NUMBER: US/09/930,871
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225,989
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 4362
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-930-871-15

Query Match      71.9%; Score 4338; DB 10; Length 4362;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATGGAGCAAAAGTGGCTTGTACCAAGAGACCTGACAGCTTCAACTCTTACACAGAGAA 60
Db      1 ATGGAGCAAAAGTGGCTTGTACCAAGAGACCTGACAGCTTCAACTCTTACACAGAGAA 60
QY      61 TCTCTGGCGCTATTTAAAGAGCGATTCGAGAAAGAAAGGCAAGAAATCCCAACAGAC 120
Db      61 TCTCTGGCGCTATTTAAAGAGCGATTCGAGAAAGAAAGGCAAGAAATCCCAACAGAC 120
QY      121 AAAAAAGATGAGAGCAAGAAATGGCCCAAGCCAAATATGACTTGGAAAGCTGGAAGAAC 180
Db      121 AAAAAAGATGAGAGCAAGAAATGGCCCAAGCCAAATATGACTTGGAAAGCTGGAAGAAC 180
QY      181 CTTCATTTATTTATGAGAGCATTCCTCCAGAGATGGTGTACAGAGCCCTGAGAGACTG 240
Db      181 CTTCATTTATTTATGAGAGCATTCCTCCAGAGATGGTGTACAGAGCCCTGAGAGACTG 240
QY      241 GACCCCTACTATATCAATAAGAAACTTTATATGTTTGAATTAAGGAAAGGCAATCTTC 300
Db      241 GACCCCTACTATATCAATAAGAAACTTTATATGTTTGAATTAAGGAAAGGCAATCTTC 300
QY      301 CGGTGAGGCAACCTGCGCTGATCAATTTTAACGCCCTCAATGCTCTTAGAAAAAT 360
Db      301 CGGTGAGGCAACCTGCGCTGATCAATTTTAACGCCCTCAATGCTCTTAGAAAAAT 360
QY      361 GGTATTAAGATTTTGTATATTCATTCATTTACAGCATCTAATTTTGTGCACTATTTGACA 420
Db      361 GGTATTAAGATTTTGTATATTCATTCATTTACAGCATCTAATTTTGTGCACTATTTGACA 420
QY      421 AACTGTGTATTATGACAAATGAGTAAACCTCCTGATTTGACAAAGAAATGTAGATAACCC 480
Db      421 AACTGTGTATTATGACAAATGAGTAAACCTCCTGATTTGACAAAGAAATGTAGATAACCC 480
QY      481 TTCACGGAATATATCTTTTGAATGACATTAATAAATTAATTCAGAGGGGATCTCTTTA 540
Db      481 TTCACGGAATATATCTTTTGAATGACATTAATAAATTAATTCAGAGGGGATCTCTTTA 540

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QY 541 GAAGATTACTTCTTCCGCGATCCATGAACTGGCTCGATTCTGATTCATTCATTT 600  
Db 541 GAAGATTACTTCTTCCGCGATCCATGAACTGGCTCGATTCTGATTCATTCATTT 600  
QY 601 GCGTACGTCACAGAGTTGTGACCTGGGCAATGTCGCGATGAGAACTTCAGACTT 660  
Db 601 GCGTACGTCACAGAGTTGTGACCTGGGCAATGTCGCGATGAGAACTTCAGACTT 660  
QY 661 CTCCGAGCATTAAGAGAGTTTCAGTCATTCAGGCTGAAACCATTTGGAGCCCTG 720  
Db 661 CTCCGAGCATTAAGAGAGTTTCAGTCATTCAGGCTGAAACCATTTGGAGCCCTG 720  
QY 721 ATCCAGTCTGGAAGAGCTCTCAGATGTAATGATCTGACTGTGTCTGTCGAGCTA 780  
Db 721 ATCCAGTCTGGAAGAGCTCTCAGATGTAATGATCTGACTGTGTCTGTCGAGCTA 780  
QY 781 TTTCCTCAATTTGGGCTGACCTGTCTCATGCGCAACCGAGAGTAATGTAATCAATGG 840  
Db 781 TTTCCTCAATTTGGGCTGACCTGTCTCATGCGCAACCGAGAGTAATGTAATCAATGG 840  
QY 841 CCTCCCAACCAATGCTTCTTGGAGAAACATAGTATAGAAAAGTAATTAAGTGAATTA 900  
Db 841 CCTCCCAACCAATGCTTCTTGGAGAAACATAGTATAGAAAAGTAATTAAGTGAATTA 900  
QY 901 AATGCTACCTTAATTAATGAATGCTCTTTGAGTTGATGCTGAAAGTCATATATCAAGAT 960  
Db 901 AATGCTACCTTAATTAATGAATGCTCTTTGAGTTGATGCTGAAAGTCATATATCAAGAT 960  
QY 961 TCAAGATATCATTAATTTCTCTGAGGAGTTTATAGTACACATATGAGAAATAGCTCT 1020  
Db 961 TCAAGATATCATTAATTTCTCTGAGGAGTTTATAGTACACATATGAGAAATAGCTCT 1020  
QY 1021 GATGACAGGCCAATGTCAGAGGAGATATATGCTGAAAGTGTAGAAAATCCCAATTA 1080  
Db 1021 GATGACAGGCCAATGTCAGAGGAGATATATGCTGAAAGTGTAGAAAATCCCAATTA 1080  
QY 1081 GCGTACCAAGCTTGTATACCTTATGTTGGCTTTTGTCTCTGTTTGCATATGACT 1140  
Db 1081 GCGTACCAAGCTTGTATACCTTATGTTGGCTTTTGTCTCTGTTTGCATATGACT 1140  
QY 1141 CAGGACTTCTGGGAAATCTTTATCACTGACATTAAGTGTCTGGGAAACCTAATG 1200  
Db 1141 CAGGACTTCTGGGAAATCTTTATCACTGACATTAAGTGTCTGGGAAACCTAATG 1200  
QY 1201 AATATTTTGTGTGTGCTATTTCTTGGGCTCATTTACCTTAATTAATTTGATCTGCT 1260  
Db 1201 AATATTTTGTGTGTGCTATTTCTTGGGCTCATTTACCTTAATTAATTTGATCTGCT 1260  
QY 1261 GTGCTGGCCATGCGCTACGAGAAACAGATACAGGCCACTTGGAAAGACAGAA 1320  
Db 1261 GTGCTGGCCATGCGCTACGAGAAACAGATACAGGCCACTTGGAAAGACAGAA 1320  
QY 1321 GAGGCCAATTTACGAGATGATTAAGCACTTAAAGAAACAGAGGAGAGCTCAGAG 1380  
Db 1321 GAGGCCAATTTACGAGATGATTAAGCACTTAAAGAAACAGAGGAGAGCTCAGAG 1380  
QY 1381 GCAAGCAACGGCACTGCTCAGAACTTCAGAGAGGCCAGTGCAGAGGAGAGCTCTCA 1440  
Db 1381 GCAAGCAACGGCACTGCTCAGAACTTCAGAGAGGCCAGTGCAGAGGAGAGCTCTCA 1440  
QY 1441 GAAAGCTCATCTGAAGCTTAAAGTTGATTCAGAGAGTCTTAAGAAAGAAATCGG 1500  
Db 1441 GAAAGCTCATCTGAAGCTTAAAGTTGATTCAGAGAGTCTTAAGAAAGAAATCGG 1500  
QY 1501 AGGAAGAAAGAAAGAAAGAGAGAGCTGCTGGGGAAGAGAAAGATGAGATTC 1560  
Db 1501 AGGAAGAAAGAAAGAAAGAGAGAGCTGCTGGGGAAGAGAAAGATGAGATTC 1560  
QY 1561 CAAAAATCTGAATCTGAGAGACAGCATCAGAGAGAAAGTTTCTGCTTCCATTTGAAGG 1620  
Db 1561 CAAAAATCTGAATCTGAGAGACAGCATCAGAGAGAAAGTTTCTGCTTCCATTTGAAGG 1620

QY 1621 AACGATTGACATATGAAAGAGGTACTCTCCACACAGCTCTTTGTGAGCATCCG 1680  
Db 1621 AACGATTGACATATGAAAGAGGTACTCTCCACACAGCTCTTTGTGAGCATCCG 1680  
QY 1681 GCGTCCCTATTTTACCAAGCGGAATATGCAAGAACCTTTTACGTTTGAAGGCGA 1740  
Db 1681 GCGTCCCTATTTTACCAAGCGGAATATGCAAGAACCTTTTACGTTTGAAGGCGA 1740  
QY 1741 GCAAGAGATGGGATCGAGAACGACTCCGAGATGATGAGCAGACACTTTGAGAT 1800  
Db 1741 GCAAGAGATGGGATCGAGAACGACTCCGAGATGATGAGCAGACACTTTGAGAT 1800  
QY 1801 AACGAGCCCTAGAGATTCCTTGTGTGGCCGACACAGCGAGAGAGCGAACAGC 1860  
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Db 4321 GCAGTTGATTCAGAAAT 4338

RESULT 4
US-09-930-871-17
; Sequence 17, Application US/09930871
; Patent No. US20020076780A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0216-USA
; CURRENT APPLICATION NUMBER: US/09/930,871
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225,989
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 4179
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-930-871-17

Query Match 68.9%; Score 4152; DB 10; Length 4179;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 ATGAGCAACAGAGCTGTATCCAGCAGAGCTGACAGCTTCAACTCTTACACAGAGAA 60
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DB 361 GCTATTAGATTTTGTGATCAATCTATATGACATGCTAATTAATGTCACATTTTGACA 420  
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QY 4141 ACTGTGACAGG 4152  
Db 4141 ACTGTGACAGG 4152

RESULT 5  
US-09-930-871-19  
; Sequence 19, Application US/09930871  
; Patent No. US20020076780A1  
; GENERAL INFORMATION:  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Mathur, Brian  
; TITLE OF INVENTION: Same  
; FILE REFERENCE: LEX-0216-USA  
; CURRENT APPLICATION NUMBER: US/09/930,871  
; PRIOR APPLICATION NUMBER: US 60/225,989  
; PRIOR FILING DATE: 2000-08-16  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 19



LENGTH: 4197  
TYPE: DNA  
ORGANISM: homo sapiens  
US-09-930-871-19

Query Match 66.4%; Score 4003; DB 10; Length 4197;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4003; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 AAAAAAGATGACGACGCAAAATGCGCCAAAGCCAAATAGTACTTGGAGCTGGAAGAAC 180  
DB 121 AAAAAAGATGACGACGCAAAATGCGCCAAAGCCAAATAGTACTTGGAGCTGGAAGAAC 180

QY 181 CTTCATTTATTTATGAGAGCATCTCCAGAGATGTTGACAGAGCCCTGGAGAGCTG 240  
DB 181 CTTCATTTATTTATGAGAGCATCTCCAGAGATGTTGACAGAGCCCTGGAGAGCTG 240

QY 241 GACCCCTACTATATCAATAAGAAACTTTTATATGATTAAGATTAAGGAGGCACTTTC 300  
DB 241 GACCCCTACTATATCAATAAGAAACTTTTATATGATTAAGATTAAGGAGGCACTTTC 300

QY 301 CGGTTAGAGCCACCTGCGCTGATCAATTTTAACTCCCTCAATCCTCTAGAGAAATA 360  
DB 301 CGGTTAGAGCCACCTGCGCTGATCAATTTTAACTCCCTCAATCCTCTAGAGAAATA 360

QY 361 GCTATTAGATTTTGTGTACATTCATTTATTCAGCATGCTATTAATGTGACTATTTTGACA 420  
DB 361 GCTATTAGATTTTGTGTACATTCATTTATTCAGCATGCTATTAATGTGACTATTTTGACA 420

QY 421 AACTGTGTGTTTATGACAAATGATTAACCTCCTGATTGGACAAAGATAGTAATACACC 480  
DB 421 AACTGTGTGTTTATGACAAATGATTAACCTCCTGATTGGACAAAGATAGTAATACACC 480

QY 481 TTCACAGGATATATCTTTTGAATCACTTATTAATAAATTAATGCAAGGGATCTGTATA 540  
DB 481 TTCACAGGATATATCTTTTGAATCACTTATTAATAAATTAATGCAAGGGATCTGTATA 540

QY 541 GAAGATTTTACTTCTCGGGATCCATGGAAGTGGCTGATTTCACTGCTATTAATTT 600  
DB 541 GAAGATTTTACTTCTCGGGATCCATGGAAGTGGCTGATTTCACTGCTATTAATTT 600

QY 601 GCGTACGTCACAGAGTTTGTGACCTGGGCAATGTCTCGGCATTTGAGAAACATTCAGAGTT 660  
DB 601 GCGTACGTCACAGAGTTTGTGACCTGGGCAATGTCTCGGCATTTGAGAAACATTCAGAGTT 660

QY 661 CTCGAGCATTTGAAGAGATTTTCAGTCATTCAGAGCTGAAACCAATTTGGGAGAGCCCTG 720  
DB 661 CTCGAGCATTTGAAGAGATTTTCAGTCATTCAGAGCTGAAACCAATTTGGGAGAGCCCTG 720

QY 721 ATCCAGTCTGTGAAGAGCTCTCAGATGTATATGATCTGCTGCTGTCTGTGAGAGCTGA 780  
DB 721 ATCCAGTCTGTGAAGAGCTCTCAGATGTATATGATCTGCTGCTGTCTGTGAGAGCTGA 780

QY 781 TTTTGTCTAATTTGGGCTGACGCTGTTTCATGGGCAACCTGAGAAATATATATCAATG 840  
DB 781 TTTTGTCTAATTTGGGCTGACGCTGTTTCATGGGCAACCTGAGAAATATATATCAATG 840

QY 841 CCGCCCAACAAGCTCTCTGAGGAAACATAGATAGAAAAAATTAATCTGTGAATTTAT 900  
DB 841 CCGCCCAACAAGCTCTCTGAGGAAACATAGATAGAAAAAATTAATCTGTGAATTTAT 900

QY 901 AATGTATACCTTATTAATGAAATGAACTGCTTGAATTTGAGTGAAGTCAATATATTAAGAT 960  
DB 901 AATGTATACCTTATTAATGAAATGAACTGCTTGAATTTGAGTGAAGTCAATATATTAAGAT 960

QY 961 TCAAGATATCATTTTCCGAGAGGTTTTTATGATGCACTACTATGTGAATTAAGTCT 1020  
DB 961 TCAAGATATCATTTTCCGAGAGGTTTTTATGATGCACTACTATGTGAATTAAGTCT 1020

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DB 1021 GATGACGGCCAAATGTCAGAGGATATATGTGTGAAGAGCTGTGAATCCCAATTAAT 1080

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DB 1081 GGTCTACAAAGCTTTATATCTTCACTTGGGCTTTTGTCTTGTGCTTGTGACTAATGACT 1140

QY 1141 CAGGACTCTGGGAAATCTTTATCACTGACATTAAGTGTGCTGTGGAAATGTCATG 1200  
DB 1141 CAGGACTCTGGGAAATCTTTATCACTGACATTAAGTGTGCTGTGGAAATGTCATG 1200

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QY 1381 GCAGCAAGGGCAATGCTCAGAGAACTTCCAGAGAGCCCAAGTGCACAGAGGAGCTCTCA 1440  
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QY 1441 GACAGCTCATCTGAAGCCTCTAAGTTAGTTCCAAAGAGTCTTAAGAAAGAAATAATCG 1500  
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QY 1621 AACCGATGACATATGAAGAGAGTACTCTCCACACAGCTTGTGTTGAGCATCCGT 1680  
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DB 1801 AACGAGAGCGGTAGAGATCTTGTGTTGCCCCGAGACAGAGGAGAGAGAGCAACAGAC 1860

QY 1861 AACCTGAGTCAGACAGATGATGATCCCGAGATCTGAGAGTGTTCACAGAGATGGGAAG 1920  
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QY 1921 ATGCAAGACACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980  
DB 1921 ATGCAAGACACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980

QY 1981 ACATGCTGTGTGAGACAGCTTCTGACAGAGGATATATGATTAAGCAGCTACTGATGAC 2040  
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QY 2101 AATGACATTTCTGAAAGATTCCTCCAAAGGCAAGACATATAGTATACCCAGATTCGA 2160  
Db 2101 AATGACATTTCTGAAAGATTCCTCCAAAGGCAAGACATATAGTATACCCAGATTCGA 2160  
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Db 2401 ACAGTAGAAGAACTGATTTTCTACTGAGATCTTTACAGCAAGAAATGTTCTGAAATATAT 2460  
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QY 2581 TTTGATGCTGAGATTTTCAAGTTGCAAGTATGCAAGTATGCTTAATATGCTTAAT 2640  
Db 2581 TTTGATGCTGAGATTTTCAAGTTGCAAGTATGCAAGTATGCTTAATATGCTTAAT 2640  
QY 2641 AAGATCATGCGCAATTTCCCTGAGGCTGCGGAAATTTAAACCTCTCTGCGCAATC 2700  
Db 2641 AAGATCATGCGCAATTTCCCTGAGGCTGCGGAAATTTAAACCTCTCTGCGCAATC 2700  
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Db 2701 GCTTCATTTTGGCGGTGCGGAGTCCGCTTTGTTGTTAAAGTATGCTTATGCTT 2760  
QY 2761 TCGAAGATGCGCAGATGATGCAACTCCACGCTGCGCATGATGATCTTCTCCACTCC 2820  
Db 2761 TCGAAGATGCGCAGATGATGCAACTCCACGCTGCGCATGATGATCTTCTCCACTCC 2820  
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Db 2821 TTTCTGATTTGTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2880  
QY 2881 GAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2940  
Db 2881 GAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2940  
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QY 3001 GCAGCCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3060  
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Db 3061 AAGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3120  
QY 3121 AAGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3180  
Db 3121 AAGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3180

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Db 3241 GGAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3300  
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QY 3361 GAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3420  
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Db 3421 ACCAAGAGAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3480  
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QY 3541 TTTACTGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3600  
Db 3541 TTTACTGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3600  
QY 3601 GGAAGAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3660  
Db 3601 GGAAGAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3660  
QY 3661 GAGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3720  
Db 3661 GAGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3720  
QY 3721 TATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3780  
Db 3721 TATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3780  
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Db 3781 TACATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3840  
QY 3841 ACCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3900  
Db 3841 ACCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3900  
QY 3901 GCAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3960  
Db 3901 GCAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3960  
QY 3961 CTGAGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4003  
Db 3961 CTGAGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4003

RESULT 6  
US-09-930-871-1  
; Sequence 1, Application US/09930871  
; Patent No. US2002076780A1  
; GENERAL INFORMATION:  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Mathur, Daniel  
; TITLE OF INVENTION: Same  
; FILE REFERENCE: LEX-0216-USA  
; CURRENT APPLICATION NUMBER: US/09/930,871  
; CURRENT FILING DATE: 2001-08-14  
; PRIOR APPLICATION NUMBER: US 60/225,989

PRIOR FILING DATE: 2000-08-16  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 5997  
TYPE: DNA  
ORGANISM: homo sapiens  
US-09-930-871-1

Query Match 66.1%; Score 3987; DB 10; Length 5997;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3987; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2044 GGAACAACCACTGAACTGAAATGAGAAAGAGAGGTCAAGTTCTTCCACGTTCCATG 2103  
DB 2011 GGAACAACCACTGAACTGAAATGAGAAAGAGAGGTCAAGTTCTTCCACGTTCCATG 2070  
QY 2104 GACTTCTAGAGATCTCTCCCAAGGCAACGACATGATGATGACCATTTCTTACA 2163  
DB 2071 GACTTCTAGAGATCTCTCCCAAGGCAACGACATGATGATGACCATTTCTTACA 2130  
QY 2164 AATACAGTGAAGACTGGAAGATCCAGGCAAGATGCCACCTGGTGGTAAATTT 2223  
DB 2131 AATACAGTGAAGACTGGAAGATCCAGGCAAGATGCCACCTGGTGGTAAATTT 2190  
QY 2224 TCCACATATCTTAAATCTGGGAGCTGTCATATTTGTTAAAGTGAACATGTTGTC 2283  
DB 2191 TCCACATATCTTAAATCTGGGAGCTGTCATATTTGTTAAAGTGAACATGTTGTC 2250  
QY 2284 AACCTGGTGTGATGAGACCCATTTGTTGACCTGGCCATCCATCTGTATTTGTTAAAT 2343  
DB 2251 AACCTGGTGTGATGAGACCCATTTGTTGACCTGGCCATCCATCTGTATTTGTTAAAT 2310  
QY 2344 ACCTTTCTATGGCCATGAGACATATCCAAATGACGACATTTCAATATGCTTACA 2403  
DB 2311 ACCTTTCTATGGCCATGAGACATATCCAAATGACGACATTTCAATATGCTTACA 2370  
QY 2404 GTAGAAACCTGTTTCACTGGGATCTTACAGACAGAAATGTTTGAATAATTTATGCC 2463  
DB 2371 GTAGAAACCTGTTTCACTGGGATCTTACAGACAGAAATGTTTGAATAATTTATGCC 2430  
QY 2464 ATGATCTCTTACTATTTATTTCCAAAGAGCTGGAATATCTTTGACGGTTTATTTGACG 2523  
DB 2431 ATGATCTCTTACTATTTATTTCCAAAGAGCTGGAATATCTTTGACGGTTTATTTGACG 2490  
QY 2524 CTAGAGCTGTAGAACTGTGACCTGCGCAATGTGGAAGGATATCTGTTCCGTTCAATT 2583  
DB 2491 CTAGAGCTGTAGAACTGTGACCTGCGCAATGTGGAAGGATATCTGTTCCGTTCAATT 2550  
QY 2584 CGATTCCTGGAGTTTTCAGAGTGGCAAAATCTTGGCCAACTTAAATATGCTAATAAG 2643  
DB 2551 CGATTCCTGGAGTTTTCAGAGTGGCAAAATCTTGGCCAACTTAAATATGCTAATAAG 2610  
QY 2644 ATGATCGGCAATTCCTGGGAGCTGTGGGAATTTAAACCTGCTCTGGCCATCATGCTC 2703  
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QY 2704 TTTCAATTTTGGCGTGGGAGCATGACGCTTGTGTAATAAGCAAAAGATTTGCTGTC 2763  
DB 2671 TTTCAATTTTGGCGTGGGAGCATGACGCTTGTGTAATAAGCAAAAGATTTGCTGTC 2730  
QY 2764 AAGATCGCAGTATTTGTCACATCCACAGCTGACATGATGATCTTCCACCTCTTC 2823  
DB 2731 AAGATCGCAGTATTTGTCACATCCACAGCTGACATGATGATGATCTTCCACCTCTTC 2790  
QY 2824 CTGATTTGTCTCCGCTGCTGTGTGGGAGTGTATGAGACCATGTGGGACTGTATGAG 2883  
DB 2791 CTGATTTGTCTCCGCTGCTGTGTGGGAGTGTATGAGACCATGTGGGACTGTATGAG 2850  
QY 2884 GTTGTGCTGTAACCAATGCTTACTGCTTATGATGATGATGATGATGATGATGATGATGAT 2943  
DB 2851 GTTGTGCTGTAACCAATGCTTACTGCTTATGATGATGATGATGATGATGATGATGATGAT 2910

QY 2944 GTGGTCTGATATCTCTTCTGGCCCTTGTGAGCTCATTTAGTCAGACAACCTTGCA 3003  
DB 2911 GTGGTCTGATATCTCTTCTGGCCCTTGTGAGCTCATTTAGTCAGACAACCTTGCA 2970  
QY 3004 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3063  
DB 2971 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3030  
QY 3064 GGAGTACCTTATGTAAGAAATATATGATATTTATTCACAGTCTTCTTATGAGAA 3123  
DB 3031 GGAGTACCTTATGTAAGAAATATATGATATTTATTCACAGTCTTCTTATGAGAA 3090  
QY 3124 CAAAGATTTTATGATGAAATTTAAACCACTGATGATCTTAAACAAAGAAAGACAGTGT 3183  
DB 3091 CAAAGATTTTATGATGAAATTTAAACCACTGATGATCTTAAACAAAGAAAGACAGTGT 3150  
QY 3184 ATGTCCATCATCAGCAGAAATTTGGGAAAGATCTGATATTTAAAGTGAATGGA 3243  
DB 3151 ATGTCCATCATCAGCAGAAATTTGGGAAAGATCTGATATCTTAAAGTGAATGGA 3210  
QY 3244 ACTAGAAGTGTATGAGAACTGGCAGCAGTGTGAAATTTACATTTGATGAAATGTAT 3303  
DB 3211 ACTAGAAGTGTATGAGAACTGGCAGCAGTGTGAAATTTACATTTGATGAAATGTAT 3270  
QY 3304 TACATGTCATTTCAATTAACAACCCAGCTTACTGTGACCTGATACCAATGCTGTAGAGAA 3363  
DB 3271 TACATGTCATTTCAATTAACAACCCAGCTTACTGTGACCTGATACCAATGCTGTAGAGAA 3330  
QY 3364 TCTGACTTTGAAATTTTAAACACGGAAGACTTATGATGATGATGATGATGATGATGATGAT 3423  
DB 3331 TCTGACTTTGAAATTTTAAACACGGAAGACTTATGATGATGATGATGATGATGATGATGAT 3390  
QY 3424 AAGAGAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3483  
DB 3391 AAGAGAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3350  
QY 3484 CCTGTAGAGAAACGCGGTAGTGAACCTGGAAGAACTTTGAACAGAAAGCTTTGTC 3543  
DB 3451 CCTGTAGAGAAACGCGGTAGTGAACCTGGAAGAACTTTGAACAGAAAGCTTTGTC 3510  
QY 3544 ACTGAAGGCTGTGTACAAAGATTTCAAGTGTGTCAATTCATGTGGAAGAGCAGAGGA 3603  
DB 3511 ACTGAAGGCTGTGTACAAAGATTTCAAGTGTGTCAATTCATGTGGAAGAGCAGAGGA 3570  
QY 3604 AAACATGCTGGAACCTGGAAGAGAGCTGTTCCGAATGATGATGATGATGATGATGATGATGAT 3663  
DB 3571 AAACATGCTGGAACCTGGAAGAGAGCTGTTCCGAATGATGATGATGATGATGATGATGATGAT 3630  
QY 3664 ACCTCATTTGTTTCAATGATTTCTCTTATGATGATGATGATGATGATGATGATGATGAT 3723  
DB 3631 ACCTCATTTGTTTCAATGATTTCTCTTATGATGATGATGATGATGATGATGATGATGAT 3690  
QY 3724 ATGATCAGGGAAGAGATTTAAGAGATGTTGAATGATGATGATGATGATGATGATGATGAT 3783  
DB 3691 ATGATCAGGGAAGAGATTTAAGAGATGTTGAATGATGATGATGATGATGATGATGATGAT 3750  
QY 3784 ATTTTCAATCTGGAATTTGCTTAAATGAGTGGGCAATGATGATGATGATGATGATGATGATGAT 3843  
DB 3751 ATTTTCAATCTGGAATTTGCTTAAATGAGTGGGCAATGATGATGATGATGATGATGATGATGAT 3810  
QY 3844 AATGCTGTGTTGCTGTGACCTTTAAATGTTGATGATGATGATGATGATGATGATGATGAT 3903  
DB 3811 AATGCTGTGTTGCTGTGACCTTTAAATGTTGATGATGATGATGATGATGATGATGATGAT 3870  
QY 3904 AATGCTGTGTTGCTGTGACCTTTAAATGTTGATGATGATGATGATGATGATGATGATGAT 3963  
DB 3871 AATGCTGTGTTGCTGTGACCTTTAAATGTTGATGATGATGATGATGATGATGATGATGAT 3930  
QY 3964 AGACCTCTAAGACCTTATCTGATTTGAAGGATGAGGTTGTTGAATGCCCTTTTA 4023  
DB 3931 AGACCTCTAAGACCTTATCTGATTTGAAGGATGAGGTTGTTGAATGCCCTTTTA 3990  
QY 4024 GGAGCAATTCATCCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4083



FILE REFERENCE: LEX-0216-USA  
CURRENT APPLICATION NUMBER: US/09/930,871  
CURRENT FILING DATE: 2001-08-14  
PRIOR APPLICATION NUMBER: US 60/225,989  
PRIOR FILING DATE: 2000-08-16  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 5889  
TYPE: DNA  
ORGANISM: homo sapiens  
US-09-930-871-3

Query Match: 64.2%; Score 3874; DB 10; Length 5889;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3874; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2044 GGAACACACGACGAACTGAAATGAGAAAGAGAAAGGCAAGTCTTCCAGCTTCCATG.2103  
DB 2011 GGAACACACGACGAACTGAAATGAGAAAGAGAAAGGCAAGTCTTCCAGCTTCCATG.2070  
QY 2104 GACTTCTAGAAAGATCTTCCAAAGGCAAGCAATAGATAGAGCAAGTCTTAC.2163  
DB 2071 GACTTCTAGAAAGATCTTCCAAAGGCAAGCAATAGATAGAGCAAGTCTTAC.2130  
QY 2164 AATACAGTAGAAGACTTGAAGATCCAGGAGAGAAATGCCACCTGTTGATTAATTT.2223  
DB 2131 AATACAGTAGAAGACTTGAAGATCCAGGAGAGAAATGCCACCTGTTGATTAATTT.2190  
QY 2224 TCCAAATATCTTAACTCTGGAGCTGTCTCCATATTGGTTAAAGTGAACATGTTGTC.2283  
DB 2191 TCCAAATATCTTAACTCTGGAGCTGTCTCCATATTGGTTAAAGTGAACATGTTGTC.2250  
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DB 2251 AACCTGGTGTGATGAGACCAATTTGACCTGGCCATCAGCATCTGATTTGATTAAT.2310  
QY 2344 ACTCTTTCAATGGCCATGAGACATATCCAAATGAGGACCAATTTCAATAATGCTTACA.2403  
DB 2311 ACTCTTTCAATGGCCATGAGACATATCCAAATGAGGACCAATTTCAATAATGCTTACA.2370  
QY 2404 GTAGAAACCTGGTTTCACTGGGATCTTTAGCAAGAAATGTTTGAATAATTAATGTC.2463  
DB 2371 GTAGAAACCTGGTTTCACTGGGATCTTTAGCAAGAAATGTTTGAATAATTAATGTC.2430  
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DB 2431 ATGATCTTACTATTAATTTCCAGAGAGGCTGGAATATCTTGACGGTTTATTTGACG.2490  
QY 2524 CTTAGCCTGGTAGACTTGGACTGCCAATGTGAAGATTAATCTGTTCCGTTCAATTT.2583  
DB 2491 CTTAGCCTGGTAGACTTGGACTGCCAATGTGAAGATTAATCTGTTCCGTTCAATTT.2550  
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DB 2551 CGATTCTCGAGTTTCAAGTTGGCAAAATCTTGGCCAAAGCTTAATATGCTAATAAAG.2610  
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DB 2611 ATCATGCGAATTTCCCTGGGGGCTGGAATAATTAACCTGCTTGGCCATCATGCTG.2670  
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DB 2671 TTCAATTTTGGCGTGGCATGACGCTTTTGGTAAAGCTACAAAGATTTGTTCTG.2730  
QY 2764 AAGATGCGAAGATTTGTAATCCAGCTGGCAATGAATGATCTTCCACTCTTC.2823  
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QY 2944 GTGCTGTAATCTTCTTGGGCTGCTTGTAGAGCAATTTAGTGAAGCAACTTGA.3003  
DB 2911 GTGCTGTAATCTTCTTGGGCTGCTTGTAGAGCAATTTAGTGAAGCAACTTGA.2970  
QY 3004 GCCACTGATGATGATGTAATGTAATTAATCTCCAAATGCTGATGATGATGATGATG.3063  
DB 2971 GCCACTGATGATGATGTAATGTAATTAATCTCCAAATGCTGATGATGATGATGATG.3030  
QY 3064 GGAGTAGCTTATGTAAGAAATAATATGAAATTTATTAACAGCTCTTATTAGGAA.3123  
DB 3031 GGAGTAGCTTATGTAAGAAATAATATGAAATTTATTAACAGCTCTTATTAGGAA.3090  
QY 3124 CAATAATTTTATGATGTAATTAACCACTGATGATGATGATGATGATGATGATG.3183  
DB 3091 CAATAATTTTATGATGTAATTAACCACTGATGATGATGATGATGATGATGATG.3150  
QY 3184 ATGTCAATCATATCAGCAGAAATTTGGAAAGATCTTACTATCTTAAAGATGTAATG.3243  
DB 3151 ATGTCAATCATATCAGCAGAAATTTGGAAAGATCTTACTATCTTAAAGATGTAATG.3210  
QY 3244 ACTCAAGTGTATAGAACTGGCAGCAGTGTGAATAATATATTTATGATGAAATGAT.3303  
DB 3211 ACTCAAGTGTATAGAACTGGCAGCAGTGTGAATAATATATTTATGATGAAATGAT.3270  
QY 3304 TACATGCTATCTTAAACCAACCCAGCTTACTGCTGATGATGATGATGATGATG.3363  
DB 3271 TACATGCTATCTTAAACCAACCCAGCTTACTGCTGATGATGATGATGATGATG.3330  
QY 3364 TCTGACTTGAATAATTTAAACAGGAACTTATGATGATGATGATGATGATGATG.3423  
DB 3331 TCTGACTTGAATAATTTAAACAGGAACTTATGATGATGATGATGATGATGATG.3390  
QY 3424 AAAGAGAACTGATGATGAAAGCACTAGCTCATGAAAGTGAAGTGAAGTGAAGTGA.3483  
DB 3391 AAAGAGAACTGATGATGAAAGCACTAGCTCATGAAAGTGAAGTGAAGTGAAGTGA.3450  
QY 3484 CCGTAGAAGAAAGCCGAGTGAAGCACTGATGATGATGATGATGATGATGATG.3543  
DB 3451 CCGTAGAAGAAAGCCGAGTGAAGCACTGATGATGATGATGATGATGATGATG.3510  
QY 3544 ACTGAAGGCTGTGTACAAAGATCAAGTGTGTCAATCAATGATGATGATGATGATG.3603  
DB 3511 ACTGAAGGCTGTGTACAAAGATCAAGTGTGTCAATCAATGATGATGATGATGATG.3570  
QY 3604 AAACAAATGATGAACTGAGAAAGAGCTGTTCCGAATAGTTGAACATTAAGTGTGAG.3663  
DB 3571 AAACAAATGATGAACTGAGAAAGAGCTGTTCCGAATAGTTGAACATTAAGTGTGAG.3630  
QY 3664 ACCCTATGTTTCAATGATGATGATGATGATGATGATGATGATGATGATGATG.3723  
DB 3631 ACCCTATGTTTCAATGATGATGATGATGATGATGATGATGATGATGATGATG.3690  
QY 3724 ATGATCAGGAAAGAGATTAAGAGATGATGATGATGATGATGATGATGATGATG.3783  
DB 3691 ATGATCAGGAAAGAGATTAAGAGATGATGATGATGATGATGATGATGATGATG.3750  
QY 3784 ATTTTCAATCTGGAATGCTTCAAAATGGGTGATGATGATGATGATGATGATG.3843  
DB 3751 ATTTTCAATCTGGAATGCTTCAAAATGGGTGATGATGATGATGATGATGATG.3810  
QY 3844 AATGCTGCTGTTGGCTGGAATCTTAAATGTTGATGATGATGATGATGATGATG.3903  
DB 3811 AATGCTGCTGTTGGCTGGAATCTTAAATGTTGATGATGATGATGATGATGATG.3870  
QY 3904 AATGCTTGGTGTACTCAGAACTGAGCAATTAATCTCAGCACTTAAGAGCTG.3963  
DB 3871 AATGCTTGGTGTACTCAGAACTGAGCAATTAATCTCAGCACTTAAGAGCTG.3930  
QY 3964 AGACCTTAAGAGCTTATCTGATTTGAAGGATGAGGATGATGATGATGATGATG.4023





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; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows
; SEQ ID NO 5
; LENGTH: 4329
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-930-871-5

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|-----------------------|----------------|--------------|----------|-------------|
| Query Match           | 38.1%          | Score 2295   | DB 10    | Length 4329 |
| Best Local Similarity | 100.0%         | Score No. 0  |          |             |
| Matches 2295          | Conservative 0 | Mismatches 0 | Indels 0 | Gaps 0      |

|    |      |   |      |
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| QY | 2044 | GGAAACAACCACTGAAACTGAAATGAAAGAGAGAGTCAAGTCTTCCAGCTTCCATG        | 2103 |
| Db | 2011 | GGAAACAACCACTGAAACTGAAATGAAAGAGAGAGTCAAGTCTTCCAGCTTCCATG        | 2070 |
| QY | 2104 | GACTTCTAGAAAGATCCTTCCCAAAGCAGCAGCAATGATATAGCCAGCATTCCTAACA      | 2163 |
| Db | 2071 | GACTTCTAGAAAGATCCTTCCCAAAGCAGCAGCAATGATATAGCCAGCATTCCTAACA      | 2130 |
| QY | 2164 | AATCACTAGAAAGACTGAAAGATCCAGCGAAATGCCACCCCTGTGGATATTAATT         | 2223 |
| Db | 2131 | AATCACTAGAAAGACTGAAAGATCCAGCGAAATGCCACCCCTGTGGATATTAATT         | 2190 |
| QY | 2224 | TCCAACTATCTTAAATCTGGAGCACTTTCATATATGGTTAAAGTAAACATGTGTC         | 2283 |
| Db | 2191 | TCCAACTATCTTAAATCTGGAGCACTTTCATATATGGTTAAAGTAAACATGTGTC         | 2250 |
| QY | 2284 | AACTGGTGTATGAGACCATTTGTTGACTCGGCCATCACCATCTGATTTGCTTAAAT        | 2343 |
| Db | 2251 | AACTGGTGTATGAGACCATTTGTTGACTCGGCCATCACCATCTGATTTGCTTAAAT        | 2310 |
| QY | 2344 | ACTCTTTCATGCGCAGTGAAGCACTATCCAAATGACGAGCATTCTCAATAAATGGTTACA    | 2403 |
| Db | 2311 | ACTCTTTCATGCGCAGTGAAGCACTATCCAAATGACGAGCATTCTCAATAAATGGTTACA    | 2370 |
| QY | 2404 | GTAAGAAACTGTGGTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAATTAATGCC     | 2463 |
| Db | 2371 | GTAAGAAACTGTGGTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAATTAATGCC     | 2430 |
| QY | 2464 | ATGAGATCCTTACTATTAATTTCCAAAGAAAGCTGGAAATACCTTGACAGGTTTAATGTGAGC | 2523 |
| Db | 2431 | ATGAGATCCTTACTATTAATTTCCAAAGAAAGCTGGAAATACCTTGACAGGTTTAATGTGAGC | 2490 |
| QY | 2524 | CTTAGCCCTGTAGAACTTGGACACCGCCAAATGTGGAAGATTAATCTGTTCTCGCTTCAATT  | 2583 |
| Db | 2491 | CTTAGCCCTGTAGAACTTGGACACCGCCAAATGTGGAAGATTAATCTGTTCTCGCTTCAATT  | 2550 |
| QY | 2584 | CGATTTGCTGGAGTTTTCACAGTTGGCCAAATCTGGCCACGTTAAATATGCTAATAAG      | 2643 |
| Db | 2551 | CGATTTGCTGGAGTTTTCACAGTTGGCCAAATCTGGCCACGTTAAATATGCTAATAAG      | 2610 |
| QY | 2644 | ATCATCGGCATTTCCGATGGGGGCGCTCGGGAATTTAACCTGTGTGGCATCATCGTC       | 2703 |
| Db | 2611 | ATCATCGGCATTTCCGATGGGGGCGCTCGGGAATTTAACCTGTGTGGCATCATCGTC       | 2670 |
| QY | 2704 | TTCAATTTTCCGCTGGTCGGCATGACGCTCTTTGGTAAAGTACAAAGATTGTCTGC        | 2763 |
| Db | 2671 | TTCAATTTTCCGCTGGTCGGCATGACGCTCTTTGGTAAAGTACAAAGATTGTCTGC        | 2730 |
| QY | 2764 | AAGATCGCCAGTATTTGTCAACTCCCAACGCTGGACATATAAGCATCTCCACATCCCTC     | 2823 |
| Db | 2731 | AAGATCGCCAGTATTTGTCAACTCCCAACGCTGGACATATAAGCATCTCTCCATCTCTTC    | 2790 |
| QY | 2824 | CTGATTTGTTCCGCGCTGTGTGGGGAGTGGATAGACCATGTGGGACTGTATGAG          | 2883 |
| Db | 2791 | CTGATTTGTTCCGCGCTGTGTGGGGAGTGGATAGACCATGTGGGACTGTATGAG          | 2850 |
| QY | 2884 | GTTCTGCTGTAAGCAGTATGCTTACTGTCTTCAATGATGCTATGATTTGGAAACCTA       | 2943 |
| Db | 2851 | GTTCTGCTGTAAGCAGTATGCTTACTGTCTTCAATGATGCTATGATTTGGAAACCTA       | 2910 |

|    |      |  |      |
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| OY | 2944 | GTGGTCCGGAATCGCTTTCGGCCCTGCTTMMGAGTCATTTAGTGCAGACACCTTGCA  | 3003 |
| Db | 2911 | GTGGTCCGGAATCGCTTTCGGCCCTGCTTMMGAGTCATTTAGTGCAGACACCTTGCA  | 2970 |
| OY | 3004 | GCCACTGATGATGATTAATGAATGAATTAATCTCCAAATTCGTGTGATAGATGCACAA | 3063 |
| Db | 2971 | GCCACTGATGATGATTAATGAATGAATTAATCTCCAAATTCGTGTGATAGATGCACAA | 3030 |
| OY | 3064 | GGAGTAGCTATGCGAAAAGAAAATATATGAATTTATTCACAAGCTCTTATAGAAA    | 3123 |
| Db | 3031 | GGAGTAGCTATGCGAAAAGAAAATATATGAATTTATTCACAAGCTCTTATAGAAA    | 3090 |
| OY | 3124 | CAAAAAGTTTATGATGAAATTAACCACTGGATGATCTAAACAAGAAACACGTGT     | 3183 |
| Db | 3091 | CAAAAAGTTTATGATGAAATTAACCACTGGATGATCTAAACAAGAAACACGTGT     | 3150 |
| OY | 3184 | ATGTCCATCATACACACGAAATTTGGGAAAGATCTTGATCTTAAAGATATAATGA    | 3243 |
| Db | 3151 | ATGTCCATCATACACACGAAATTTGGGAAAGATCTTGATCTTAAAGATATAATGA    | 3210 |
| OY | 3244 | ACTCAAGTGTATAGGAACTGGCAGCAGTGTGAAAAATACATTATGTAGAAAGTAT    | 3303 |
| Db | 3211 | ACTCAAGTGTATAGGAACTGGCAGCAGTGTGAAAAATACATTATGTAGAAAGTAT    | 3270 |
| OY | 3304 | TACATGTCATTCATAAACCAACCCCACTCTTACGTGTACGTACCAATTCGTAGAGAA  | 3363 |
| Db | 3271 | TACATGTCATTCATAAACCAACCCCACTCTTACGTGTACGTACCAATTCGTAGAGAA  | 3330 |
| OY | 3364 | TCTACTTGTAAATTTAAACACGGAAGACTTATAGTATGATCGGATCTGGAAAGAC    | 3423 |
| Db | 3331 | TCTACTTGTAAATTTAAACACGGAAGACTTATAGTATGATCGGATCTGGAAAGAC    | 3390 |
| OY | 3424 | AAAGAGAACTGAATGAAAGACAGTAGCTCATCAGAAAGTAGCAGTGTGACATCGCGCA | 3483 |
| Db | 3391 | AAAGAGAACTGAATGAAAGACAGTAGCTCATCAGAAAGTAGCAGTGTGACATCGCGCA | 3450 |
| OY | 3484 | CCTGTAGAAAGACGCCCGTAGTGGAACTGGAAGAACTCTTGAACACAGACTTGTTC   | 3543 |
| Db | 3451 | CCTGTAGAAAGACGCCCGTAGTGGAACTGGAAGAACTCTTGAACACAGACTTGTTC   | 3510 |
| OY | 3544 | ACTGAAAGCTGTGACAAATATCAAGTGTGCAATGATGTAAGTGAAGAAAGACAGAA   | 3603 |
| Db | 3511 | ACTGAAAGCTGTGACAAATATCAAGTGTGCAATGATGTAAGTGAAGAAAGACAGAA   | 3570 |
| OY | 3604 | AAACAATGTGGAACCTGAGAGAGAGCTGTTCCGAATAGTTGAACATTAACGTGTAG   | 3663 |
| Db | 3571 | AAACAATGTGGAACCTGAGAGAGAGCTGTTCCGAATAGTTGAACATTAACGTGTAG   | 3630 |
| OY | 3664 | ACCTTCATTTTTCATGANTTCTCTTAGTAGTGTGTCTGTGGCATTTGAAATATATAT  | 3722 |
| Db | 3631 | ACCTTCATTTTTCATGANTTCTCTTAGTAGTGTGTCTGTGGCATTTGAAATATATAT  | 3690 |
| OY | 3724 | ATTGATCAGGAAAGACGATTAAAGAGATGGTGGAAATGCGCAAAAGTTTACTTAC    | 3783 |
| Db | 3691 | ATTGATCAGGAAAGACGATTAAAGAGATGGTGGAAATGCGCAAAAGTTTACTTAC    | 3750 |
| OY | 3784 | ATTTTCATCTGGAATGCTTCAAAATGAGTGGCATATGCGTATCAAAATATTTAC     | 3843 |
| Db | 3751 | ATTTTCATCTGGAATGCTTCAAAATGAGTGGCATATGCGTATCAAAATATTTAC     | 3810 |
| OY | 3844 | AATGCGCTGTGTGTGGTGGACTTCTTAATTTGATGTTTCATGTGCTAGTTTAAACGA  | 3903 |
| Db | 3811 | AATGCGCTGTGTGTGGTGGACTTCTTAATTTGATGTTTCATGTGCTAGTTTAAACGA  | 3870 |
| OY | 3904 | AATGCGCTGTGTGTGGTGGACTTCTTAATTTGATGTTTCATGTGCTAGTTTAAACGA  | 3963 |
| Db | 3871 | AATGCGCTGTGTGTGGTGGACTTCTTAATTTGATGTTTCATGTGCTAGTTTAAACGA  | 3930 |
| OY | 3964 | AGACCTCTAAGAGCCTTATCTGCATTTGAAAGGATAGGGTGGTGTGAATCCCTTTTA  | 4023 |
| Db | 3931 | AGACCTCTAAGAGCCTTATCTGCATTTGAAAGGATAGGGTGGTGTGAATCCCTTTTA  | 3990 |
| OY | 4024 | GGAGCAATTCATCATCATGAAATGTGCTGTGGTTGTCTTATATCTCGCTAATTTTC   | 4083 |



|||||  
Db 3991 GGAGCAATTCATCCATCATATGATGCTTCGTTGCTTATATTCGTGCTAATTTTC 4050  
QY 4084 AGCATCAGGGCGTAAATTTTGTGCTGCAATTTCTACCCCTGATTAACCCACACT 4143  
Db 4051 AGCATCAGGGCGTAAATTTTGTGCTGCAATTTCTACCCCTGATTAACCCACACT 4110  
QY 4144 GGTGACAGTTTGACATCGAAGACGTGAATATCATCTGATTTGCTAAACTAATAGA 4203  
Db 4111 GGTGACAGTTTGACATCGAAGACGTGAATATCATCTGATTTGCTAAACTAATAGA 4170  
QY 4204 AGAATGAGACTGCTCGATGGAATAATGTAAGTAACTTTGATTAATGAGATTGGG 4263  
Db 4171 AGAATGAGACTGCTCGATGGAATAATGTAAGTAACTTTGATTAATGAGATTGGG 4230  
QY 4264 TATCTCTTTTGTCTCAAGTTGCCCATTTCAAGATGATGATTAATGATGACAGA 4323  
Db 4231 TATCTCTTTTGTCTCAAGTTGCCCATTTCAAGATGATGATTAATGATGACAGA 4290  
QY 4324 GTTGATCCAGAAAT 4338  
Db 4291 GTTGATCCAGAAAT 4305

RESULT 9  
US-09-930-871-7

Sequence 7, Application US/09930871  
Patent No. US20020076780A1  
GENERAL INFORMATION:  
APPLICANT: Turner, C. Alexander Jr.  
APPLICANT: Mathur, Brian  
TITLE OF INVENTION: NO. US20020076780A1 Human Ion Channel Proteins and Polynucleot  
FILE REFERENCE: LEX-0216-USA  
CURRENT APPLICATION NUMBER: US/09/930,871  
CURRENT FILING DATE: 2001-08-14  
PRIOR APPLICATION NUMBER: US 60/225,989  
PRIOR FILING DATE: 2000-08-16  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 7  
LENGTH: 4146  
TYPE: DNA  
ORGANISM: homo sapiens  
US-09-930-871-7

Query Match 35.0%; Score 2109; DB 10; Length 4146;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2104 GACTTCTTGAAGATCTTCCCAAGGCAAGCAAGCAATAGATATGACCGCATTTCA 2163  
Db 2071 GACTTCTTGAAGATCTTCCCAAGGCAAGCAAGCAATAGATATGACCGCATTTCA 2130  
QY 2164 AATACAGTGAAGACTGAAGATCCAGGAGAAATGCCACCGCTGGTGAATATTT 2223  
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QY 2224 TCCACATATTTCTAATCTGGGACGTCTTCATATTTGTTAAAGTGAACATGTTGC 2283  
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QY 2284 AACCTGCTGATGAGACCATTTGTTGACCTGGCCATACACATCTGATTTGCTTAAT 2343  
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QY 3244 ACTACAGTGTATAGAACTGGCAGCAGTGTGAAATTAATATATGATGAAAGTAT 3303  
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Db 3271 TACATGCTATCATTAACCAACCCAGCTTACTGTCAGCTGTCACATTTCTGTAGAGAA 3330  
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3544 ACTGAGAGCGTGTACAAAGATTCAGTGTGTCAATCATGTGAGAAAGAGCAGAGGA 3603  
3511 ACTGAGAGCGTGTACAAAGATTCAGTGTGTCAATCATGTGAGAAAGAGCAGAGGA 3570  
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3571 AAACATGTGTGAACCTGAGAGAGAGCTGTTCCGAATGATGAACATTAAGCTGTTGAG 3630  
3664 ACCTTATGTGTTTCATGATTCCTCTAGTAGTGAGTGCTGCTGATTTGAGATATATAT 3723  
3631 ACCTTATGTGTTTCATGATTCCTCTAGTAGTGAGTGCTGCTGATTTGAGATATATAT 3690  
3724 ATTGATCAGGAGAAAGAGATTAAGAGAGATGTTGGAATATGCTGACAAAGTGTTCACCTTAC 3783  
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3751 ATTTTCATTTTGAATGCTTCTTAATAATGGGTGGCAATGCTATCAACATATTTGACC 3810  
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3811 AATGCGTGGTGGTGGGAGCTCTTAATGTTGATGTTTCATTTGCTGACATTTTAACAGCA 3870  
3904 AATGCGTGGTGGTGGGAGCTCTTAATGTTGATGTTTCATTTGCTGACATTTTAACAGCA 3963  
3871 AATGCGTGGTGGTGGGAGCTCTTAATGTTGATGTTTCATTTGCTGACATTTTAACAGCA 3930  
3964 AGACCTCTAAGAGCTTATCTGATTTGAAGGAGATGAGGTGTTGGAATGCCCTTTTA 4023  
3931 AGACCTCTAAGAGCTTATCTGATTTGAAGGAGATGAGGTGTTGGAATGCCCTTTTA 3990  
4024 GAGGCAATTCATCATCATGATGATGCTGCTGTTGTTTATATTCGCGTAATTTTC 4083  
3991 GAGGCAATTCATCATCATGATGATGCTGCTGTTGTTTATATTCGCGTAATTTTC 4050  
4084 AGCATCATGGCGCTAATTTGTTGCTGCGCAATTTACACATGATTAACACCAACT 4143  
4051 AGCATCATGGCGCTAATTTGTTGCTGCGCAATTTACACATGATTAACACCAACT 4110  
4144 GGTGACAGG 4152  
4111 GGTGACAGG 4119

RESULT 10  
US-09-930-871-9  
Sequence 9, Application US/09930871  
Patent No. US20020076780A1  
GENERAL INFORMATION:  
Applicant: Turner, C. Alexander Jr.  
Applicant: Mathur, Daniel  
Applicant: Mathur, Brian  
TITLE OF INVENTION: Same  
FILE REFERENCE: LEX-0216-USA  
CURRENT APPLICATION NUMBER: US/09/930,871  
PRIOR FILING DATE: 2001-08-14  
PRIOR APPLICATION NUMBER: US 60/225,989  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 9  
LENGTH: 4164  
TYPE: DNA  
ORGANISM: homo sapiens  
US-09-930-871-9

Query Match 33.3%; Score 2011; DB 10; Length 4164;  
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;  
Matches 2011; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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61 TCTCTTGGCGCTATTTGAAGAGCGATTTGAGAAAGGCAAGAAATCCCAACAGAC 120  
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121 AAAAAGATGACGACGAAATGGCCCAAGCCAAATGTACTTGAAGTGAAGGAAAC 180  
181 CTTCATTTATTTATGAGAGCATTTCCACAGATGAGTGTGACAGCCCTGAGAGACTG 240  
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241 GACCCCTACTATATCAATTAAGAAACCTTTATATGATTAATAAGGAGGAGCCATCTC 300  
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361 GCTATTAAGATTTTGTGATCATTTATTCAGATGCTAATTAATGTCATATTTTGA 420  
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421 AACTGTGTGTTTATGACATGAGTAACCTGCTGATTTGAAGAAAGATTAAGATAC 480  
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481 TTACAGGAAATATATCTTTGAATCACTTAATAAATTTGCAAGGGAATCTGTTTA 540  
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541 GAAGATTTTACTTCTTCCGAGATCCATGAGAGCTGCTGATTTCACTGATTAATTA 600  
601 GCGTAGTCTACAGAGTTTGTGACCTGGGCAATGCTCGGCAATTAATTAATTAAT 660  
601 GCGTAGTCTACAGAGTTTGTGACCTGGGCAATGCTCGGCAATTAATTAATTAAT 660  
661 CTCGAGCATTTGAAGAGATTTAGTATTCAGAGGCTGAGGAAACCATTTGGGAGCCCTG 720  
661 CTCGAGCATTTGAAGAGATTTAGTATTCAGAGGCTGAGGAAACCATTTGGGAGCCCTG 720  
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721 ATCCAGTCTGTGAAGAGCTCTGAGATTAATGATTCCTGAGCTGTTCTGTCGAGCGTA 780  
781 TTGCTCTAATTTGGGCTGACGCTGTTTATGAGGCACTGAGAAATTAATTAATTAAT 840  
781 TTGCTCTAATTTGGGCTGACGCTGTTTATGAGGCACTGAGAAATTAATTAATTAAT 840  
841 CTCGACCAAGTCTCTCTGAGAGAAACATTAATTAATTAATTAATTAATTAATTAAT 900  
841 CTCGACCAAGTCTCTCTGAGAGAAACATTAATTAATTAATTAATTAATTAATTAAT 900  
901 AATGATCACTTTAATGAAGAGCTGTTGATTTGATGAGTGAAGTCAATTAATTAAT 960  
901 AATGATCACTTTAATGAAGAGCTGTTGATTTGATGAGTGAAGTCAATTAATTAAT 960  
961 TCAAGATATCATTTATCTGAGAGGTTTATGATGACATCACTATGATGAAGTATGCT 1020  
961 TCAAGATATCATTTATCTGAGAGGTTTATGATGACATCACTATGATGAAGTATGCT 1020  
1021 GATGACAGGCAATGCTCAGAGGATATATGCTGTGAAGAGCTGATGAAGTATTAAT 1080

|    |      |  |      |
|----|------|--|------|
| Db | 1021 | GATCAGAGCCAAATGTCACAGAGGGAATATATGTGTGTGAAGAAAGCTGTGATGAATAATCCCAATATAT | 1080 |
| QY | 1081 | GGCTACACAAAGCTTTGATACCTTCAGTGTGGCTTTTGTCTCTGTTCGACTAATGACT             | 1140 |
| Db | 1081 | GGCTACACAAAGCTTTGATACCTTCAGTGTGGCTTTTGTCTCTGTTCGACTAATGACT             | 1140 |
| QY | 1141 | CAGGACTCTGGGAAAAATCTTTTCAACATGACATTAACGTCGCTGGGAAAAACGTACATG           | 1200 |
| Db | 1141 | CAGGACTCTGGGAAAAATCTTTTCAACATGACATTAACGTCGCTGGGAAAAACGTACATG           | 1200 |
| QY | 1201 | ATATTTTGTGTGGTCATTTTCTTGGGCTCATCTTCTACCTAATATAATTTGATCCGTGACT          | 1260 |
| Db | 1201 | ATATTTTGTGTGGTCATTTTCTTGGGCTCATCTTCTACCTAATATAATTTGATCCGTGACT          | 1260 |
| QY | 1261 | GTGTGGGCATGGCCTTACGAGAAACAGAAATCAAGGCCACTTGGAAGAAACAGAA                | 1320 |
| Db | 1261 | GTGTGGGCATGGCCTTACGAGAAACAGAAATCAAGGCCACTTGGAAGAAACAGAA                | 1320 |
| QY | 1321 | GAGGCCCAATTTTCAGCAGATGATTTGAACGCTTAAAAAGCAACAGAGGCACTCAGAC             | 1380 |
| Db | 1321 | GAGGCCCAATTTTCAGCAGATGATTTGAACGCTTAAAAAGCAACAGAGGCACTCAGAC             | 1380 |
| QY | 1381 | GCAGCAACGGCAACTGCTCTAGAACATTTCCAGAGACCCAGTGCACGACGCGCTTCTCA            | 1440 |
| Db | 1381 | GCAGCAACGGCAACTGCTCTAGAACATTTCCAGAGACCCAGTGCACGACGCGCTTCTCA            | 1440 |
| QY | 1441 | GACAGCTCATCTGAAAGCCTTAAGTTGAGTTCCAGAGTGTCTAAGAAAGAAAGAAATCG            | 1500 |
| Db | 1441 | GACAGCTCATCTGAAAGCCTTAAGTTGAGTTCCAGAGTGTCTAAGAAAGAAAGAAATCG            | 1500 |
| QY | 1501 | AGGAAAGAAAAAACAAGAAAGCAAGTGTGTGGGGAAGAGAAAGATGAGATGAATTC               | 1560 |
| Db | 1501 | AGGAAAGAAAAAACAAGAAAGCAAGTGTGTGGGGAAGAGAAAGATGAGATGAATTC               | 1560 |
| QY | 1561 | CAAAATCTAATCTGGAGGACACATCAGAGAGAAAGTTTGGTCTCCATTTGAAGG                 | 1620 |
| Db | 1561 | CAAAATCTAATCTGGAGGACACATCAGAGAGAAAGTTTGGTCTCCATTTGAAGG                 | 1620 |
| QY | 1621 | AACCGATTCACATATGAAAAAGAGTACTCTCCACACACAGTCTTTGTGAGCATCCGT              | 1680 |
| Db | 1621 | AACCGATTCACATATGAAAAAGAGTACTCTCCACACACAGTCTTTGTGAGCATCCGT              | 1680 |
| QY | 1681 | GGCTCCCTAATTTTCACCAAGGCGAAATATACAGAACAAAGCCTTTCAGCTTTAAGAGGCGA         | 1740 |
| Db | 1681 | GGCTCCCTAATTTTCACCAAGGCGAAATATACAGAACAAAGCCTTTCAGCTTTAAGAGGCGA         | 1740 |
| QY | 1741 | GCAAGAGATGTGGGATCTGGAACGACTTCGCGAGATGATGAGACACAGCACTTTGAGAGAT          | 1800 |
| Db | 1741 | GCAAGAGATGTGGGATCTGGAACGACTTCGCGAGATGATGAGACACAGCACTTTGAGAGAT          | 1800 |
| QY | 1801 | AACGAGAGCCGTGAGATTTCTTGTGTGGCCCGACGACAGGAGAGAGAGCGCAACAGC              | 1860 |
| Db | 1801 | AACGAGAGCCGTGAGATTTCTTGTGTGGCCCGACGACAGGAGAGAGAGCGCAACAGC              | 1860 |
| QY | 1861 | AACCTGAGTCAGACACAGTAGTATCCCGAGATGCTGGCAGTGTTCACGCAATAGGAGAG            | 1920 |
| Db | 1861 | AACCTGAGTCAGACACAGTAGTATCCCGAGATGCTGGCAGTGTTCACGCAATAGGAGAG            | 1920 |
| QY | 1921 | ATGCAACAGCACTGTGGAATTTGCAATGTGTGGTTTCTTGTTGGTGGAGCACTTCAGTTCCT         | 1980 |
| Db | 1921 | ATGCAACAGCACTGTGGAATTTGCAATGTGTGGTTTCTTGTTGGTGGAGCACTTCAGTTCCT         | 1980 |
| QY | 1981 | ACATCGCCTGTTGAGACGCTTCGCCAGAGG   | 2011 |
| Db | 1981 | ACATCGCCTGTTGAGACGCTTCGCCAGAGG   | 2011 |

RESULT 11

US-09-864-761-10189/c

Sequence 10189 Application US/09864761

Patent No. US2002048763A1

GENERAL INFORMATION:

```

APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL F
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aecmca-x-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax sequence Listing Engine vers. 1.1
SEQ ID NO 10189
LENGTH: 1992
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC010127.3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.6
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.4
US-09-864-761-10189

Query Match      19.6%; Score 1181; DB 10; Length 1992;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4850 TAGGATGATGTTCTCCCGCGAGTATAGAAAGAAATATTCGTGTCGCCCTACCCGTTCGCGAG 4909
Dn 1447 TAGGATGATGTTCTCCCGCGAGTATAGAAAGAAATATTCGTGTCGCCCTACCCGTTCGCGAG 1388
QY 4910 TGATCCGCTCTTGCTAGGATTGGCCGAATCCTACGCTTGATCAAGAGCAAGAGGCGATCC 4969
Dn 1387 TGATCCGCTCTTGCTAGGATTGGCCGAATCCTACGCTTGATCAAGAGCAAGAGGCGATCC 1328
QY 4970 GCAGCGCTGCTCTTCTTGATGATGATGTCCTCTGCGGTGTTTAACATCGGCTCTTAC 5029
Dn 1327 GCAGCGCTGCTCTTCTTGATGATGATGTCCTCTGCGGTGTTTAACATCGGCTCTTAC 1268

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|    |      |  |      |
|----|------|--|------|
| OY | 5030 | TCCTCCAGTCAATGATATCATACGCCATCTTTGGGATGTCACAACTTGTGCTATGTTAGA   | 5089 |
| Db | 1267 | TCCTTCAGTATATGATATCATACGCCATCTTTGGGATGTCACAACTTGTGCTATGTTAGA   | 1208 |
| OY | 5090 | GGGAAATTGGGATGATGACATGTCACACTTTGGAGACTTTGGCAACAGCATGATCTGCC    | 5149 |
| Db | 1207 | GGGAAATTGGGATGATGACATGTCACACTTTGGAGACTTTGGCAACAGCATGATCTGCC    | 1148 |
| OY | 5150 | TATTTCCAATTACAACTCTCTGCTGGGATGGATGCTTACACCCATTTCTCAACAGTA      | 5209 |
| Db | 1147 | TATTTCCAATTACAACTCTCTGCTGGGATGGATGCTTACACCCATTTCTCAACAGTA      | 1088 |
| OY | 5210 | AGCCACCAGACTGAGACCTTAATAAAGTTAACCTTGGAGCTCAGCTTAAGGAGACCTGTG   | 5269 |
| Db | 1087 | AGCCACCAGACTGAGACCTTAATAAAGTTAACCTTGGAGCTCAGCTTAAGGAGACCTGTG   | 1028 |
| OY | 5270 | GGAAACCATCTGTGGAAATTTCTTTTGTCTAGTTACATCATCATCTCTCGTGTG         | 5329 |
| Db | 1027 | GGAAACCATCTGTGGAAATTTCTTTTGTCTAGTTACATCATCATCTCTCGTGTG         | 968  |
| OY | 5330 | TGGTGAACATGTCATCATCGCGGTACCTGTGGAGAACTTCAGCTGTCTCTACTGAAGAAATG | 5389 |
| Db | 967  | TGGTGAACATGTCATCATCGCGGTACCTGTGGAGAACTTCAGCTGTCTCTACTGAAGAAATG | 908  |
| OY | 5390 | CAGAGCCTCTAGTGAAGAGATGACCTTTGAGATGTTCTATAGGTTTGGAGAAAGTTTGATC  | 5449 |
| Db | 907  | CAGAGCCTCTAGTGAAGAGATGACCTTTGAGATGTTCTATAGGTTTGGAGAAAGTTTGATC  | 848  |
| OY | 5450 | CCGATGCAACTCAGTTTCATGGAATTTGAAAAATTAATCTCAGTTTGACACTCGCTTGAC   | 5509 |
| Db | 847  | CCGATGCAACTCAGTTTCATGGAATTTGAAAAATTAATCTCAGTTTGACACTCGCTTGAC   | 788  |
| OY | 5510 | CGCCTTCATCTGTGCCAACCAACAAACCTCAGCTCATTTGCCATTTGCCATGG          | 5569 |
| Db | 787  | CGCCTTCATCTGTGCCAACCAACAAACCTCAGCTCATTTGCCATTTGCCATGG          | 728  |
| OY | 5570 | TGATGTGTGACCGGATCCATCTGCTGTGATATCTTAATTTCCTTTCAAAAGGGGCTTCAG   | 5629 |
| Db | 727  | TGATGTGTGACCGGATCCATCTGCTGTGATATCTTAATTTCCTTTCAAAAGGGGCTTCAG   | 668  |
| OY | 5630 | GAGAGATGAGAGATGATGCTCTACGAATACAGATGAGAAAGCATTCATGGCTTCCA       | 5689 |
| Db | 667  | GAGAGATGAGAGATGATGCTCTACGAATACAGATGAGAAAGCATTCATGGCTTCCA       | 608  |
| OY | 5690 | ATCCTTCAGAGTCTCTCTATCACCACTACATCTACTTAAAGGAAAACAAAGAGAG        | 5749 |
| Db | 607  | ATCCTTCAGAGTCTCTCTATCACCACTACATCTACTTAAAGGAAAACAAAGAGAG        | 548  |
| OY | 5750 | TATCTGCTGTCATTAATTCAGCGCTGTTACAGACGCCACTTTTAAAGGAACTGTAAAC     | 5809 |
| Db | 547  | TATCTGCTGTCATTAATTCAGCGCTGTTACAGACGCCACTTTTAAAGGAACTGTAAAC     | 488  |
| OY | 5810 | AAGCTTCCTTACGTACATTAATAAACAAATTAAGAAGTGGGGCTATCTTCTTAAGAAG     | 5869 |
| Db | 487  | AAGCTTCCTTACGTACATTAATAAACAAATTAAGAAGTGGGGCTATCTTCTTAAGAAG     | 428  |
| OY | 5870 | AAGCATGATTAATGACAGAAATTAAGAAACATCTAATTAACGAAAAACAGATCTGACCA    | 5929 |
| Db | 427  | AAGCATGATTAATGACAGAAATTAAGAAACATCTAATTAACGAAAAACAGATCTGACCA    | 368  |
| OY | 5930 | TGTCACTGACGTTGTCCACCTTCTATAGACCGGGGTACAAAGCAATTTGGAAAAAC       | 5989 |
| Db | 367  | TGTCACTGACGTTGTCCACCTTCTATAGACCGGGGTACAAAGCAATTTGGAAAAAC       | 308  |
| OY | 5990 | ATGAGCAAGAGCAAAAGATGAAAAAAGCCAAAGGAAATTA 6030                  |      |
| Db | 307  | ATGAGCAAGAGCAAAAGATGAAAAAAGCCAAAGGAAATTA 267                   |      |

RESULT 12  
US-09-864-761-18334/c  
; Sequence 18334, Application US/09864761  
; Patent No. US20020048763A1

```

1 GENERAL INFORMATION:
2 APPLICANT: Penn, Sharon G.
3 APPLICANT: Rank, David R.
4 APPLICANT: Hanzel, David K.
5 APPLICANT: Chen, Wensheng
6 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
7 TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
8 FILE REFERENCE: Aecm1ca-X-1
9 CURRENT APPLICATION NUMBER: US/09/864,761
10 CURRENT FILING DATE: 2001-05-23
11 PRIOR APPLICATION NUMBER: US 60/180,312
12 PRIOR FILING DATE: 2000-02-04
13 PRIOR APPLICATION NUMBER: US 60/207,456
14 PRIOR FILING DATE: 2000-05-26
15 PRIOR APPLICATION NUMBER: US 09/632,366
16 PRIOR FILING DATE: 2000-08-03
17 PRIOR APPLICATION NUMBER: GB 24263.6
18 PRIOR FILING DATE: 2000-10-04
19 PRIOR APPLICATION NUMBER: US 60/236,359
20 PRIOR FILING DATE: 2000-09-27
21 PRIOR APPLICATION NUMBER: PCT/US01/00666
22 PRIOR FILING DATE: 2001-01-30
23 PRIOR APPLICATION NUMBER: PCT/US01/00667
24 PRIOR FILING DATE: 2001-01-30
25 PRIOR APPLICATION NUMBER: PCT/US01/00664
26 PRIOR FILING DATE: 2001-01-30
27 PRIOR APPLICATION NUMBER: PCT/US01/00669
28 PRIOR FILING DATE: 2001-01-30
29 PRIOR APPLICATION NUMBER: PCT/US01/00665
30 PRIOR FILING DATE: 2001-01-30
31 PRIOR APPLICATION NUMBER: PCT/US01/00668
32 PRIOR FILING DATE: 2001-01-30
33 PRIOR APPLICATION NUMBER: PCT/US01/00663
34 PRIOR FILING DATE: 2001-01-30
35 PRIOR APPLICATION NUMBER: PCT/US01/00662
36 PRIOR FILING DATE: 2001-01-30
37 PRIOR APPLICATION NUMBER: PCT/US01/00661
38 PRIOR FILING DATE: 2001-01-30
39 PRIOR APPLICATION NUMBER: PCT/US01/00670
40 PRIOR FILING DATE: 2001-01-30
41 PRIOR APPLICATION NUMBER: US 60/234,687
42 PRIOR FILING DATE: 2000-09-21
43 PRIOR APPLICATION NUMBER: US 09/608,408
44 PRIOR FILING DATE: 2000-06-30
45 PRIOR APPLICATION NUMBER: US 09/774,203
46 PRIOR FILING DATE: 2001-01-29
47 NUMBER OF SEQ ID NOS: 49117
48 SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
49 SEQ ID NO 18334
50 LENGTH: 1194
51 TYPE: DNA
52 ORGANISM: Homo sapiens
53 FEATURE:
54 OTHER INFORMATION: MAP TO AC010127.2
55 OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.1
56 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.87
57 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.3
58 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
59 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 7.9
60 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.6
61 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.3
62 OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.3
63 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.94
64 OTHER INFORMATION: NT HIT: M91803.1, EVALU0.00e+00
65 OTHER INFORMATION: SWISSPROT HIT: P04774, EVALU0.00e+00
66 OTHER INFORMATION: EST_HUMAN HIT: AL120392.1, EVALU0.100e-129
67 US-09-864-761-18334

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| QY | 4850 | TAGGATAGTTCTTGGCGAGCTATGAAAGATTTGGTGGCCCTCAGCTGTTCCGAG          | 4909 |
| Db | 1157 | TAGGATAGTTCTTGGCGAGCTATGAAAGATTTGGTGGCCCTCAGCTGTTCCGAG          | 1098 |
| QY | 4910 | TGATCCGTCCTGCTAGAGATTGGCCGAATCCPACGTCGTATCAAGAGCAAGGGGAGATCC    | 4969 |
| Db | 1097 | TGATCCGTCCTGCTAGAGATTGGCCGAATCCPACGTCGTATCAAGAGCAAGGGGAGATCC    | 1098 |
| QY | 4970 | GCACGCTGCTTGTGCTTGGATGATGTCCTTCTGCGTGTGTTAACATGCGGCTCTAC        | 5029 |
| Db | 1037 | GCACGCTGCTTGTGCTTGGATGATGTCCTTCTGCGTGTGTTAACATGCGGCTCTAC        | 978  |
| QY | 5030 | TCTTCCAGCATGTTTCATCTACGCCATCTTGGGATGTCACACTTGGCTCATGTGTAGA      | 5089 |
| Db | 977  | TCTTCCAGCATGTTTCATCTACGCCATCTTGGGATGTCACACTTGGCTCATGTGTAGA      | 918  |
| QY | 5090 | GGAAGATTGGGATGCGATGACATGTTCAACTTTTGAGACCTTTGGCAACAGCATGATCTGCC  | 5149 |
| Db | 917  | GGAAGATTGGGATGCGATGACATGTTCAACTTTTGAGACCTTTGGCAACAGCATGATCTGCC  | 858  |
| QY | 5150 | TATTCCAAATTAACAACCTCTGCTGGGTGGGATGGATTGCTAGCACCCATCTCAACAGTA    | 5209 |
| Db | 857  | TATTCCAAATTAACAACCTCTGCTGGGTGGGATGGATTGCTAGCACCCATCTCAACAGTA    | 798  |
| QY | 5210 | AGCCACCCGAGCTGAGACCCCTAATAAAGTTAACCCTTGGAAGCTCATTTAAGGAGACTGTG  | 5289 |
| Db | 797  | AGCCACCCGAGCTGAGACCCCTAATAAAGTTAACCCTTGGAAGCTCATTTAAGGAGACTGTG  | 738  |
| QY | 5270 | GGAACCCATCGTTGGAAATTTCTTTTGTGACGTTACATCATCATCTCTCCGCTGTG        | 5329 |
| Db | 737  | GGAACCCATCGTTGGAAATTTCTTTTGTGACGTTACATCATCATCTCTCCGCTGTG        | 678  |
| QY | 5330 | TGGTGAACATGTATACATCGCGGTCACTCGTGGAGAACCTTCAGTGTGCTACTGAGAAATGTG | 5389 |
| Db | 677  | TGGTGAACATGTATACATCGCGGTCACTCGTGGAGAACCTTCAGTGTGCTACTGAGAAATGTG | 618  |
| QY | 5380 | CAGAAGCTGTGAGTGAAGATGACTTTGAATGTTCTATGAGTGTGGGAAAGTTTGATC       | 5449 |
| Db | 617  | CAGAAGCTGTGAGTGAAGATGACTTTGAATGTTCTATGAGTGTGGGAAAGTTTGATC       | 558  |
| QY | 5450 | CCGATGGAACGACAGTTCATGAGATTTGAAATAATCTACAGTTGCAGTGGGCTGTGAC      | 5509 |
| Db | 557  | CCGATGGAACGACAGTTCATGAGATTTGAAATAATCTACAGTTGCAGTGGGCTGTGAC      | 498  |
| QY | 5510 | CGCCTTCATCTGCGCAACAACAACAACCTCAGCTCATTCGCCATGATTTGGCCATGCG      | 5569 |
| Db | 497  | CGCCTTCATCTGCGCAACAACAACAACCTCAGCTCATTCGCCATGATTTGGCCATGCG      | 438  |
| QY | 5570 | TGAGTGTGACCGGATCCACTGCTGTTGATATCTTATTTGCTTTTCAAAAGCGGGTCTAG     | 5629 |
| Db | 437  | TGAGTGTGACCGGATCCACTGCTGTTGATATCTTATTTGCTTTTCAAAAGCGGGTCTAG     | 378  |
| QY | 5630 | GAGAGAGTGGAGATGAGATGCTCTPACGAATACAGATGGAAGAGGATTCATGGCTTCCA     | 5689 |
| Db | 377  | GAGAGAGTGGAGATGAGATGCTCTACGAATACAGATGGAAGAGGATTCATGGCTTCCA      | 318  |
| QY | 5690 | ATTCCTTCCAAGTCTCCTATCAGCCCACTCACTACTTAAACGAAACAGAGAGAG          | 5749 |
| Db | 317  | ATTCCTTCCAAGTCTCCTATCAGCCCACTCACTACTTAAACGAAACAGAGAGAG          | 258  |
| QY | 5750 | TATCTGCTGTCAATTATCAGCGTGTCTTACAGCGCCACTTTTAAAGCGAACTGTAAAC      | 5809 |
| Db | 257  | TATCTGCTGTCAATTATCAGCGTGTCTTACAGCGCCACTTTTAAAGCGAACTGTAAAC      | 198  |
| QY | 5810 | AAAGTTCCTTACCTACATAATAAACAATAATCAAAGTGGGGCTAATCTCTTATAAAG       | 5869 |
| Db | 197  | AAAGTTCCTTACCTACATAATAAACAATAATCAAAGTGGGGCTAATCTCTTATAAAG       | 138  |
| QY | 5870 | AAGACATGATTAATGACAGAAATAAATGAAAACTCTATTACAAAAAACTGATCTGACCA     | 5929 |
| Db | 137  | AAGACATGATTAATGACAGAAATAAATGAAAACTCTATTACAAAAAACTGATCTGACCA     | 78   |
| QY | 5930 | TGTCCATCGACGCTTGTCCACCTTCTATGACCGGGGTGACAAAGCAATTGTGGAAAAAC     | 5989 |

[illegible]

Query Match 18.9% Score 1141: DB 10; Length 1178;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4850 TAGGTATGTTCTTGGCCGAGTGTATAGAAAAGTATTCGTGTCCTTACCTGTTCCGAG 4909  
DB 1141 TAGGTATGTTCTTGGCCGAGTGTATAGAAAAGTATTCGTGTCCTTACCTGTTCCGAG 1082

QY 4910 TGATCCGTCTTGTAGAGATTTGGCCGAATCCTACGTGTATCAAGAGCAAGGGGATCC 4969  
DB 1081 TGATCCGTCTTGTAGAGATTTGGCCGAATCCTACGTGTATCAAGAGCAAGGGGATCC 1022

QY 4970 GCAGGTCGTCTTGTGTTGATGATGTCCTCTGCGTGTGTTAACTGAGGCTCTAC 5029  
DB 1021 GCAGGTCGTCTTGTGTTGATGATGTCCTCTGCGTGTGTTAACTGAGGCTCTAC 962

QY 5030 TCTTCCTAGTCATGTATCATACGCCATCTTGGGATGTCCAACTTGGCTATGTAGA 5089  
DB 961 TCTTCCTAGTCATGTATCATACGCCATCTTGGGATGTCCAACTTGGCTATGTAGA 902

QY 5090 GGGAGTGGGATGATGACATGTTCAACTTGGACCTTGGCAAGCATGATCTGCC 5149  
DB 901 GGGAGTGGGATGATGACATGTTCAACTTGGACCTTGGCAAGCATGATCTGCC 842

QY 5150 TATTCCAAATTACAACTCTGCTGGTGGATGATGCTGACACCATTTCTCAACATA 5209  
DB 841 TATTCCAAATTACAACTCTGCTGGTGGATGATGCTGACACCATTTCTCAACATA 782

QY 5210 AGCCACCCGAGTGTGACCCCTAATAAGTTAACCTGGAAGTGTAGTAAGGAGACGTG 5269  
DB 781 AGCCACCCGAGTGTGACCCCTAATAAGTTAACCTGGAAGTGTAGTAAGGAGACGTG 722

QY 5370 GGAACCATCTGTGGAATTTCTTTTGTCACTACATCATATCTCTCTGTTG 5329  
DB 721 GGAACCATCTGTGGAATTTCTTTTGTCACTACATCATATCTCTCTGTTG 662

QY 5330 TGGGAACATGTATCATGCGGCTCATCTCGAAGAACTTCACTGTTCTAGAGAAAGTG 5389  
DB 661 TGGGAACATGTATCATGCGGCTCATCTCGAAGAACTTCACTGTTCTAGAGAAAGTG 602

QY 5390 CAGAGCCCTGAGTGGAGATGATGATGTTGATGATGATGATGATGATGATGATG 5449  
DB 601 CAGAGCCCTGAGTGGAGATGATGATGATGATGATGATGATGATGATGATGATG 542

QY 5450 CCGATGCACTCATGTTGATGATGATGATGATGATGATGATGATGATGATGATG 5509  
DB 541 CCGATGCACTCATGTTGATGATGATGATGATGATGATGATGATGATGATGATG 482

QY 5510 CGCCTCTCAATCTGCCACAAACCAAAACCTCCAGTCACTGATGATGATGATG 5569  
DB 481 CGCCTCTCAATCTGCCACAAACCAAAACCTCCAGTCACTGATGATGATGATG 422

QY 5570 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5629  
DB 421 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 362

QY 5530 GAGAGAGTGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 5589  
DB 361 GAGAGAGTGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 302

QY 5590 ATCTTCCAAAGTCTCTATACGCAATCATCTACTTAAAGGAAAGAGAGAG 5749  
DB 301 ATCTTCCAAAGTCTCTATACGCAATCATCTACTTAAAGGAAAGAGAGAG 242

QY 5750 TATCTGTCATATTATCAGGTCCTTACAGAGCCACTTTTAAAGGAAAGTAAAC 5809  
DB 241 TATCTGTCATATTATCAGGTCCTTACAGAGCCACTTTTAAAGGAAAGTAAAC 182

QY 5810 AAGCTTCCTTACGTACAAATTAACAAATCAAAAGTGGGCTTAATCTTTTAAAG 5869  
DB 181 AAGCTTCCTTACGTACAAATTAACAAATCAAAAGTGGGCTTAATCTTTTAAAG 122

QY 5870 AAGCATGATTAATTGACAGATTAATGAATAAATCTATTAAGAAAAATGATCTGACCA 5929

DB 121 AAGCATGATTAATTGACAGATTAATGAATAAATCTATTAAGAAAAATGATCTGACCA 62

QY 5930 TGTCCACTGAGAGCTTGTCCACCTTCTATGACCGGTGACAAAGCAATGTGAAAAAC 5989  
DB 61 TGTCCACTGAGAGCTTGTCCACCTTCTATGACCGGTGACAAAGCAATGTGAAAAAC 2

QY 5990 A 5990  
DB 1 A 1

RESULT 14  
US-09-864-761-1576/c  
Sequence 1576, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David R.  
APPLICANT: Chen, Wensheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
FILE REFERENCE: Aeomica-X-1  
CURRENT APPLICATION NUMBER: US/09/864,761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263,6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
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PRIOR APPLICATION NUMBER: PCT/US01/00668  
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PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 1576  
LENGTH: 969  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AC010127.2  
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL - 2.1  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL - 0.87  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL - 2.3





Query Match 4.4%; Score 268; DB 10; Length 347;  
Best Local Similarity 99.7%; Pred. No. 3e-131;  
Matches 318; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 3035 TCCAAATGCTGTGATAGGATGACAAAGAGTACCTTATGTGAAAAGAAAATATATG 3094  
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QY 3215 AACTGACTATCTTAAGATGTAAATGGAACCTACAGTGTATAGGAACTGGCAGAGTG 3274  
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DB 329 TTGAAAAATACATTATTGA 347  
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Search completed: April 22, 2003, 23:20:13  
Job time : 412 secs

GenCore version 5.1.4.p5.4578  
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OM protein - nucleic search, using frame\_plus.p2n model

Run on: April 22, 2003, 18:38:50 ; Search time 7575 seconds  
(without alignments)  
7718.487 Million cell updates/sec

Title: US-09-930-871-12

Perfect score: 10397  
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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-OUTFM-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-2000000000  
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Database :

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12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_da:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
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30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htg\_mus:\*  
34: em\_htg\_pln:\*  
35: em\_htg\_rod:\*  
36: em\_htg\_mam:\*  
37: em\_htg\_vrt:\*  
38: em\_sy:\*  
39: em\_htgo\_hum:\*  
40: em\_htgo\_mus:\*  
41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result<br>No. | Score   | Query<br>Match | Length | DB<br>ID     | Description         |
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| 2             | 10367   | 99.7           | 8378   | 6 AX164171   | AX164171 Sequence   |
| 3             | 10321.5 | 99.3           | 6046   | 9 AY043484   | AY043484 Homo sapi  |
| 4             | 10321   | 99.3           | 8378   | 6 AX164172   | AX164172 Sequence   |
| 5             | 10320.5 | 99.3           | 5997   | 6 AX391130   | AX391130 Sequence   |
| 6             | 10273   | 98.8           | 8131   | 6 AF225985   | AF225985 Homo sapi  |
| 7             | 10253   | 98.6           | 8398   | 10 RNSCDIR   | X03638 Rat brain m  |
| 8             | 10253   | 98.6           | 8399   | 10 RNSCDIR   | M22253 Rattus norv  |
| 9             | 10197   | 98.1           | 5922   | 6 AX391142   | AX391142 Sequence   |
| 10            | 10124.5 | 97.4           | 5889   | 6 AX391132   | AX391132 Sequence   |
| 11            | 9025.5  | 86.8           | 8349   | 6 AX164203   | AX164203 Sequence   |
| 12            | 9025.5  | 86.8           | 8349   | 6 AX164204   | AX164204 Sequence   |
| 13            | 9022.5  | 86.8           | 6328   | 9 HDMHBAX    | M94055 Human volta  |
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| 15            | 8967.5  | 86.3           | 8552   | 9 RNSCDIR    | M22253 Rattus norv  |
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| 17            | 8488.5  | 81.6           | 6599   | 9 HSA251507  | AF225987 Homo sapi  |
| 18            | 8468.5  | 81.5           | 9112   | 6 AX164235   | AX164235 Homo sapi  |
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| 23            | 8344.5  | 80.3           | 8378   | 5 AF123593   | AF123593 Cynops py  |
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| 25            | 7877    | 75.8           | 6452   | 6 AR107904   | AR107904 Sequence   |
| 26            | 7876    | 75.8           | 5952   | 10 RND79568  | U79568 Rattus norv  |
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| 28            | 7861.5  | 75.6           | 6371   | 6 AR107905   | AR107905 Sequence   |
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| 30            | 7841    | 75.4           | 5955   | 4 OCUC35238  | U35238 Oryctolagus  |
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| 32            | 7755.5  | 74.6           | 6586   | 6 AF0493240  | AF0493240 Rattus no |
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| 34            | 7736.5  | 74.4           | 5937   | 10 AF049617  | AF049617 Mus muscu  |
| 35            | 7720.5  | 74.3           | 5977   | 6 AR181335   | AR181335 Sequence   |
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| 37            | 7720.5  | 74.3           | 6556   | 6 AF0493239  | AF0493239 Rattus no |
| 38            | 7712.5  | 74.2           | 6586   | 6 AR181360   | AR181360 Sequence   |
| 39            | 7685.5  | 73.9           | 7053   | 6 BD012084   | BD012084 Human sod  |
| 40            | 7685.5  | 73.9           | 7053   | 6 E37451     | E37451 Sodium chan  |
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| 43            | 7525.5  | 72.4           | 6826   | 6 AR181339   | AR181339 Sequence   |
| 44            | 7525.5  | 72.4           | 6826   | 10 RATSCEP6A | U39018 Rattus norv  |
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RESULT 1

#### ALIGNMENTS

AX391140  
 LOCUS AX391140 6030 bp DNA linear PAT 19-MAR-2002  
 DEFINITION Sequence 11 from Patent WO0214498.  
 ACCESSION AX391140  
 VERSION AX391140.1 GI:19584237  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE  
 1 Turner C.A., Mathur B. and Mathur D.  
 TITLE Novel human ion channel proteins and polynucleotides encoding the  
 same  
 JOURNAL Patent: WO 0214498-A 11 21 FEB-2002;  
 Lexicon Genetics Incorporated (US)  
 FEATURES  
 source /db\_xref="taxon:9606"  
 1. 6030  
 Location/Qualifiers  
 BASE COUNT 1786 a 1190 c 1345 g 1706 t 3 others  
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 Alignment Scores:  
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 Score: 10393.00 Matches: 2009  
 Percent Similarity: 100.00% Conservative: 0  
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Db 1861 AACTGATCTAGACCAAGTAGATCATCCGAGATGTCGCAAGTCTTCCAGCGATGGGAAG 1920
Oy 641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyProSerValPro 660
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RESULT 2



AX164171 AX164171 8378 bp DNA linear PAT 22-JUN-2001  
 LOCUS Sequence 1 from Patent WO0138564.  
 DEFINITION AX164171  
 ACCESSION AX164171  
 VERSION AX164171.1 GI:14545110  
 KEYWORDS  
 SOURCE  
 ORGANISM human.  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE  
 1 (bases 1 to 8378)  
 Rouleau, G.A., Latreliere, R.G., Rochefort, D., Cossette, P. and  
 Ragsdale, D.  
 TITLE  
 Local for idiopathic generalized epilepsy, mutations thereof and  
 method using same to assess, diagnose, prognosis or treat epilepsy  
 JOURNAL  
 Patent: WO 0138564-A 1 31-MAY-2001;  
 Mcgill University (CA)  
 FEATURES  
 source  
 1. 8378  
 Location/Qualifiers  
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 ORIGIN  
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 Score: 10367.00 Matches: 2006  
 Percent Similarity: 99.85% Conservative: 0  
 Best Local Similarity: 99.85% Mismatches: 3  
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[illegible]

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| Db  | 241      | GACCCCTACTATATCAAAAGAAACCTTTATGATATGATTAAGGAGAGCCATCTTC        | 300    |        |        |          |
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| Db  | 361      | GCTATTAGATTTTGGTACATTCATTATTCAGCATGCAATTAATGATGACATATTGGCA     | 420    |        |        |          |
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 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 8378)  
 AUTHORS Rouleau G.A., Lafreniere R.G., Rochefort D., Cossette P. and  
 Ragsdale D.  
 TITLE Local for idiopathic generalized epilepsy, mutations thereof and  
 method using same to assess, diagnose, prognosis or treat epilepsy  
 Patent: WO 0138564-A 2 31-MAY-2001;  
 JOURNAL

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 QY 121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140  
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 QY 141 AsnCysValPheMetThrMetSerAsnProProAspTyrThrLysAsnValGluTyrThr 160  
 DB 686 AACGTGTGTGTATGACAAATGAGTAACCTCTGATTTGGCAAGAGATGTAGAAATACACC 745  
 QY 161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180  
 DB 746 TTACACGAGATTAATATCTTTTGAATCACTTATTAATAATTTCAAGGGAGATTTCTTTA 805  
 QY 181 GluAspPheThrPheLeuArgAspProTyrAsnTyrLeuAspPheThrValIleThrPhe 200  
 DB 806 GAGGATTTTACTTCTCTGCGGATTCATGGAAGTGGCTGATTTTCACTGATTTACATTT 865  
 QY 201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220  
 DB 866 GCGTTGTGTAACAAATTTGAAACCTAGGCAATTTTCACTCTTGCACATTTCAAGAGTC 925  
 QY 221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValAlaIleLeu 240  
 DB 926 TTGAGAGCTTGAAGAACTATTTGATTCAGAGGCTGAAACCAATGTGGAGAGCCCTG 985  
 QY 241 IleGluSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260  
 DB 986 ATCAGCTGTGGAAGAGCTCTCAGATTAATGATCTGCTGCTGCTGACAGCGTA 1045  
 QY 261 PheAlaLeuIleGlyLeuGluLeuPheMetGlyAsnLeuArgAsnLysCysIleGluTyr 280  
 DB 1046 TTTCCTCTAATTTGGGCTGACGCTGTTCATGAGGCAACCTGAGAAATTAATGATTAACATG 1105

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|----|------|---|------|
| QY | 281  | ProProThrAsnAlaSerLeuGIuGIuHISerIleGIuLysAsnIleThrValAsnTyr     | 300  |
| Db | 1106 | CCGCCACCAATGCTCTCTGGAGGAACATGATATGAAAAGAAATATTAACGTGTAATAT      | 1165 |
| QY | 301  | AsnGIythrIeuIleAsnGIuThrValPheGIuPheAspTrpLysSerTyrIleGIuAsp    | 320  |
| Db | 1166 | AATGGTACACTTATTAATTAATGAAACTGTCTTGGATTTGGATCGAAGTCAATATTCAAAT   | 1225 |
| QY | 321  | SerArgTyrHisTyrPheLeuGIuGIyPheLeuAspAlaLeuLeuCYsGIYAsnSerSer    | 340  |
| Db | 1226 | TCAAGATATTCATATTTTCCCGAGAGGCTTTTTRAGATGCCTACTATGTGGAATATGCTCT   | 1285 |
| QY | 341  | AspAlaGIyLeuCYsProGIuGIyTyrMetCYsValLysAlaGIYArgAsnProAsnTyr    | 360  |
| Db | 1286 | GATCAGAGCCAAATGTCCAGAGGATATATGTGTGTAAGAAAGCTGTATGAAATCCCAATAT   | 1345 |
| QY | 361  | GIYtyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr    | 380  |
| Db | 1346 | GGCTACCAAGCTTTGATACCTTCACGTGGCTTTTGTGCTTTCCTTTCGACTAATGACT      | 1405 |
| QY | 381  | GIAspPheTrpGIuAsnLeuTyrGIuLeuThrLeuArgAlaAlaGIYtyrThrTyrMet     | 400  |
| Db | 1406 | CAGAGCTTCCTGGGAAATCTTTATCAACAGACATTACGTGCTGCTGGGAAACGTACATG     | 1465 |
| QY | 401  | IlePhePheValIeuValIlePheLeuGIySerPheTyrLeuIleAsnLeuIleuVala     | 420  |
| Db | 1466 | ATATTTTTGTATTTGGTCATTTCTTGGGCTCATTCCTACCTAATTAATTTGATCCTGGCT    | 1525 |
| QY | 421  | ValValAlaMetAlaTyrGIuGIuGIuAsnGIuAlaThrLeuGIuGIuAlaGIuGIuLys    | 440  |
| Db | 1526 | GTGGTGCCATGGCTTCACGGAGAACAAATTCAGGCCACCTTGGAAGAGACAGAACAGAA     | 1585 |
| QY | 441  | GIuValaGIuPheGIuInuMetIleGIuGIuIleuLysGIuGIuInuAlaIleGIuIn      | 460  |
| Db | 1586 | GAGGCCAATTTTACAGCAGATGATTGACACGCTTAAANACCAACAGAGAGAGCTCAGAG     | 1645 |
| QY | 461  | AlaAlaThrAlaThrAlaSerGIuHISerArgGIuProSerAlaAlaGIYArgLeuSer     | 480  |
| Db | 1646 | GCACACACGGCAACTGCTCAGAACATTCACAGAGAGCCAGTGCAGAGAGGCGCTCA        | 1705 |
| QY | 481  | AspSerSerSerGIuAlaSerTyrLysLeuSerSerTyrSerAlaLysGIuArgArgAsnArg | 500  |
| Db | 1706 | GACAGCTCACTCAAGAGCTCTTAAGTTGAGCTTCCAGAGAGTCTTAAGAAAGAAAGAAATCGG | 1765 |
| QY | 501  | ArgtyrAsnArgLysGIuInuGIuInuSerGIyGIuGIuLysAspGIuAspGIuPhe       | 520  |
| Db | 1766 | AGCAAGAAAGAAACAGAAAGAGCACTGTGGTGGGGAAGAAAGATGAGATGAATTC         | 1825 |
| QY | 521  | GIuLysSerGIuSerGIuAspSerIleArgArgLysGIYPheArgPheSerIleGIuGIY    | 540  |
| Db | 1826 | CAAAAATCTAATCTGAGGACACACATCAGAGAGAAAGTTTTCGCTTCTCATTTGAAGG      | 1885 |
| QY | 541  | AsnArgLeuThrTyrGIuLysArgTyrSerSerProHISerLeuSerLeuSerIleArg     | 560  |
| Db | 1886 | AACCGATGTCAATATGAAAGAGAGTCTCTCCGCCACACAGCTTTTGTGAGCAATCCGT      | 1945 |
| QY | 561  | GIySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGIYArg    | 580  |
| Db | 1946 | GGCTCCCTAATTTTACCACAGGCGAAATTACCAACAAAGCTTTTTCAGCTTTTAAAGGGCGA  | 2005 |
| QY | 581  | AlaLysAspValGIYSerGIuAsnAspPheAlaAspAspGIuHISerThrPheGIuAsp     | 600  |
| Db | 2006 | GCAAGAGATTTGGGATCTGAAACGACTTCCGAGATGATGAGCC-AGCAACCTTTGAGGAT    | 2064 |
| QY | 601  | AsnGIuSerArgArgAspSerLeuPheValProArgArgHISGIYGIuLysArgArgAsnSer | 620  |
| Db | 2065 | AACGAGAGCGCGTAGAGATTCCTTTGTGTGGCCCGACGACACGAGAGAGAGAGCAACGC     | 2124 |
| QY | 621  | AsnLeuSerGIuThrSerArgSerSerArgMetLeuAlaValPheProAlaAsnGIYLys    | 640  |
| Db | 2125 | AACCTGAGTACAGACAGATAGTATCCCGAGATCTGGCAGTGTTCACGCAATATGGAGAG     | 2184 |

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|----|------|---|------|
| QY | 664  | MethISerThrValAspCysAsnGlyValValSerLeuValGlyIProSerValPro       | 660  |
| Db | 2185 | ANGCACACACACTGGGGATGTGCAAGGTGTGTCTTGGTGTGGACCTTCACCTGCT         | 2244 |
| QY | 661  | ThrSerProValGlyGlnLeuLeuProGlnValIleLeuSerProAlaThrAsp          | 680  |
| Db | 2245 | ACATGCTGTGGACACGCTTCTCCAGAGGTATATATGATAGCCACTACTGATGAC          | 2304 |
| QY | 681  | AsnGlyThrThrGluThrGluMetArgLysArgArgSerSerPheHisValSer          | 700  |
| Db | 2305 | AATGGACACACACTGAAAGTGAATGAGAAAGAGCAAGTCTTCCACGCTTCC             | 2364 |
| QY | 701  | MetAspPheLeuGlnAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu    | 720  |
| Db | 2365 | ATGGACTTCTTCAAGAAAGATCCCTCCCAAGGCAACGAGCATGTATACCGACATTC        | 2422 |
| QY | 721  | ThrAsnThrValGlnGluLeuGlnGluSerArgGlnLysCysProProGlySerPyrLys    | 740  |
| Db | 2425 | ACAATATACAGTAGAAGAACTTGAAAGATCCAGGACACAAATGCCACCGTGGTAGTAA      | 2484 |
| QY | 741  | PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValHisVal       | 760  |
| Db | 2485 | TTTTCCAAACATATTTCTTAATCTGGGAGATGTCTCCATATGTGGTAAATGAAACATGTT    | 2544 |
| QY | 761  | ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu    | 780  |
| Db | 2545 | GTCACACCGGTGTGATGGAGCCCATTTGTGTGACCTGGCATCACCATCTGTATTTGCTTA    | 2604 |
| QY | 781  | AsnThrIleuPheMetAlaMetGlnHisTyrProMetThrAspHisPheAsnAsnValLeu   | 800  |
| Db | 2605 | AATATCTCTTTTCAGGGCAGGAGGACACTATCCAAATAGCAGCCATTCATATATGTGCTT    | 2664 |
| QY | 801  | ThrValGlnAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle    | 820  |
| Db | 2665 | ACAGTAGGAACCTGGTTTTCACGTGGGATCTTACAGCAAGAAATGTTTGTGAATATATTT    | 2724 |
| QY | 821  | AlaMetAspProTyrTyrTrpPheGlnGluGlyTyrPasnIlePheAspGlyPheIleVal   | 840  |
| Db | 2725 | GCCATGGATCTCTTACTATTTATTTTCCAGAAAGCGTGGAATATCTTGACGCTTATTTGTG   | 2784 |
| QY | 841  | ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGlnGlyLeuSerValLeuArgSer    | 860  |
| Db | 2785 | ACGCTTACCTGGTAGAACTTGGACTCGCAATGAGTGAAGATATCTGTCTTCGCTCA        | 2844 |
| QY | 861  | PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle    | 880  |
| Db | 2845 | TTTGCATTTGCGGAGAGTTTTCAGTTGCGCAAAATCTTGGCCAAACGTATAATTCGTATTA   | 2904 |
| QY | 881  | LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle    | 900  |
| Db | 2905 | AAGATCATCGGCATTTCCGTGGGGGCTGTGGAAATTTAAACCTGCTTGGCATCATC        | 2964 |
| QY | 901  | ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal    | 920  |
| Db | 2965 | GCTTCATTTTTGGCGGTGGCGGACATCCACTTTGGTGAAGCTACAAACATATGCTCTC      | 3024 |
| QY | 921  | CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer    | 940  |
| Db | 3025 | TGCAGATCGCCGACTGATGTCTCAACTCCACGCTGGACACATGAATGACTTCTCCACTCC    | 3084 |
| QY | 941  | PheLeuIleValPheArgValLeuCysGlyLysIleTrpIleGluThrMetTrpAspCysMet | 960  |
| Db | 3085 | TTTCGATGTGTTCCCGCGTGTGTGTGGGAGATGGATAGAACCATGTGGGACGTATG        | 3144 |
| QY | 961  | GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn    | 980  |
| Db | 3145 | GAGGTGTGTGTCAAGCCATGTGCTTACTAGTCTTCATATGTGTATGTGTGTAAGAAC       | 3204 |
| QY | 981  | LeuValValLeuAsnLeuPheLeuAlaIleLeu***SerSerPheSerAlaAspAsnLeu    | 1000 |
| Db | 3205 | CTAGTGTCTGATATCTTCTTGTGGCCCTGTCTGAGCTCATTTAGTGACACACACTT        | 3264 |
| QY | 1001 | AlaAlaThrAspAspAsnGlnMetAsnAsnLeuGlnIleAlaValAspArgMetHis       | 1020 |

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|----|------|---|------|
| Db | 3265 | GCAGCCACTATATGATATGTAATGAATGATTAATCTCCAAATTCGCTGGATAGCATCGAC    | 3324 |
| Qy | 1021 | LysGIyValaIaTyRValLysaRgLySIeTyRGuIuPheIIeGIInGInSerPheIIeaRg   | 1040 |
| Db | 3325 | AAAGAGTACTCTATGCGAAAGAAAATAATATGTAATTAATCAACAGCTCTCATTAGG       | 3384 |
| Qy | 1041 | LysGIuLySIleLeuaspGcIIuLySProLeuaspApPheAsnAsnLyLyAspSer        | 1060 |
| Db | 3385 | AAACAAAAGATTATAGTATGAAATTAACCACTGTATGATCTAAACACAAAGAACAGT       | 3444 |
| Qy | 1061 | CysMetSerAsnIsthr**GIuIIeGIyLysAsPLeuAsPtyrLeuLyAsPValAsn       | 1080 |
| Db | 3445 | TGRTATGCCAATATATACAGCAGAAATTTGGGAAAAGATCTTGACTATCTTAAAGATGTAAAT | 3504 |
| Qy | 1081 | GIyThrThrSerGIyIIeGIyThrGIySerValGIuLySTyRIIeIeAspGIuSer        | 1100 |
| Db | 3505 | GGAACTCAAGTGTATAGAACTGGCACAGCTGTGAAAATACTATATGATGAAGAAT         | 3564 |
| Qy | 1101 | AsPtyrMetSerPheIIeAsnAsnProSerLeuThrValThrProIIeAlaValGIy       | 1120 |
| Db | 3565 | GATTACATGTGCATTCATTAACAACCCCACTCTTACTGTGACTGTACCAATATGCTGTAGGA  | 3624 |
| Qy | 1121 | GIuSeraspPheGIuAsnLeuAsnThrGIuAspPheSerSerGIuSerAsPLeuGIuGIu    | 1140 |
| Db | 3625 | GAATCTGACTTTGAATATTTAAACCGGAACCTTATAGTAGAATCGGATCTGGAAAGA       | 3684 |
| Qy | 1141 | SerLySGIuLySLeuAsnGIuSerSerSerSerSerGIuGIySerThrValAsPIIeGIy    | 1160 |
| Db | 3685 | AGCAAAAGAAACATGATGAACCACTACTACTATCAGAAAGTAGACATGCTGGACATCGGC    | 3744 |
| Qy | 1161 | AlaProValGIuGIuGIuInProValValGIuProGIuGIuThrLeuGIuProGIuAlaCys  | 1180 |
| Db | 3745 | GCACCTGTAGAAAGACGCCCTGATGGAGAACTGTGAAGAACTCTTGAACCAAGACTTGT     | 3804 |
| Qy | 1181 | PheThrGIuGIyCysValGIuAspPheLyCysCysGInIIeAsnValGIuGIuGIyArg     | 1200 |
| Db | 3805 | TTTCTATAGAGCTGTGTACAAATATCAAGTGTGTCAATATCAATGTGAAGAAAGGACGA     | 3864 |
| Qy | 1201 | GIyLySGInTrPTpAsnLeuAspArgThrCysPheArgIIeValGIuHISAsnTrPhe      | 1220 |
| Db | 3865 | GGAAACAAATGGTGGAAACCTGAGAAAGAGCTGTTCCTCGAATGTTGAACATATACGTGTT   | 3924 |
| Qy | 1221 | GIuThrPheIIeValPheMetIIeLeuLeuSerSerGIyAlaLeuAlaPheGIuAspIle    | 1240 |
| Db | 3925 | GAGACCTTCATTTGTTTCAAGATTTCTTCCTTAGAGTGCGTCTGGCATTTGAGATATTA     | 3984 |
| Qy | 1241 | TyrIIeAspGIuAspArgLySThrIIeLySThrMetIeGIuTyRAlaAspLyValPheThr   | 1260 |
| Db | 3985 | TATATTCATACGCGAAAGACGATTAAGACAGATGTGGATATATGTCAGCAAGGTTTTCACT   | 4044 |
| Qy | 1261 | TyrIIePheIIeLeuGIuMetIeLeuLySTpValAlaTyRGIyTyRGIuThrTyRPh       | 1280 |
| Db | 4045 | TACATTTTCATCTCGAAATGCCTCTTAAATGGGTGGCATATGGGCTATCAAAA-TATTTC    | 4103 |
| Qy | 1281 | ThrAsnAlaTrpCysTrpLeuaspPheLeuIIeValAspValSerLeuValSerLeuThr    | 1300 |
| Db | 4104 | ACCAATCGCGTGGTGGCTGGACCTTCAATATGTTGATGTTTCAATGTGCTAGTTTACA      | 4163 |
| Qy | 1301 | AlaAsnAlaLeuGIyTyRSerGIuLeuGIyAlaIIeLySerLeuArgThrLeuArgAla     | 1320 |
| Db | 4164 | GCAATATCGTTGGGTGTACTCAGAACTTGGAGCCATCAAAATCTCTCAGACACTAAGACT    | 4223 |
| Qy | 1321 | LeuArgProLeuArgAlaLeuSerArgPheGIuGIyMetArgValValValAsnAlaLeu    | 1340 |
| Db | 4224 | CTGAGACCTTAAAGACCTTATCTCCATTTTGAAGGGATATAGGGGTGTGTGAATGCCCTT    | 4283 |
| Qy | 1341 | LeuGIyAlaIIeProSerIIeMetAsnValLeuLeuValCysLeuIIePheThrPheIIe    | 1360 |
| Db | 4284 | TTAAGAGCAATTCATCCATCATGAAATATGCTTGTGTGTATATTCGTGGCTAAT          | 4343 |
| Qy | 1361 | PheSerIIeMetGIyValAsnLeuPheAlaGIyLySPheTyRHSISySIleAsnThrThr    | 1380 |

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|----|------|---|------|
| Db | 4344 | TTTCAGCATCANGGGCGTAAATTTGTTGGCTGGCAAAATTCCTACACGTATTAACACACA    | 4403 |
| Qy | 1381 | ThcGlyspargPheaspIleGluaspValAsnAsnHisThrAspCysLeuLysLeuIle     | 1400 |
| Db | 4404 | ACTGGTACAGGTTTGGACATCGAAGCGTAAATATCATCTGATTTGGCTAAACATAATA      | 4463 |
| Qy | 1401 | GluThrGsnGluThrAlaArgTPlysAsnValLysValAsnPheaspAsnAlaGlyPhe     | 1420 |
| Db | 4464 | GAAGAAATGAGACGCTCGATGGAAATAAGTAAAGTAACTTGATGATATATGAGATTT       | 4523 |
| Qy | 1421 | GlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTyrMetaspIleMetTyrAla    | 1440 |
| Db | 4524 | GGGTATCTCTCTTTCGTTCAAGTTGGCACATTCGAAAGATGATGATATATATGATGA       | 4583 |
| Qy | 1441 | AlaValAspSerArgAsnValGluLeuGlnProLysTyrGluGlnSerLeuTyrMetCyr    | 1466 |
| Db | 4584 | GCACCTTATTCAGAAATGTGGAACTCCACCTCAAGTATGAAGAAAGTCTGTACATGAT      | 4644 |
| Qy | 1461 | LeuThrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIleGly    | 1480 |
| Db | 4664 | CTTACTCTGTATTTATTCATCATCTTTGGGCTCTTCTCACTTCAGACCTGTTATGAT       | 4703 |
| Qy | 1481 | ValIleIleAspAsnPheAsnGlnGlnLysLysLysPheGlyGlyGlnAspIlePheMet    | 1500 |
| Db | 4704 | GTCATCATAGATATTTTCAACGACGCAAAAAGATTTGGAGGTCAACATCTTTTANG        | 4765 |
| Qy | 1501 | ThrGluGlnGlnLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLysProGln    | 1520 |
| Db | 4764 | ACAGAAACAGACGAAAGATTACTAATATGCAATGAAAAATTAGATCGAAAAACCGCA       | 4823 |
| Qy | 1521 | LysProIleProArgProGlyAsnLysPheGlnGlyMetValPheaspPheValThrArg    | 1544 |
| Db | 4824 | AAGCCTATACCTGCACCGAGAAACAAATTTCAAGGAATGGCTTTGATCTGTATCCAGCA     | 4883 |
| Qy | 1541 | GlnAlaPheaspIleSerIleMetIleLeuIleCysLeuAsnMetValThrmMetVal      | 1566 |
| Db | 4884 | CAATTTTGGACATAAACATCATGATTCCTATCTGTCTTAACATGGTCAATGATGATGG      | 4944 |
| Qy | 1561 | GluThrAspAspGlnSerGluTyrValThrThrIleLeuSerArgIleAsnLeuValPhe    | 1586 |
| Db | 4944 | GAACACAGTACCGACGACTGAATATGTACATCAACATTTTGCACGATCATCTGGGTTC      | 5003 |
| Qy | 1581 | IleValLeuPheThrGlyGlyCysValLeuLysLeuIleSerLeuArgHisTyrTyrPhe    | 1600 |
| Db | 5004 | ATTTGGCTATTTACTGGAGAGGTGTACTAACTCATCTCTCTACGCAATTAATATTTT       | 5063 |
| Qy | 1601 | ThrIleGlyTyrAsnIlePheAspPheValValValIleLeuSerIleValGlyMetPhe    | 1620 |
| Db | 5064 | ACCAATTGATGGAATATTTTGTGATTTGTGTGTGTCTATCTCTCAATTGTAGATATGTT     | 5122 |
| Qy | 1621 | LeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPheArgValIleArgLeu    | 1640 |
| Db | 5124 | CTTGGCGAGCGTANAGAAAGATATTTGGTGTCCCTACCTGTGCGAGATGCCGTCT         | 5183 |
| Qy | 1641 | AlaArgIleGlyArgIleLeuArgLeuIleLysGlyValAlaLysGlyIleArgThrLeuLeu | 1666 |
| Db | 5184 | GCTAGGATTTGGCCCAATCTCATGCTGTATCAAGAGACAAAGGGATCCGACGGCTGC       | 5244 |
| Qy | 1661 | PheAlaLeuMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPheLeuVal       | 1688 |
| Db | 5244 | TTTGGTTGATGAGATGCCCTTCCGCTGGCTGTTAACATCGGCTCTTACTCTTCCATGTC     | 5303 |
| Qy | 1681 | MetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgGluValGly    | 1700 |
| Db | 5304 | ATGTTCACTACGCCATCTTTGGGATGTCCAACTTTCCTATTTTAAGACGGAAGTTGGG      | 5366 |
| Qy | 1701 | IleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPheGlnIle    | 1720 |
| Db | 5364 | ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCGCAAT     | 5423 |
| Qy | 1721 | ThrThrSerAlaGlyTyrPaspGlyLeuLeuAlaProIleLeuAsnSerLysProProAsp   | 1744 |
| Db | 5424 | ACAACCTCTGCTGGCTGGAGATGTTCTGTACGCCCATTTCTCAACAGTATAGCCACCGAC    | 5483 |

QY 1741 CysaspProbaunlyValAsnProGlySerSerVallysglyaspCysglyAsnProSer 1760  
 DB 5484 TGTGACCTTAATAAGTTAACTGGAAGCTCAGTTAAGGAGACTGGGAGACCACT 5543  
 QY 1761 ValGlyIlePhePheValSerTyrIleIleIleSerPheValValAsnMet 1780  
 DB 5544 GTTGGAAATTTCTTTTGTTCAGTTACATCATCTCCGTTGCTGGTGAACATG 5603  
 QY 1781 TyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGluProLeu 1800  
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 QY 1881 GluMetAspAlaLeuArgIleGluMetGluIleuArgPheMetAlaSerAspProSerIle 1900  
 DB 5904 GAGATGATCTCTACGAAATACAGATGGAAGAGGATTCAGCTTCAATCTTCCAG 5963  
 QY 1901 ValSerTyrGluProIleThrThrThrLeuIleArgIleGluGluGluValSerAlaVal 1920  
 DB 5964 GTCTCTATAGCAACCACTCAGTCTTAAACGAAACCAAGAGAGATCTGCTGTC 6023  
 QY 1921 IleIleGluArgAlaTyrArgArgIleLeuLeuIleuArgThrValIleGluAlaSerPhe 1940  
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 QY 1961 IleAspArgIleAsnGluAsnSerIleThrGluIleThrAspLeuThrMetSerThrAla 1980  
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 QY 1981 AlaCysProProSerTyrAspArgValThrIleProIleValGluIleGluIleGlu 2000  
 DB 6204 GCTTGCCACCTTCTTATGACCGGGTACAAAGCAATGTGGAAAAACATGACAAAGAA 6263  
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 VERSION AX391130.1 GI:19584232  
 KEYWORDS  
 SOURCE human.  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE  
 1 Turner, C.A., Mathur, B. and Mathur, D.  
 Novel human ion channel proteins and polynucleotides encoding the  
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 JOURNAL Patent: WO 0214498-A 1 21-FEB-2002;

FEATURES  
 SOURCE location/Qualifiers  
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 Alignment Scores:  
 Pred. No.: 0 Length: 5997  
 Score: 10320.50 Matches: 1998  
 Percent Similarity: 99.45% Conservative: 0  
 Best Local Similarity: 99.45% Mismatches: 0  
 Query Match: 99.26% Indels: 11  
 DB: 6 Gaps: 1  
 US-09-930-871-12 (1-2009) x AX391130 (1-5997)  
 QY 1 MetGluIleThrValIleuValProGlyProAspSerPheAsnPheThrArgGlu 20  
 DB 1 ATGAGCAACACAGTGTCTTGTACACAGACCTCAGACTTCACTTCTCAGAGAA 60  
 QY 21 SerLeuAlaIleGluArgArgIleAlaGluIleuIleuIleuIleuIleuIleuIleu 40  
 DB 61 TCTCTGGGCTATTGAAGACGATTCGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120  
 QY 41 LysIleAspAspAspGluAsnGlyProIleProAsnSerAspLeuGluAlaGlyIleAsn 60  
 DB 121 AAAAAAATGACGACGAAAGAGCCCAAGCCAAATGTGACTTGGAAGCTGGAAGAAC 180  
 QY 61 LeuProPheIleTyrGlyAspIleProGluMetValSerGluProLeuGluAspLeu 80  
 DB 181 CTTCATTTATTATGAGACATCTCTCAGAGATGGTGTGAGAGCCCTGAGAGACCTG 240  
 QY 81 AspProTyrTyrIleAsnlySlyThrPheIleValLeuAsnlySlyIleAlaIlePhe 100  
 DB 241 GACCCCTATATATCAATAGAAAACCTTTATATGATATGATATGAGAGAGAGAGAGAG 300  
 QY 101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgIle 120  
 DB 301 CGGTTTCAAGTCCACCTCTGCTTACATTTTAACTCCCTCAATCTCTTAGAGAAATA 360  
 QY 121 AlaIleIleIleuValIleHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140  
 DB 361 GCTATTAGATTGTGGACATCTATTATTCAGCATGTCAATATAGTCCACTATTATGACA 420  
 QY 141 AsnCysValPheMetThrMetSerAsnProProAspThrPheIleAsnValAlaIleTyr 160  
 DB 421 AACTGTGTGTTTATGACAAATGACATGACCTCTCTGATTTGACAAAGAAATGTAGATACAC 480  
 QY 161 PheThrGlyIleTyrThrPheGluSerLeuIleuIleuIleuIleuIleuIleuIleu 180  
 DB 481 TTCACAGAAATATATCTTGTGATCTTATATAAATATATGCAAGGAGATCTGTGTTA 540  
 QY 181 GluAspPheThrPheLeuArgAspProTyrAsnThrPheAsnPheThrValIleThrPhe 200  
 DB 541 GAAGATTTCCTTCTCTGCGGATCCATGGAACCTGCTGATTCATCTGCTATACATTA 600  
 QY 201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220  
 DB 601 GCGAGCTCACAAGATTTGTGGACCTGGCAATGTCTCGGATTTGACAAACATTCAGAGTT 660  
 QY 221 LeuArgAlaLeuIleuIleuSerValIleProGlyLeuIleuIleuIleuIleuIleuIleu 240  
 DB 661 CTCCGAGCATTTGAAGAGATTCAGTTCATTCAGAGCTGGAACCAATGTGGAGGCTG 720  
 QY 241 IleGluSerValIleuIleuSerAspValMetIleuThrValPheCysIleuSerVal 260  
 DB 721 ATCCAGTCTGTGAAGAGCTCTCAGATGATATGCTCTGACTGTCTGTCTGAGAGTGA 780  
 QY 261 PheAlaLeuIleuIleuGluIleuPheMetGlyAsnLeuArgAsnlySlyIleGlnIle 280  
 DB 781 TTTCGCTATTTGGGCTGCGACCTGTTCATGCGCACTGAGAGATTAATATATACATGG 840

QY 281 ProProthrasnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300  
| | | | |  
Db 841 CCGCCACCAATGCTCTCTGGAGAACTAGATAGAAAGAAATATACCTGGAAATTAT 900  
QY 301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTyrPheSerTyrIleGlnAsp 320  
| | | | |  
Db 901 AATGGTACCTTATTAATAAATGCTCTTGGAGTTGACTGGAAAGCAATATATCAAGAT 960  
QY 321 SerArgTyrHisTyrPheLeuGluGluPheLeuAspAlaLeuLeuGlyAsnSerSer 340  
| | | | |  
Db 961 TCAGATATCATATATTTCTCGAGGGTTTTTATGATGCATCATATGTGGAATACCTCT 1020  
QY 341 AspAlaGlyGlnCysProGluGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360  
| | | | |  
Db 1021 GATGCAGGCGCAATGCTCCAGAGGATATATGTGTGTAAGAGCGTGAATCCCAATTAT 1080  
QY 361 GlyTyrThrSerPheAspThrPheSerTyrPheLeuSerLeuPheArgLeuMetThr 380  
| | | | |  
Db 1081 GGTTCACACAGCTTGATACCTTCAAGTTGGCTTTTCTCTGTTCTGACTTAATGACT 1140  
QY 381 GluAspPheThrGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlySerThrTyrMet 400  
| | | | |  
Db 1141 CAGGACTCTGGGAAATCTTATATCAATGACATTAACGTGCTGGGAAACGTACATG 1200  
QY 401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleAla 420  
| | | | |  
Db 1201 AATTTTTGTGTGTGCTATTTCTTGGGCTCATTTCTACTAATAATTTGATCCGGCT 1260  
QY 421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440  
| | | | |  
Db 1261 GTGTGGCCATGGCCCTACAGAGAACAGAAATCAGGCCACTTGGAAACAGAAAGAAA 1320  
QY 441 GluAlaGluPheGluGlnMetIleGluGlnLeuLysGluGlnGluAlaGlnGln 460  
| | | | |  
Db 1321 GAGGCCGAATTTCCAGAGATGATTAACAGCTTAAAGAACACAGAGGAGCTCAGCAG 1380  
QY 461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480  
| | | | |  
Db 1381 GCAGAGAGGCAAGCTCCACAGAACTCCAGAGAGCCAGTGCACAGAGGAGGCTCTCA 1440  
QY 481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500  
| | | | |  
Db 1441 GACAGCTCATCTGAAACCTCTTAAGTTGAGTCCCAAGAGTCTTAAGAGAAAGAAATCCG 1500  
QY 501 ArgLysLysArgLysGlnLysGlnLysGlnLysGlnLysGlnLysArgLysGlnLys 520  
| | | | |  
Db 1501 AGGAAAGAAAGAAAGAAAGAGAGAGCTGTGGGGGAAAGAGAAAGATAGAGTAATTC 1560  
QY 521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540  
| | | | |  
Db 1561 CAAAAATCTGAATCTGAGGAGACATCAGAGAGAAAGGTTTTGCTTCCATTGAAAGG 1620  
QY 541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560  
| | | | |  
Db 1621 AACCGATGACATATGAAAAAGAGGTACTCTCCACACAGCTTGTGTTGACATCCGT 1680  
QY 561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerGlyArgLys 580  
| | | | |  
Db 1681 GCTCCCTATTTTCAACAGGCGCAATATACAGAAACAGCTTTTCAAGCTTTAAGAGCGCG 1740  
QY 581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGlnHisSerThrPheGluAsp 600  
| | | | |  
Db 1741 GCAGAGGATGTGGATCTAGAAAGCACTTCGAGATGATGAGCACAGCACTTTGAGGAT 1800  
QY 601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620  
| | | | |  
Db 1801 AACGAGAGCGTGAAGATCTCTTGTGTGCCCCGAGAGAGAGAGAGAGAGAGAGAGAG 1860  
QY 621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValPheProAlaAsnGlyLys 640  
| | | | |  
Db 1861 AACCTAGTCAGACAGCACTAGGCTCATCCCGATGCTGCGAGCTGTTTCCAGCGAATGGAGAG 1920

QY 641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660  
| | | | |  
Db 1921 ATGCACAGACACTGTGATGCATATGATGTGTCTCTGTTGGTGGAGCTTCACTTCT 1980  
QY 661 ThrSerProValGlyGlnLeuLeuProGluValIleIleLysPheProAlaThrAspAsp 680  
| | | | |  
Db 1981 ACATCGCTGTGGAGAGCTTCTGCGCAGAG----- 2010  
QY 681 AsnGlyThrThrGluThrGluMetArgLysArgArgSerSerPheHisValSer 700  
| | | | |  
Db 2011 ----GGAAACAACACTGAATGAAATGAAAGAAAGAGGCAAGTTCTTCCAGCTTCC 2067  
QY 701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720  
| | | | |  
Db 2068 ATGACATTTCTAGAAAGATCCTTCCAAAGGACAGCAATGATGATGACCACTTCTA 2127  
QY 721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTyrPheLys 740  
| | | | |  
Db 2128 ACAAAATACAGTAAACAACTGTAAGAAATCCAGCAGCAAAATGCCCACTGTGTATAA 2187  
QY 741 PheSerAsnIlePheLeuIleThrAspCysSerProTyrThrLeuLysValHisVal 760  
| | | | |  
Db 2188 TTTTCCACATATTTCTTAATCTGGACTGTCTTCCATATTTGGTTAAAGTAACATGTT 2247  
QY 761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780  
| | | | |  
Db 2248 GTCAACCTGGTGTGATGAGCCATTTGTGACTGGCCATCAGCATCTGATGTCTTA 2307  
QY 781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnValLeu 800  
| | | | |  
Db 2308 AATACCTTTTCAATGAGCCATGAGCACTATCCAAATCAGGACCATTTCAATATGTGCTT 2367  
QY 801 ThrValGlyAsnLeuValPheThrArgLysIlePheThrAlaGluMetPheLeuLysIle 820  
| | | | |  
Db 2368 ACAGTGGAACTGTGTTTCACTGGAGATCTTACAGCAAAATGTTCTGAAATATAT 2427  
QY 821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTyrPheAsnIlePheAspGlyPheIleVal 840  
| | | | |  
Db 2428 GCCATGATCCTTAATATATATTTCCAAAGAGCTGGAATATCTTGAAGGTTTATATGTC 2487  
QY 841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860  
| | | | |  
Db 2488 ACCCTTACCTGTGTAAACCTTGACATCCGCCAAATGTGAAGATATATCTGTTCCCGTCA 2547  
QY 861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTyrProThrLeuAsnMetLeuIle 880  
| | | | |  
Db 2548 TTTGATTTGCTGGAGTTTTCAGATTGGCAAAATCTTGCCCAAGTTAAATATGCTAATA 2607  
QY 881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900  
| | | | |  
Db 2608 AAGATCATGGCAATTCCTGGGGGCTGTGGGAAATTTAACCTCGTCTGGCCATCATC 2667  
QY 901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920  
| | | | |  
Db 2668 GTCCTATTTTTCCTGGTGGGAGATGACAGCTTGTGGTAAAGCTTAACAAAGATGTGTC 2727  
QY 921 CysLysIleAlaAspSerPysGlnLeuProArgTyrPheHisMetLysAspPheHisSer 940  
| | | | |  
Db 2728 TGCAGATGGCGGTATGTTGTAACCTCCAGCGTGCACATGTAATGATGCTTCCCACTCC 2787  
QY 941 PheLeuIleValPheArgValLeuGlyGlyGlyTyrIleGluThrMetPheAspCysMet 960  
| | | | |  
Db 2788 TTCTCATTTGTGTTCCGCGTGTGTGTGGAGATGATGATGAGCAATGTGGAGCTGATG 2847  
QY 961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980  
| | | | |  
Db 2848 GAGCTTGTGGTCAACCAATGCTCCTTACTGCTTCATGATGTGTCATGGATGGAAAC 2907  
QY 981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu\*\*\*SerSerPheSerAlaAspAsnLeu 1000  
| | | | |  
Db 2908 CTAAGTGTCTGTGAATCTTCTTGGCTTGTATAGCTCATATTTGTGTGACGAACTT 2967  
QY 1001 AlaAlaThrAspAspAsnGlnMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020



|    |      |  |      |
|----|------|--|------|
| Db | 2968 | GCACCCCTGATGCTGTAATGAAATGAATTAATCTCCAAATTCGCTGGATGATGCATGCAC   | 3027 |
| Qy | 1021 | LYSGIYVALAATYRYVALLYSARGLYSIETYRGUPEHLEGINGLNSerPheILEaR       | 1040 |
| Db | 3028 | AAAGAGTACTTATGTGGAABAAAABAAATATATGAATTTATTCACACACTCCTCATTAAG   | 3087 |
| Qy | 1041 | LYSGINLYSILEeUaSPGIUuILEYsProLeuASPLeuASnASnLYsASpSer          | 1060 |
| Db | 3088 | AAACAAAGATTTTAGTGAATTAATTAACCACTTGATGATCTTAACACAAAGAAAGACGT    | 3147 |
| Qy | 1061 | CysMetSerSnHStr**GUuILEGIYsASPLeuASTYrLEuLYsASpVALsn           | 1080 |
| Db | 3148 | TGTGTGTCACATCATACARCAAGAAATTTGGAAAGATCTTGACTATCTTAAGATGTAAAT   | 3207 |
| Qy | 1081 | GLYThrHSerGIYILEGIYThRGYsSerSerVALGIuLYsTYrILEASPGLuser        | 1100 |
| Db | 3208 | GGAACTCAAAAGTGATATAGCAACTGGCAGACAGTGTGAAAATATACATTAATGATGAAGT  | 3267 |
| Qy | 1101 | ASPTYrMetSerPheILEASnASnProSerLeuThrVALThrVALProILEALVALcLY    | 1120 |
| Db | 3268 | GATATACATGTCATTCATTAACAACCCAGCTTACTGACTGTACCAATTCGTGTAGA       | 3327 |
| Qy | 1121 | GLuserASPheGLuASnLEuASnThRGUuASPheSerSerGLuserASPheUGlu        | 1140 |
| Db | 3328 | GAATCTACCTTTGAAAAATTTAAACAGGGAAGCTTATGATGAACTCGGAAGAA          | 3387 |
| Qy | 1141 | SerLYSGIuLYsLEuASnGLuserSerSerSerSerGLYGLYSerThrVALAspILEGLY   | 1160 |
| Db | 3388 | AGCAAAAGAAACTGAATGAAGACAGTACTCATCGAAGATGACACTGTGACATCGGC       | 3447 |
| Qy | 1161 | ALAProVALGIuGLuInProVALGIuProGLuGLUThrLEuGLuProGLuALAcYS       | 1180 |
| Db | 3448 | GCACCTGTAGAAAGACAGCCCGTAGTGGAAACCGAAGAAACTCTTGAACCGAAGCTGT     | 3507 |
| Qy | 1181 | PheThrGLuGLYcYSVALGIuAqPheLYsCYSGLINILEASnVALGIuGLUcLYaR       | 1200 |
| Db | 3508 | TTTCACTGAAGCGCTGTGCAAAAGATTTCAAGTGTTCCAATCAATGATGGAAGAGCGGA    | 3567 |
| Qy | 1201 | GLYsYSGINTPRPAuLEuAATGATGTThrCysPheARGILEVALGHLHISAsnTPhe      | 1220 |
| Db | 3568 | GGAAACAAATGGTGGAAACCGTAAGAGAGAGCTGTTCGGAATGCTTGAACATTAACGTGT   | 3627 |
| Qy | 1221 | GLUThrPheILEVALPheMETILELeuLeuSerSerGLYALALEuALAPheGLuASpILE   | 1240 |
| Db | 3628 | GAGACCTTCATTTGTTTCATGATTCCTTAGTAGTGGCTCTGGCATTTGAAGATATA       | 3687 |
| Qy | 1241 | TYrILEASpGLuARGLYsThrILEYsThrMetLeuGLUThrALIASpLYsVALPheThr    | 1260 |
| Db | 3688 | TATATTGATCAGCGAAAGAGATTAAGACAGCTTGGAATATGCTGCAGACAGGTTCCTACT   | 3747 |
| Qy | 1261 | TYrILEPheILELeuGLuMETILEuLeuLYsSTRPVALALATYrGLYTYrGLUThrTYrPhe | 1280 |
| Db | 3748 | TATATTTCATCTGGAAATGCTTCTTAAGATGGGTGGCAATAGGCTATCAACATTAATTC    | 3807 |
| Qy | 1281 | ThrASnALATrPCysSTRPLeuASPheLEuILEVALASpVALSerLEuVALSerLEuThr   | 1300 |
| Db | 3808 | ACCAATGCTGGTGTGGCGGACTTCCTTAATGTGATGCTTCATTTGGTCAGTTAAACA      | 3867 |
| Qy | 1301 | ALASnALALEuGLYTYrSerGLULeuGLYALALEYsSerLEuARGThrLEuARGAL       | 1320 |
| Db | 3868 | GCAATATGCTTGGGTGTACTCAGAACTTGGAGCCATCAATCTCTCAGACACTTAAGACT    | 3927 |
| Qy | 1321 | LEuARGProLeuARGALALEuSERARGPheGLUuMETARGVALVALASnALALEu        | 1340 |
| Db | 3928 | CTGAGACCTCTTAAGAGCTTATCTCGATTTGAAGGAGATAGGGGTGTGTGAATCCCTT     | 3987 |
| Qy | 1341 | LEuGLYALALEProSerILEMetASnVALLEuLEuVALCYsLEuILEPheThrPLeuILE   | 1360 |
| Db | 3988 | TTAGAGCAATTCATCATCATGATATGCTCTTGCTTGTCTTATATCTGCGTAAAT         | 4047 |
| Qy | 1361 | PheSerILEMetGLYALASnLEuPheALAGLYsPheTYrHISCYsILEASnThrThr      | 1380 |

|    |      |   |      |
|----|------|---|------|
| Dd | 4048 | TTTGACATCAATGGGCGTAATTTGTTTGGCTGGCAAAATTCACCACTGATTAATACCCACA   | 4107 |
| Qy | 1381 | ThrGlyspArpGheaspIleGluaspValAsnaspHisfhrAspCysLeuLysLeuIle     | 1400 |
| Dd | 4108 | ACTGGTGACAGGTTTGACATCGAAGACGTGAATTAATCATACTGATGTGCTAAACTATA     | 4167 |
| Qy | 1401 | GluArgasnGluThrAlaArgTfPlyshAsnValLysValAsnPhaspAspValGlyPhe    | 1420 |
| Dd | 4168 | GAAGAAGATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTGAAATAACTAGATATT    | 4227 |
| Qy | 1421 | GlyPyrLeuSerLeuLeuGluValAlaThrPheLysGlyTrpMetAspIleMetfYrAla    | 1440 |
| Dd | 4228 | GGGATCTCTCTTGCTTCAAGTGGCCACTTCGCAAAAGATGGATGATTAATGATGACA       | 4287 |
| Qy | 1441 | AlaValAspSerArgaspValGluLeuGlnProLysTyrGluGlnSerLeuTyrMetfYr    | 1460 |
| Dd | 4288 | GCAGTGAATTCAGAAATGTGGAACTCCAGCCCAAGTAAAGAAAGCTGTACTGAT          | 4347 |
| Qy | 1461 | LeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIleGly    | 1480 |
| Dd | 4348 | CTTACTTGTGTTATTTTCATCATCTTGGGTCCTTCACCTTGAACTGTTATTGGT          | 4407 |
| Qy | 1481 | ValIleIleAspAsnPhespAsnGlnGluLysLysPheGlyGlyGlnAspIlePheMet     | 1500 |
| Dd | 4408 | GTCAATCAATGTAATTTTCAACCGACGAGAAAAGAAATGGAGGTCAACACTCTTAATG      | 4467 |
| Qy | 1501 | ThrGluGlnGluLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLysProGln    | 1520 |
| Dd | 4468 | ACAAGAACAGCAAGAAATACTTAATGCAATGAAATAAAATTGATGATCGAAAAACCGCA     | 4527 |
| Qy | 1521 | LysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheValThrArg    | 1540 |
| Dd | 4528 | AAGCCTATACCTCGACCGAGAAACAAATTTCAAGAAATGCTTGACTTGCTGAACCGA       | 4587 |
| Qy | 1541 | GluValPheaspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMetfYrAla    | 1560 |
| Dd | 4588 | CAAGTTTGTGACATACCAATCAATCATGATTCATCTGCTTAACATGGTCACAAATGATGGTG  | 4647 |
| Qy | 1561 | GluThrAspAspGlnSerGluTyrValThrIleLeuSerArgIleAsnLeuValPhe       | 1580 |
| Dd | 4648 | GAACAGATGACCGAGATGAAATGTGACTACCAATTTTGTACGCATCATCTGGTGTTC       | 4707 |
| Qy | 1581 | IleValLeuPheThrGlyGlyCysValLeuLysLeuIleSerLeuArgHisTyrTyrPhe    | 1600 |
| Dd | 4708 | ATTGGCATTTACTGGAGAGGTGATACGTAACATCATCTCTACGCAATTAATATTT         | 4767 |
| Qy | 1601 | ThrIleGlyTyrPheAsnIlePheaspPheValValIleLeuSerIleValGlyMetfYrPhe | 1620 |
| Dd | 4768 | ACCAATGGATGGAATTAATTTTGATTTTGCTGGCTGTCAATCTCTCAATGTAGATGTTT     | 4827 |
| Qy | 1621 | LeuAlaGluLeuIleGlyLysTyrPheValSerProThrLeuPheArgValIleArgLeu    | 1640 |
| Dd | 4828 | CTTGCCAGACTGATAGAAAGATTTTCGTCTCCCTCAACCTGTTCGAGTGAATCCGCTT      | 4887 |
| Qy | 1641 | AlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgfYrLeuLeu    | 1660 |
| Dd | 4888 | GCTAGATTTGGCCGAATCTACGTGATCAAGAAAGAGCAAGGGGATCGCACGCTGCTC       | 4947 |
| Qy | 1661 | PheAlaLeuMetMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuPheLeuVal       | 1680 |
| Dd | 4948 | TTTGCTTTGATGAGATGCTCCCTTCGCTGGCTGTTTAACATGGGCTCTTACTTCTTACTG    | 5007 |
| Qy | 1681 | MetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgGluAlaGly    | 1700 |
| Dd | 5008 | ATGTTCACTACGCCAATCTTGGGATGTCCAACTTGCTTAATGTAAGGGGAATGTGGG       | 5067 |
| Qy | 1701 | IleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPheGlnIle    | 1720 |
| Dd | 5068 | ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGATATGTGCTATTCCAATTT       | 5127 |
| Qy | 1721 | ThrThrSerAlaGlyTyrPaspGlyLeuLeuAlaProIleLeuAsnSerLysProProAsp   | 1740 |
| Dd | 5128 | ACAACCTCTGCTGCTGGATGATGATGCTAAGCACCACTTCTCAACAGTAAGCACCCGAC     | 5187 |





QY 21 SerLeuAlaIleIleGluArgGlyIleAlaGluIleValAlaLysAsnProLysProAsp 40  
 DB |||||  
 DB 79 TCCTTCGGCGCTATTGAAAGACCATTTGCAGAAAGAAAGCAAGATCCCAACCCAGAC 138  
 QY 41 LysLysAspAspAspGluLysGluProLysProAsnSerAspLeuAlaGlyLysAsn 60  
 DB |||||  
 DB 139 AAAAAAGATGACAGCAAAATGGCCCAAGCAAAATAGTACCTGGAAAGCTGGAAAGAAC 138  
 QY 61 LeuProPheIleIleGlyLysPheProGluMetValSerGluProLeuGluAspLeu 80  
 DB |||||  
 DB 199 CTTCATTAATTAATTAATGAGCATCTCCAGAGATGCTGCAGAGCCCTGGAGAGCCTG 258  
 QY 81 AspProTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100  
 DB |||||  
 DB 259 GACCCCTACTATATCAATTAAGAAAGAACTTTATAGTATGATTAAGAAAGAGGCCATCTTC 318  
 QY 101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120  
 DB |||||  
 DB 319 CGGTCAGTGCACCTCTGCTGATCATTTTAACCTCCATCATCTCTTAGGAAATA 378  
 QY 121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140  
 DB |||||  
 DB 379 GCTAATTAAGATTTGGTACATTCATTAATCAAGCATGCTAATTAATGCTAATTTTGACA 438  
 QY 141 AsnCysValPheMetThrMetSerAsnProProAspTyrThrLysAsnValGluTyrThr 160  
 DB |||||  
 DB 439 AACTGTGCTGTTTATGACATGATGATTAACCTCCCTGATTTGCAGAAAGATGATGATACCC 438  
 QY 161 PheThrGlyIleIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180  
 DB |||||  
 DB 499 TTCACAGGAATATATATCTTTGAAATCACTAATAAATATATTCAGAGGGATCTGTTTA 558  
 QY 181 GluAspPheThrPheLeuArgAspProTyrPheSerThrLeuAspPheThrValIleThrPhe 200  
 DB |||||  
 DB 559 GAAGATTTTACTTCTCTGGGATTCATGGAAGTGGCTGCTCATTTCACTGTCATTAATTT 618  
 QY 201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220  
 DB |||||  
 DB 619 GCGTACGTACAGAGATTTTGGACCTGGGCAATGCTCCGCAATTTGAGAAATTCAGAGT 678  
 QY 221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValAlaLeu 240  
 DB |||||  
 DB 679 CTCGAGCATTTGAAAGAGATTCAGTCATTCAGAGCTGAAACCAATTTGGGAGGCCCTG 738  
 QY 241 IleGluSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260  
 DB |||||  
 DB 739 ATCCAGTCTGTGAAGAGCTCTCAGATGATATGATCTGCTGTTCTGTGAGCGTA 738  
 QY 261 PheAlaLeuIleGlyLeuGluIlePheMetGlyAsnLeuArgAsnLysCysIleGluThr 280  
 DB |||||  
 DB 799 TTTCCTTAATTTGGCTGCGACGCTGTCATGGGCAACCTCGAGAAATAAATGATATACAAATGG 858  
 QY 281 ProProThrAsnAlaSerLeuGluGluLysSerIleGluLysAsnIleThrValAsnTyr 300  
 DB |||||  
 DB 859 CCTCCACCAACATGCTCTTGGAGAAACATAGATTAAGAAAGAAATTAATCTGGAATTA 918  
 QY 301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTyrLysSerTyrIleGluAsp 320  
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 DB 919 AATGAGTACCTTAATTAATGAATGCTCTTGAATTTGACGGAAGCATATATTAACAAGAT 978  
 QY 321 SerArgTyrHisTyrPheLeuGluGluPheLeuAspAlaLeuMetCysGlyAsnSerSer 340  
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 DB 979 TCAAGATTAATCAATTAATTCGCGAGGCTTTTAAAGATGACACTAATGTAAGAAATACCTCT 1038  
 QY 341 AspAlaGlyLysCysProGluGlyTyrMetCysValLysAlaGlyLysArgAsnProAsnTyr 360  
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 DB 1039 GATGAGGCAATGCTCAGAGGATATATGCTGTGAAGAGCTGTGAAGATCCCAATTA 1098  
 QY 361 GlyTyrThrSerPheAspThrPheSerThrAlaPheLeuSerLeuPheArgLeuMetThr 380  
 DB |||||  
 DB 1099 GGTACACAGAGCTTGAATACCTTCAGTGGGCTTCTGCTGTTTGCATTAATGACT 1158

QY 381 GluAspPheThrPheLysLeuLysIleGluThrLeuArgAlaIleAlaGlyLysThrTyrMet 400  
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 DB 1159 CAGACATTCGGGAAAATCTTTATCAACTGATACATTAAGCTGCTCGGAAAGGTAATG 1218  
 QY 401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleValAla 420  
 DB |||||  
 DB 1219 ATATTTTGTGTGTGTGATTTCTTGCGGCTCAATTCATTAATTAATTTGATCTGCT 1278  
 QY 421 ValValAlaMetAlaTyrGluGluGluAsnGluAlaThrLeuGluIleAlaGluLys 440  
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 DB 1279 GTGGTGGCCATGTGCTACGAGGAACAGAAATCAGGCCACCTGGAAAGACGAAAGAA 1338  
 QY 441 GluAlaGluPheGluGluMetIleGluGluIleLysIleGluGluIleAlaGluGlu 460  
 DB |||||  
 DB 1339 GAGGCCGAATTTGAGAGATGATTAACAGCTTAATAAGCAAGAGAGGAGGCTCAGACAG 1398  
 QY 461 AlaAlaThrAlaThrAlaSerGluLysSerArgGluProSerAlaAlaGlyLysLeuSer 480  
 DB |||||  
 DB 1399 GCAGCAAGGCAACCTGCTCAGAAACATTCAGAGAGCCCGCTCAGCAGGCAAGCTCTCA 1458  
 QY 481 AspSerSerSerGluLysSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500  
 DB |||||  
 DB 1459 GACAGCTCATCTGACCTCTTAAGTTGAGTTCCAAAGAGCTTAAGAGAAAGAAATTCGG 1518  
 QY 501 ArgLysLysArgGlyGluLysGluIleSerGlyGluGluLysAspGluAspGluPhe 520  
 DB |||||  
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 QY 521 GluLysSerGluSerGluLysSerIleArgArgGlyGlyPheArgPheSerIleGluGly 540  
 DB |||||  
 DB 1579 CAATAATCTGAATCTGAGGACACATCAGAGAGAAAGTTTGCTTCTCATTTGAAGAGG 1638  
 QY 541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGluSerLeuLeuSerIleArg 560  
 DB |||||  
 DB 1639 AACGATTTGACATTAATAAAGAGTACTCTCCACACAGACTTTGTTGAGACATCCGT 1698  
 QY 561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580  
 DB |||||  
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 DB |||||  
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Qy 861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880  
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Db 2926 AACCTAGTGTCTGAATCTCTTCTGGCTTGTCTTGACGCTCATTTAGTGCAGACAC 2985  
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Qy 1000 LeuAlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMet 1019  
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Qy 1060 SerCysMetSerAsnHisThr--GluIleGlyLysAspLeuAspTrpLeuLysAspVal 1079  
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Qy 1080 AsnGlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTrpIleIleAspGlu 1099  
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Qy 1340 LeuLeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeu 1359  
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Db 4066 ATTTTCAGCATCATGAGCCCTAAATTTGTTGCTGGCAAAATTCACACATGTTTACACAC 4125  
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Qy 1380 ThrThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspLysLeuLysLeu 1399  
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Qy 1440 AlaAlaValAspSerArgAsnValGluLeuGlnProLysTrpGluIleSerLeuTrpMet 1459  
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Db 4306 GCGACAGTTGATTCAGAAATGTGGAACCTCCAGCTCAATATGCAAAAGTGTGACAG 4365  
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Qy 1460 TyrLeuTrpPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIle 1479  
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Db 4366 TATCTTACTTGTATTTTTCATCATCTTGGTCTCTTTTCACCTTGAACCTGTTTAT 4425  
|||||

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|----|------|--|------|
| QY | 1480 | glyValIleIleAspAsnPheAsnGlnGlnIleuIysIysPheGlyGlyGlnAspIlePhe    | 1439 |
| Db | 4426 | GGTCATCATGATNGATATTTCAACACGACGAAAAAGAGATTGGAGGTCACAGACATCTT      | 4485 |
| QY | 1500 | MetThrGlnGlnGlnIleuIysIysIrrYrrAsnAlaMetIysIysLeuGlySerIysIysPro | 1519 |
| Db | 4486 | ATGACAGAGAACGAGAAAGAAATCTTAATGCAAGAAAAAATTTGAGATCAAAAAACG        | 4545 |
| QY | 1520 | GlnIysProIleProArgProGlyAsnIysPheGlnIleMetValPheAspPheValThr     | 1539 |
| Db | 4546 | CAAAAGCCTATACCTGCACACGAAAAAATTTCAAGAAATGCTTTGGACTTCGTAAAC        | 4605 |
| QY | 1540 | ArgGlnValPheAspIleSerIleMetIleuIleCysLeuAsnMetValThrMetMet       | 1559 |
| Db | 4606 | AGACAGATTTTGCATCAATGACATCAAGATTCATCTCATCTTAACATGGTCACATGATG      | 4665 |
| QY | 1560 | ValGlnThrAspAspGlnSerGlyIrrValThrThrIleuSerArgIleAsnLeuVal       | 1579 |
| Db | 4666 | GTGAAACAGATGACGAGATGAAATGTGACTACCATTTGGTCACGATCAATCTGGTG         | 4725 |
| QY | 1580 | PheIleValIleuPheThrGlnGlyCysValIleuIysLeuIleSerLeuArgHisTyrTyr   | 1599 |
| Db | 4726 | TTCAATGTGCTAATTAAGTGAAGAGTGTGACAGAAACATCATCTCTACGCCATTAATAT      | 4785 |
| QY | 1600 | PheThrIleGlyTyrAsnIlePheAspPheValValIleLeuSerIleValGlyMet        | 1619 |
| Db | 4786 | TTTACCATTTGGATGGAATATTTTGGATTTGGTGGTGCATTCCTCATGTAGTATG          | 4845 |
| QY | 1620 | PheLeuAlaGlnLeuIleGlyIysIrrPheValSerProThrIleuPheArgValIleArg    | 1639 |
| Db | 4846 | TTTTTCCGACGATGAGAGAAAGATTTTCGATCCCTACCCGTCGAGTATCCGT             | 4905 |
| QY | 1640 | LeuAlaIrrGlyIleGlyArgIleLeuAlaGlnIleIysGlyAlaIysGlyIleArgThrLeu  | 1659 |
| Db | 4906 | CTTGTCTGATTTGGCCCAATCCTACCTGTGATCAAGACCAAGAGGATCCGACCGTG         | 4965 |
| QY | 1660 | LeuPheAlaLeuMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuPheLeu           | 1679 |
| Db | 4966 | CTCTTTCCTTGGATGATGATGCCCTTCTCGGCTGTTAACATCGGCGCTCTACTCTCTA       | 5025 |
| QY | 1680 | ValMetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaIrrValIysArgIleVal     | 1699 |
| Db | 5026 | GTCAATGTCATCACGCCCATCTTGGGATGTCCAACTTGGCTATGTAAAGGAGGATTT        | 5085 |
| QY | 1700 | GlyIleAspAspMetPheAsnPheGlyuThrPheGlyAsnSerMetIleCysLeuPheGln    | 1719 |
| Db | 5086 | GGGATCCATGATACATTTTCAACTTGTGACCTTGGCAACACCATGATCTGCTAATTCAA      | 5145 |
| QY | 1720 | IleThrThrSerAlaGlyTyrAspGlyLeuLeuAlaProIleLeuAsnSerIysProPro     | 1739 |
| Db | 5146 | ATTACAACTCTGCTGGCTGGATGGATTTGTCAGCACCATTTCCAAACAGTAACCCACC       | 5205 |
| QY | 1740 | AspCysAspProAsnIysValAsnProGlySerSerValIysGlyAspCysGlyAsnPro     | 1759 |
| Db | 5206 | GACTGTACCCCTAATTAATTAACCTCGGACACTCAGTTAAGGAGACATGGGAAACCA        | 5265 |
| QY | 1760 | SerValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValValAsn        | 1779 |
| Db | 5266 | TCTGTGGGAATTTCTTTTGTGACGTTATACATCAATATCTTCCGTGTGGTGGAAC          | 5325 |
| QY | 1780 | MetTyrIleAlaValIleLeuGlnAsnPheSerValAlaThrGlnIleuSerAlaGlnPro    | 1799 |
| Db | 5326 | ATGTACATCGCGGTATCTCTGAGAACTTCAGTGTGCTACTGAGAAAGTGACAGACCT        | 5385 |
| QY | 1800 | LeuSerGlnAspAspPheGlyMetPheTyrGlnValTrrGlyIysPheAspProAspAla     | 1819 |
| Db | 5386 | CTGAGTCAGAGATCACTTTAGATGTTTATGAGGTTTGGAGAGATTTGATCCGAGATCA       | 5445 |
| QY | 1820 | ThrGlnPheMetGlnPheGlyIysLeuSerGlnPheAlaAlaIleuGlnProIleu         | 1839 |
| Db | 5446 | ACTCAGTTCAGAAATTTAAAAAATTAATCTCAGTTTGCAGCTGGCGTTGAACGCCCTCTC     | 5505 |

|    |      |   |      |
|----|------|---|------|
| Oy | 1840 | AasnpproglInProasnllyseuglnlneulllealameLaspleunPrometvalsergly | 1859 |
| Dd | 5506 | RatfctccCAACAACCAAACTCCAGCCTCATGGATCGGATGTGGCAATGGTGGT          | 5565 |
| Oy | 1860 | AspargllleHisCysleusnpilleLeupePhaIaphethrLysArgValIeuglyguSer  | 1879 |
| Dd | 5566 | GACCGGATCCATGTCCTTGATATCTTATTGGCTTTACAAACGGGCTTCAGAGAGA         | 5625 |
| Oy | 1880 | GIylglumetasPalaleunArglleglmnetglugluArgphemetalaseranProser   | 1899 |
| Dd | 5626 | GGAGAGATGGATGCTCTMGAAATACAGATGAAGAAGGCATCATGGCTTCCAATCCTTCC     | 5685 |
| Oy | 1900 | LysValserTyrrGlhProIlethrThrmPrlleuLysArgLySglngluIuvalseAla    | 1919 |
| Dd | 5666 | AMGGCTCTTAACAGCCATCACTACTCTTTAAAACGAAAAACAAGAGAAATATCTGCT       | 5745 |
| Oy | 1920 | ValllelelglnarGalAtyrArgArghIsleuleuLysArgThrValIySglnaIaser    | 1939 |
| Dd | 5746 | GCATATTATCACGGTGTACAGAGGCCACCCTTTAAGCGAACGTATAAACACCTTCC        | 5805 |
| Oy | 1940 | PheTrTyrrashLysAsnLyslleLysgllyglialaIsnleuIleLysglunspMet      | 1959 |
| Dd | 5806 | TTTTAGTCAATAAAAAACAAATCAAGGTGGCGCTAAATCTTATAAAAAAACAACATG       | 5865 |
| Oy | 1960 | IlelleasPargIIeasnglunsnserllePrgIuvLysThrAspleuthrMetserThr    | 1979 |
| Dd | 5866 | ATATTTGACAGATATAAGAAACCTATTTACAGAAAAAACGATCTGCATGTCCACT         | 5925 |
| Oy | 1980 | AlaalacysProProSerTyrrAspargValThryLysProIleValgluYshHsgluIn    | 1999 |
| Dd | 5926 | GCAGCTTGCCACCTTCATATGACCGGGGTGACAAAGCCCAATGTGTGAATAAACATGACGA   | 5985 |
| Oy | 2000 | GIucglylsAspgluLysAlalySgltylys                                 | 2009 |
| Dd | 5986 | GAAGGCAAAAGATGAAAAAGCCAAAGGGA                                   | 6015 |

RESULT 7  
RNSCPJR RNSCPJR

|            |   |          |      |        |                 |
|------------|---|----------|------|--------|-----------------|
| LOCUS      | RNSCPJR   | 8398 bp  | mRNA | linear | ROD 12-SEP-1993 |
| DEFINITION | Rat Brain mRNA for sodium channel protein. I.                     |          |      |        |                 |
| ACCESSION  | X03638  |          |      |        |                 |
| VERSION    | X03638.1  | GI:57216 |      |        |                 |
| KEYWORDS   | glycoprotein; sodium channel.                                     |          |      |        |                 |
| SOURCE     | Rattus norvegicus.  |          |      |        |                 |
| ORGANISM   | Rattus norvegicus.  |          |      |        |                 |
|            | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |          |      |        |                 |
|            | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;     |          |      |        |                 |
|            | Rattus.   |          |      |        |                 |

REFERENCE  
AUTHORS Noda,M., Ikeda,T., Kayano,T., Suzuki,H., Takeshima,H., Kurasaki,M.,  
Takahashi,H. and Numa,S.  
Existence of distinct sodium channel messenger RNAs in rat brain  
Nature 320 (6058), 188-192 (1986)

JOURNAL MEDLINE 86146901  
PUBMED 3754035

FEATURES  
SOURCE location/Qualifiers  
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 Best Local Similarity: 98.11% Mismatches: 14  
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 QY 21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluAlaLysAsnProLysProAsp 40  
 Db 312 TCTCTTGACGCTATGTGAAGGCGCATTCGAGAAAGAAAGCTTAAGATCCCAAGCCAGAC 371

QY 41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuAlaGlyLysAsn 60  
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 QY 121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140  
 Db 612 GCTATTAAGATTTGGTATCATCATATTCAGCATGTTAATTAATTAATGTCACCTATTGTGACG 671  
 QY 141 AsnGlyValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160  
 Db 672 AACTGCTATTTATGACAAATGATTAACCTCTGACCTGACGACAAAGAAATGATAGATACAC 731  
 QY 161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180  
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|    |      |   |      |
|----|------|---|------|
| Qy | 401  | IllePhePheValIleValIlePheLeuGlySerPheTyrIleuIleAsnIleuIleuLa    | 420  |
| Db | 1452 | ATAATTTTTCGCTGGCTCATTTTCCTGGCTCATTTCTACCTGTAACCTTGATCTCGGCT     | 1511 |
| Qy | 421  | ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluLaIaGluGln      | 440  |
| Db | 1512 | GTGGTGGCCATGGCCATTATGAGAAACAGAACACAGGCCACATTTGGAGAGAGCTGACACGAA | 1571 |
| Qy | 441  | GluValaGluPheGluGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaIaIaGlnGln  | 460  |
| Db | 1572 | GAGCAGAGGTTTCAGCAGATGCTGGAGCACTCAACAGACAGAGCAACCCACACAG         | 1631 |
| Qy | 461  | AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer    | 480  |
| Db | 1632 | CGGGCGGACGACACAGCATGATGAAGACATTCACAGGGAGCCACAGTGCACGGGCGCTCTCA  | 1691 |
| Qy | 481  | AspSerSerSerGluAlaSerLysLysSerSerLysSerAlaLysGluLysArgTrpAsnArg | 500  |
| Db | 1692 | GATAGCTCTTCAGAAAGGCTCCAAAGTTGAGTTCAAAGAGCGCTAAAGAAAGGCGGAATGG   | 1751 |
| Qy | 501  | ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspIlePhe    | 520  |
| Db | 1752 | AGGAAAAAAGAAAAACAGAAAGAGAGCTGCGAGGGGGAAGAAAGATGATGATGAATTC      | 1811 |
| Qy | 521  | GlnLysSerGluSerGluAspSerIleLeuArgLysGlyPheArgPheSerIleLeuLys    | 540  |
| Db | 1812 | CACAAATCCGAGTCCGAAGATACATCAGAGAGGAAAGGCTTCCTCCATGACAAAGG        | 1871 |
| Qy | 541  | AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuAsnSerIleArg    | 560  |
| Db | 1872 | AACAGACTGACCTTATGAAAAAGAGTACTCTTCCCACTACAGTCTCTGTGGACATTCG      | 1931 |
| Qy | 561  | GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgLysArg    | 580  |
| Db | 1932 | GGCTACACTGTTTTCCCGAGACGCAATAGACAGAAACAGCTTTTCAGCTTCAGAGGGCA     | 1991 |
| Qy | 581  | AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp    | 600  |
| Db | 1992 | CGGAGAGACCTGGGGTCTGGAAATGATTTTCCGAGCAAGACACAGCACCTTCCAGGAC      | 2051 |
| Qy | 601  | AsnIleuSerArgArgAspSerLeuPheValProArgArgHisGlyLysArgTrpAsnSer   | 620  |
| Db | 2052 | AATAGAGCAGAGACAGACACTCTCTGTTTGTTCGCCGAAGCAATGGAGAGCGACGACACGT   | 2111 |
| Qy | 621  | AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValPheProAlaAsnGlyLys    | 640  |
| Db | 2112 | AACCTCAGCCAAACACAGACATCTCCGCCAATCTGGCGGGCTTCCAGCAAGCGGAAAG      | 2171 |
| Qy | 641  | MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro    | 660  |
| Db | 2172 | ATGCAACGACAGAGTGGATGTCATATGGATGTGGTTCCTTGATGGGCGGACCCCTGGTCCG   | 2231 |
| Qy | 661  | ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp    | 680  |
| Db | 2232 | ACATTCGCGCAGTTGACAGCTTCTGCGCAGAGGTGATATATGATAGCCACATCATGATAC    | 2291 |
| Qy | 681  | AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerPheHisValSer       | 700  |
| Db | 2292 | AATGGAACAACACTACTGAAATCTGAGATGAGAAAGAGAGGTCAAGTCTTTCATATTTCC    | 2351 |
| Qy | 701  | MetAspPheLeuGluAspProSerGlnArgGlnAlaMetSerIleAlaSerIleLeu       | 720  |
| Db | 2352 | ATGCACTTTCTTGGAGATCTCTCCAGAGGCAAAAGGCAATAGACATTTGCCAGCATTTA     | 2411 |
| Qy | 721  | ThrAspThrValGluGluGluGluGluGluGluGlnLysCysProProCysTrpTyrLys    | 740  |
| Db | 2412 | ACAATATCAGAGTGAAGACATGAGAAATCCAGACAAATATGTCACCTGTTGGATATA       | 2471 |
| Qy | 741  | PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal    | 760  |
| Db | 2472 | TTTTTCCAAACATATTTTAAATTTTGGACATGTCTCCATATATGGCTTAAAGATTAAACATAT | 2531 |
| Qy | 761  | ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu    | 780  |

|   |      |   |      |
|---|------|---|------|
| D | 2532 | GTCAACCTGGTTGTGATGAGCCCAATTGTGACCTGGCACTTACATTCATTCGTAATGTGTTA  | 2591 |
| O | 781  | AsnThrLeuPheMetAlaMetGluHisTyr-ProMetThrAspHisPheAsnValLeu      | 800  |
| D | 2592 | ATAACCTTTTCATGGGCATGAGACATACCCTCATGCTGACATATTCATCATCTACTT       | 2651 |
| O | 801  | ThrValGlyAsnLeuVal-PheThrGly-IlePheThrAlaGluPheLeuLysIleIle     | 820  |
| D | 2652 | ACAGTAGGAACCTTGTTTCACAGGGAGTCTCACAGCAAGAAATGTTCTGAAAAATCATTT    | 2711 |
| O | 821  | AlaMetAspProTyrTyrTyrPheGlnGluTyrAsnIlePheAspLysPheIleVal       | 840  |
| D | 2712 | GCCATGAGACCTTCACTATATATTTCCAAAGAGGGCTGGAAATCTTGTATGTTTCATTGTG   | 2771 |
| O | 841  | ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluLysLeuSerValLeuArgSer    | 860  |
| D | 2772 | ACACCAACCTGGTAGAATCTTGCCCTTGCCAAATGTGGAAAGGTATCATGTTCTCCGTCCA   | 2831 |
| O | 861  | PheArgLeuLeuArgVal-PheLysLeuAlaLysSerTyrProThrLeuAsnMetLeuIle   | 880  |
| D | 2832 | TTCACAGCTGCTCCAGATCTTCAAGTTGGCAAAATGCTGGGCCACACTGAAATGTCATTT    | 2891 |
| O | 881  | LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle    | 900  |
| D | 2892 | AAGATCAATGGCAACTGTGTGGGGCCACTGTGGCACTGACCTGTTGCTGGCCATCATTC     | 2951 |
| O | 901  | ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspGlyVal    | 920  |
| D | 2952 | GTTCTCATTTTGGCGGTGGGATGCGATCCACTTGTGGCAAAAGTTCAAAATGTTGTC       | 3011 |
| O | 921  | CysLysIleAlaSerAspCysGlnLeuProArgTyrPheIleMetAsnAspPheHisSer    | 940  |
| D | 3012 | TGCAAAATTTGCACTGACATGCAAACTCCCGCGTGGCAATGACACATCTTCCACATCC      | 3071 |
| O | 941  | PheLeuIleVal-PheArgValLeuCysGlyGluTyrIleGluThrMetTyrAspCysMet   | 960  |
| D | 3072 | TTCCTGATCGATTCCGAGTCTGTGTGGGAGATGATAGACCATGTGGGACATGCAATG       | 3131 |
| O | 961  | GluValAlaGlyGlnAlaMetCysIleuThrVal-PheMetMetValMetValIleGlyAsn  | 980  |
| D | 3132 | GAGGTCCGGGTCAAGCCATGTGCTTACTGTTCTATGATGGTCATGGTGTATGGAGAC       | 3191 |
| O | 981  | LeuValValLeuAsnLeuPheLeuAlaLeuLeu**SerSer-PheSerAlaAspAsnLeu    | 1000 |
| D | 3192 | CTTGGGTCCTGAACCTTTTCTTGCGCTTGCTCTGAGCTCATTTAGTSCAACACACTT       | 3251 |
| O | 1001 | AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis    | 1020 |
| D | 3252 | GCAGCACTGTGACATGACCAAGAAATGACAACTTCAAAATGCTGTGTGACAGATGCAC      | 3311 |
| O | 1021 | LysGlyValAlaTyrValLysArgGlyLysIleTyrGluPheIleGlnGlnSerPheIleArg | 1040 |
| D | 3312 | AAAGAGTAGTCTTATGTAAGAAAAATATATAGATTTATTCACAGCTTCTTGTATGG        | 3371 |
| O | 1041 | LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnLysLysAspSer       | 1060 |
| D | 3372 | AAACGAAAGATCCATAGTAAATTAAGCACTTGATGATCTTAAACAACGAAAGAACAT       | 3431 |
| O | 1061 | CysMetSerAsnHisThr**GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn     | 1080 |
| D | 3432 | TGTACATCTAACACACAGACAGATGGGAAGATCTGAGCTGATGAAAGATGTGAT          | 3491 |
| O | 1081 | GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspLysSer    | 1100 |
| D | 3492 | GGAACCAAGATGGCAATAGGAGCCGACAGATGTGAAATATCATATCATGATGAGAGT       | 3551 |
| O | 1101 | AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly    | 1120 |
| D | 3552 | GACTACATGTCATTCATTAACCAACCCACGCTTACCGTACTGTGCCCATTTGCTGTGGGA    | 3611 |
| O | 1121 | GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGln    | 1140 |







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Db 792 GAAGATTACTTCTCTGTCGACCATGAACTGGCTGACTTCTGCTCATTTACATTC 851  
Oy 201 AATATYValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220  
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Db 852 GATATGTACAGGAGTTTGTGACCTGGGCAATGTCTCAGCGTTGAGAACATTCACAGATT 911  
Oy 221 LeuArgAlaLeuArgThrIleSerValIleProGlyLeuArgThrIleValGlyAlaLeu 240  
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Db 912 CTTCCGACATTTGAAAAAATATCATCATCCAGGCTGAGACCATCTGGGGGCCCG 971  
Oy 241 IleGlnSerValIleArgLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260  
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Db 972 ATCCAGTCTGTGAAGAGCTCTCTGACGTATGATCTCAACGCTGTCTGTCTCAGTGTG 1031  
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Db 1032 TTTGGCTTAATCGGGTGTGACGTTTTCATGCGGCACTGAGAAATAAGTGTACAGTGG 1091  
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Db 1152 AACGGACACTTGTAAATGAACCGTGTGTGAATTTGACTGGAAATCATATTCATCAAGC 1211  
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Db 1572 GAAGCAGAGTTTACAGAGATGCTGGAGCACTGAAAGAGCAGAGCCGACAGCAG 1631  
Oy 461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480  
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Db 1632 GCGGCGGACAGCAACAGCATCAGAAATTTCCAGGGAGCCAGCTGACGCGGACGCTCTCA 1691  
Oy 481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500  
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Db 1692 GATAGCTCTTCAGAGAGCTCCAAAGTTGATGATCAAGAGCCCTAAAGAGAGCGGAATCGG 1751  
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Db 1752 AGAAAAAGAAAAAGAAAGAGCACTCTGAGAGGGAAGAAAGATGATGATGATTC 1811  
Oy 521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGlnGly 540  
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Db 1812 CACAAATCCGAGTCCGAAGATAGCATCAGAGAGAGGCGCTCCGCTTCATGAGAGGG 1871  
Oy 541 AsnArgLeuThrTrpGluLysArgTrpSerProHisGlnSerLeuLeuSerIleArg 560  
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Db 1872 AACAGACTGACCTATGAAAAAGAGTACTCTTCCCATCATGACTCTGTTGAGCATTCGC 1931  
Oy 561 GlySerLeuPheSerProArgArgAsnSerArgTrpHisSerLeuPheSerPheArgGlyArg 580  
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Db 1932 GGCCTCACTGTTTCCCGAGAGCCAAATAGCAGAAAGCTTTTTCAGCTTCACAGGGGCA 1991  
Oy 581 AlaLysAspValGlySerGluAsnAspPheAlaAspAlaGlnHisSerThrPheGluAsp 600  
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Db 1992 GCGAAGAGCGTGGGTGTGAAATGATTTTGGGAGATGAGCAGACACCTTCAGAGAC 2051  
Oy 601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620  
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Db 2052 AATGAGAGCAGAGAGACACTCTCTGTTTCCCGGAAGACATGAGAGCGAGCAACAGT 2111  
Oy 621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValPheProAlaAsnGlyLys 640  
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Db 2112 AACCTCAGCCAAACAGAGATCTCCCGAATCTGCGGGGCTTCAGCAAAACGGGAG 2171  
Oy 641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660  
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Db 2172 ATCCACAGCAGACTGGATGCAATGATGTGTGTTCTTCTGGTGGCGGACCTCGGTCCG 2231  
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Db 2712 GCCATGAGACCTTACATTTATTTTCCAAAGGCGCTGGAATATCTTGAATGTTTCATTTG 2771  
Oy 841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860  
|||||  
Db 2772 ACACTGACCTGTGAGAACTTGGCTTGCCAATGTGAAAGGTTATATCAGTTCTCCGTCA 2831  
Oy 861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880  
|||||  
Db 2832 TTTCCGACTGCTCCGAGCTTCAATGTTGCAAGAGGCTGCGCCACATGACATGCTCATTT 2891  
Oy 881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValIleAlaIleIle 900  
|||||  
Db 2892 AAGATTCATCGCAACTCGGTGGGCGCACTGGCACTGACCTGTGGTGGCATCATTC 2951  
Oy 901 ValPheIlePheAlaValAlaGlyMetGlnLeuPheGlyLysSerTrpLysAspCysVal 920  
|||||  
Db 2952 GTCTTCAATTTTGGCGGTGGTGGCATGACGCTGTCCGCAAAATTTTCAAAAGATTTGTCTC 3011

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|----|------|---|------|
| OY | 921  | CysLysIleAlaSerAspCysGlnLeuProArgTyrHisMetAsnAspPheHisSer       | 940  |
| Db | 3012 | TCGAAAATATGGCAATGACTGCAAACTCCCGCTGGCACATGAAACACTTCTCCACATCC     | 3071 |
| OY | 941  | .PheLeuIleValPheArgValLeuCysGlyGluTyrIleGluThrMetCysPysMet      | 960  |
| Db | 3072 | TTCCGATCGGTTCGCCAGAGTCGTGTGGGGATGGATAGACCACTGTGGGACGTGCATG      | 3131 |
| OY | 961  | GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn    | 980  |
| Db | 3132 | GAGGCGGGGTCAAGCCATGTGCTTACTGTCTTCATGATGCTCATGTGATATGAGAAC       | 3191 |
| OY | 981  | LeuValValLeuAsnLeuPheLeuAlaLeuLeu**SerSerPheSerAlaAspAsnLeu     | 1000 |
| Db | 3192 | CTTGTGGTCCGTAACCTCTTCTGGCCCTTCTCTGAGCTCAATTAGTTCACACAACCTT      | 3251 |
| OY | 1001 | AlaAlaThrAspAspAsnGlnMetAsnAsnLeuGlnIleAlaValAspArgMetHis       | 1020 |
| Db | 3252 | GCACCCACTGCAGTATGCAACGAATATGAAACACTTCAATATGCTGTGGACAGATGAC      | 3311 |
| OY | 1021 | LysGlyValAlaTyrValLysArgLysIleTyrGluPheAlaGlnGlnSerPheIleArg    | 1040 |
| Db | 3312 | AAAGAGACTGTTATGTAATAAGAAAAATATAGATTTATTCACAGCTCTTGTGTAGG        | 3371 |
| OY | 1041 | LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnLysLysAspSer       | 1060 |
| Db | 3372 | AAACAGAAAGATCTAGATGAATTAAGCCACTTGATGATCTAAACACAGAAAGACAAT       | 3431 |
| OY | 1061 | CysMetSerAsnHisThr**GluIleGlyLysAspLeuAspTyrIleuLysAspValAsn    | 1080 |
| Db | 3432 | TGTATCATCTTAACCAACAGACAGAGATTTGGGAAAGATCTGAGCTGTCAAAATGTGAT     | 3491 |
| OY | 1081 | GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleLeuAspGlnSer    | 1100 |
| Db | 3492 | GGAACCAAGAGTGGCATRAGGACCGGACGACGTGTGAAAATACTATCTTATATAGACT      | 3551 |
| OY | 1101 | AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly    | 1120 |
| Db | 3552 | GACTACATGTCATCTAATAAACAACCCAGCCTCACCTGACTGTGGCCATTCCTGTGGGA     | 3611 |
| OY | 1121 | GlnSerAspPheGlnAsnLeuAsnThrGluAspPheSerSerGlnSerAspLeuGluGlu    | 1140 |
| Db | 3612 | GAGTCTGACTTGAAACTTAACACAGAGACTTTAGCAGATCAATCAATCTAACAAATA       | 3671 |
| OY | 1141 | SerLysGlnLysLeuAsnGlnUserSerSerSerSerGlnGlySerThrValAspIleGly   | 1160 |
| Db | 3672 | AGCAAAAGAAACTCAACAGAAAGACTGATGTTCTCTCAAGAGAAACACATGATACATCGG    | 3731 |
| OY | 1161 | AlaProValGlnGlnGlnProValValGluProGluGluThrLeuGlnProGluAlaCys    | 1180 |
| Db | 3732 | GGCGCTGGGAGAAAGCCTGTGCATGAGAAACAGAAAGAAACCTTGAGCCGCAACTGCC      | 3791 |
| OY | 1181 | PheThrGlnGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg    | 1200 |
| Db | 3792 | TTCACTGAAGCTGTGTGCAGAAATTCAGTCACTGTCATATCAAGTGTGGAAGAAAGAGA     | 3851 |
| OY | 1201 | GlyLysGlnTyrPheAsnLeuArgArgThrCysPheArgIleValGlnHisSerPhe       | 1220 |
| Db | 3852 | GGAAACACGTGTGTGAACCTTGGAGAGAGCTGTTCCGATATGTTGAGACAACTGGTTT      | 3911 |
| OY | 1221 | GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle    | 1240 |
| Db | 3912 | GAGACCTTCAATGTGTTCAATGATTCCTCCTCAGTATAGTGTGCGCTTGAGAGATATA      | 3971 |
| OY | 1241 | TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr    | 1260 |
| Db | 3972 | TACATGATATGCGAAAGAAATCAACAGACATGCTGATATGCAGACAAAGTTTACT         | 4031 |
| OY | 1261 | TyrIlePheIleLeuGluMetLeuLeuLysTyrPheValAlaTyrGlyTyrGlnThrTyrPhe | 1280 |
| Db | 4032 | TACATTTTATCTCGGAGATGCTCTCAATATGGTATGCTTACGGGTATCAACAGTATTC      | 4091 |

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| OY | 1281 | Thsasnlatprcysrtpleuasrphelieu11eValAspvalSerleuValSerleuThr     | 1300 |
| Db | 4092 | ACCAATGCGTGGTGTGGCGGACCTTCATATGGTGAATGGTTCATGGTCAGTTAAACA        | 4151 |
| OY | 1301 | AlaasnAlaLeuglyTySerGluLeuglyAla1eLysSerLeuArgThrLeuArgLa        | 1320 |
| Db | 4152 | GCAATGCGTTGGTTACTGTGAACTTGGGGCCATCAAGTCCCTTAAGGACCTAAGACT        | 4211 |
| OY | 1321 | LeuArgProLeuArgAlaLeuSerArgpheGluGlyMetArgValValAlaAlaLeu        | 1340 |
| Db | 4212 | CTGAGACCCCTAAGAGCCTTATACAGATTGAAGGGATGAGGGTGGTTGTGAATCCCTG       | 4271 |
| OY | 1341 | LeuGlyAla1eProSer11eMetAsnValLeuLeuValCysLeu11ePheThrLeu11e      | 1360 |
| Db | 4272 | TTAGAGCAATTCATCCATCAATCAAGAAATGGCTTCGGTTGGCTTAATTCGGCTAAT        | 4331 |
| OY | 1361 | PheSer11eMetGlyValAsnLeuPheAlaGlyLysPheThrHisCys11eAlaSerThr     | 1380 |
| Db | 4332 | TTTCAGCATCGGCGCTAAATTTGTTGGCGAAATTCACCACTGGGTGAACCCACA           | 4391 |
| OY | 1381 | ThrGlyAspArgPheAsp11eGluAspValAsnAsnHisThrAspCysLeuLysLeu11e     | 1400 |
| Db | 4392 | ACTGGTGACACATTGTGAGATCACGAAAGTCATTAATCATCTGATGGCTAAACTATA        | 4451 |
| OY | 1401 | GluArgAsnGluThrAlaArgTTPlysAsnValLysValAsnPheAspAsnValGlyPhe     | 1420 |
| Db | 4452 | GAAGAAGATGAGACTGCCGCGGTGGAATAATGTGAAGTAATCTGTGAATAGTAGATT        | 4511 |
| OY | 1421 | GlyTyreSerLeuLeuGlnValAlaThrPheLysGlyTPPmetAsp11eMetArgLa        | 1440 |
| Db | 4512 | GGGATCTCTCTTGGCTCAAGTTGGGACGTTAAAGGTTGGATGCAATCATGTATCA          | 4571 |
| OY | 1441 | AlaValAspSerArgAsnValGluLeuGlnProLysTyrgluSerLeuTyreTyr          | 1460 |
| Db | 4572 | GCAATTGATTCCAGAAATGTGGAACGCGACCTAAGTATGAGAAAGCCTGACATGAC         | 4631 |
| OY | 1461 | LeuTyrrPheVal11ePhe11e1ePheGlySerPhePheThrLeuAsnLeuPhe11eGly     | 1480 |
| Db | 4632 | CTGTACTTCGTCATCTTCATCATCTTCGCGCTGGCTTCCTACCTAAATCTATTCACGT       | 4691 |
| OY | 1481 | Val11eLeuAspAsnPheAsnGlnGlnLysLysPheGlyGlyGlnAsp11ePheMet        | 1500 |
| Db | 4692 | GTCATCATAGCAACATTCACACGACGAAAGAAAGATTGGAGGTCAACATCTTAATG         | 4751 |
| OY | 1501 | ThrGluGluGlnLysLysTyrrTyrrAsnAlaMetLysLysLeuGlySerLysGlyProGln   | 1520 |
| Db | 4752 | ACAAGAAGACGAAAGAAATCTTAATGCATGAGAAATTGGATCAAAAAGCCACAA           | 4811 |
| OY | 1521 | LysPro11eProArgProGlyAsnLysPheGlnGlyMetValPheAspPheValThrArg     | 1540 |
| Db | 4812 | AAGCCTATCCCTGACCTGGAAACAAATTTCAAGGATGTGCTTGACTTTGTAAACGA         | 4871 |
| OY | 1541 | GlnValPheAsp11eSer11eMet11eLeu11eCysLeuAsnMetValThiMetVal        | 1560 |
| Db | 4872 | CAAGTGTTCACATCAACACATCAATCCATCTGTCAACATGTGATCAACATGATGGTG        | 4931 |
| OY | 1561 | GluThrAspAspGlnSerGlyTyrrVal11eThrThr11eLeuSerArg11eAsnLeuValPhe | 1580 |
| Db | 4932 | GAACGAGTATCCAGACGACTTATGTGACACAGATTTGTACAGTATACCTGGTGTCC         | 4991 |
| OY | 1581 | 11eValLeuPheThrGlyGlyCysValLeuLysLeu11eSerLeuArgHisTyrrTyrrPhe   | 1600 |
| Db | 4992 | ATGTGCTGTTCACCGGCGAGTCCGTCGCGAAGTCATCTCCCTCCGCAATTATTAATTC       | 5051 |
| OY | 1601 | Thr11eGlyTyrrAsn11ePheAspPheValValVal11eLeuSer11eValGlyMetPhe    | 1620 |
| Db | 5052 | ACCATTCGCTGCAATATTTTTCATTTTGTGGTGGTCATCCCTTCATTTGTAGGAATGTT      | 5111 |
| OY | 1621 | LeuAlaLeuLeu11eGlyLysTyrrPheValSerProThrLeuPheArgVal11eArgLeu    | 1640 |
| Db | 5112 | CTTCGGAGCTGATAAAGAAGATTTTCGTGTCCTCCATCCGTTCCGAGTATCCGCTG         | 5171 |
| OY | 1641 | AlaArg11eGlyArg11eLeuArgLeu11eLysGlyAlaLysGly11eArgThrLeuLeu     | 1660 |

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 QY 1681 MetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValIysArgIleValGly 1700  
 Db 5292 ATGTCATCTACGCCATCTTTGGGATGTCACATTTGCTTATTTAGAGGAGAGTTGGA 5351  
 QY 1701 IleAspAspMetPheAsnPheGlyIleuThrPheGlyAsnSerMetIleCysLeuPheGlnIle 1720  
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 QY 1901 ValSerTyrGlnProIleThrThrThrLeuIysArgIysGlnIleValSerAlaVal 1920  
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 Db 6012 ATCATTTACGCGCTTACAGGCGCCACCTTTTGAACGCAACATAAACAAGCTTATTC 6071  
 QY 1941 ThrTyrAsnIysAsnIysIleIysGlyIleValAsnLeuIleIysGlyAspMetIle 1960  
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 QY 1961 IleAspArgIleAsnGluAsnSerIleThrGlnIleThrAspLeuThrMetSerThrAla 1980  
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 QY 1981 AlaCysProProSerTyrAspArgValIleThrIysProIleValGluIysHisGlnGln 2000  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE  
 1 Turner,C.A., Mathur,B. and Mathur,D.  
 Novel human ion channel proteins and polynucleotides encoding the  
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 Patent: WO 0214498-A 13 21 -FEB-2002;  
 JOURNAL Lexicon Genetics Incorporated (US)  
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 QY 41 LysIysAspAspAspGluAsnGlyProIysProAsnSerAspLeuGluAlaGlyIysAsn 60  
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 841 CCTCCACCAATGCTTCCTTCGAGAGAACATGATAGAAAAGATATATACGTGATAT 900  
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 Qy 321 SerArgTyrHisThrPheLeuGluGluPheLeuAspAlaLeuLysGlyAsnSerSer 340  
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 Db 841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860  
 2521 ACGCTTACCTGCTGTAAGTCTGAGACTGCCCAATGCGAAGGATATATGTTCTCCGTTCA 2580  
 Qy 861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTyrProThrLeuAsnMetLeuIle 880  
 2581 TTTCGATTTGCTGCGAGTTTTCAGTTGCAAAATTTTGGCCAAACGTAAATATGCTATATA 2640  
 Qy 881 LysIleIleGlyAsnSerValGlyValAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900  
 2641 AAGATCATCGGCAATTCGTTGGGCGCTCTGGGAATTTTAACTTGTCTTGCCATCATC 2700  
 Db 901 ValPheIlePheAlaValAlaGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920  
 2701 GCTTCATATTTTGGCGTGCGGATGACGCTTGTGTTAAAGCTACAAAGATTTGTGTC 2760



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| OY | 921  | CysLysIleLeaSerAspCysGlnLeuPheOatgTTPHisMetAsnAspPhePheHisSer   | 940  |
| Db | 2761 | TCCAAGATCCGACGAGATGTGTCAACTCCACCGCTGGCACATGAAATGACTTCTCCACTCC   | 2820 |
| OY | 941  | PheLeuIleValPheArgValLeuCysGlyGluTTPriLeGluThrMetTrpAspCysMet   | 960  |
| Db | 2821 | TTCCGATTTGTCTCCGCTGCTGTGTGGGAGTGAAGACCAATGGGCACTGTATG           | 2880 |
| OY | 961  | GluValAlaGlyGlnAlaMetCysLeuThrValPheMetCysValMetValIleGlyAsn    | 980  |
| Db | 2881 | GAGGTGCTGGTCAGAACCATGTGGCTTACTGTCTTCATATGATGTCAATGGTGATGGAAAC   | 2940 |
| OY | 981  | LeuValIleValLeuAsnIleuPheLeuAlaLeuLeu**SerSerPheSerAlaAspAsnLeu | 1000 |
| Db | 2941 | CTAGTGGTCCCTGAATCTCTTCTGGCGCTTGTMTAGCTCATTTGTGCAGCAACCTT        | 3000 |
| OY | 1001 | AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis    | 1020 |
| Db | 3001 | GGAGCCACTGAGAGATGATATATATAATGAATTAATCTCCAAATGCTGTGATAGAGTAC     | 3060 |
| OY | 1021 | LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg    | 1040 |
| Db | 3061 | AAGAGATGCTTATATGTGTAAGAAAAAATATATGATTTATTCACAGTCCCTTCATTAG      | 3120 |
| OY | 1041 | LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSer    | 1060 |
| Db | 3121 | AAACAAAGATTTTGTAGTGAATTAATTAACCATGTGATGATCTTAACAAACAAGAAACAGT   | 3180 |
| OY | 1061 | CysMetSerAsnHisThr**GluIleGlyLysAspLeuAspTyrIleuLysAspValAsn    | 1080 |
| Db | 3181 | TGTATGTCCAAACAACAACAACAAGAAATGGGAAAGACTTGACTTCTTAAAGTGTAAAT     | 3240 |
| OY | 1081 | GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer    | 1100 |
| Db | 3241 | GGAATCACAAGGTGRTATAGGAATGGCACAGCTGTGGAAAAATACATTATGTATGATGAAGT  | 3300 |
| OY | 1101 | AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly    | 1120 |
| Db | 3301 | GATTCATGTCAATCATATAAACAACCCAGTCTTACTGTCACTGATCCAAATTCGTGTAGA    | 3360 |
| OY | 1121 | GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu    | 1140 |
| Db | 3361 | GAACTGTCACTTGTGAATAATTAAACGGAAGACTTTAGTGAATCGATCTCGGAAGAA       | 3420 |
| OY | 1141 | SerLysGluLysLeuAsnGluSerSerSerSerSerGlySerThrValAspIleGly       | 1160 |
| Db | 3421 | ACCAAAAGAAACTGATATAAAGCACTACTCTCAAGAAAGTACACTGTGGACATCGGC       | 3480 |
| OY | 1161 | AlaProValGluGluGlnProValAlaGluProGluGluThrLeuGluProGluAlaCys    | 1180 |
| Db | 3481 | GCACCTGTAGAAAGAACACGCCCGTAGTGGAACTCGAAAGAACTTTGAACCAAGAGCTGT    | 3540 |
| OY | 1181 | PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluArg       | 1200 |
| Db | 3541 | TTCACTGGAAGGCTGTGTACAAAGATTCAGATGTGTCAATCAATCAATGTGGAAGAGGAGA   | 3600 |
| OY | 1201 | GlyLysGlnTTPTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTTPhe     | 1220 |
| Db | 3601 | GGAAAAACAATGTGGAACTGTGAAGAGACGTGTTTCCGAATGTTGAACTTAATCTGTTT     | 3660 |
| OY | 1221 | GluThrPheIleValPheMetIleLeuLeuSerSerGlyValaLeuAlaPheGluAspIle   | 1240 |
| Db | 3661 | GGAGCCCTCATTTGTTTCATGATGCTCCCTTAGAGTGAGTGCTCTGGCATTTGGAAGATATA  | 3720 |
| OY | 1241 | TyrIleAspGluArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr    | 1260 |
| Db | 3721 | TATATTGATCAGAGAAAGACGATTAAGACGATTTGGAAATATGCTGACAAAGTTTTCAC     | 3780 |
| OY | 1261 | TyrIlePheIleLeuGluMetLeuLeuLysTTPValAlaTyrGlyTyrGlnThrTyrPhe    | 1280 |
| Db | 3781 | TGCAATTTATCTGTGAAGATGCTTCAAAATGGTGTGCATATGCAATGCAACATATATTC     | 3840 |

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| QY | 1281 | ThrsnAlatrcpYstrpleuaspPheleuIlleValaspValSerleuValSerleuThr  | 1300 |
| Db | 3841 | ACCAATGCCCTGGTGTGGCGAGACTCTTAATGTGTGAATGTTTCATTGGTCAAGTTTAACA | 3900 |
| QY | 1301 | AlaAsnAlaleuGlyTrSerGluLeuGlyAlaIlleLysSerleuArgThrleuArgLa   | 1320 |
| Db | 3901 | GCAATGGCTTGGGTTACTGACAACTTGGAGCATTAATATCTCTACGGACACTAGAGACT   | 3960 |
| QY | 1321 | LeuArgProLeuAgaAlaLeuSerArgPheGluGlyMetArgValValAlaAsnAlaLeu  | 1340 |
| Db | 3961 | CTGAGACCTCTAAGAGCCTTATCTGCATTTGAAGGAGTAGAGGTTGTGTGAATGCCCTT   | 4020 |
| QY | 1341 | LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheThrleuIle  | 1360 |
| Db | 4021 | TTAGAGGCAATTCATCCATCATCAATGATGCTTGGTTGTCTTAATATTCGGCTAAT      | 4080 |
| QY | 1361 | PheSerIleMetGlyValAsnLeuPheIleGlyLysPheThrHisCysIleAsnThrThr  | 1380 |
| Db | 4081 | TTTCGATCATAGGGCGTAATTTGTTGGCGAATTTTACACTGTATTAACACCA          | 4140 |
| QY | 1381 | ThrGlyAspArgPheAspIleGlyAspValAsnAsnHisThrAspCysLeuLysLeuIle  | 1400 |
| Db | 4141 | ACTGGTAGCAGTTTGACATCCGAAGCGTAATATCATACATGATGGCTAAACTATA       | 4200 |
| QY | 1401 | GluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValCylPhe  | 1420 |
| Db | 4201 | GAAAGAAATGAGACTGCTCATAGGAAATAATGTAAAGTAAACTTTGATTAATCTAGCAAT  | 4260 |
| QY | 1421 | GlyTrpLeuSerLeuLeuGluValAlaThrPheLysGlyTrpMetAspIleMetGlyAla  | 1440 |
| Db | 4261 | GGGATCTCTTGGTCTCAAGTTGCCACATTTAAAGATGAGATGAATTAATGTATCA       | 4320 |
| QY | 1441 | AlaValAspSerArgAsnValGluLeuGluProLysTrpGluGluSerLeuTrpMetTrp  | 1460 |
| Db | 4321 | GCAGTGTATTCAGAAATGTGGAACTCCAGCCTAATGAAGAAAGCTGTGACATGTAT      | 4380 |
| QY | 1461 | LeuTrpPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIleGly  | 1480 |
| Db | 4381 | CTTACTTGTATTATTTATTCATCATCTTTGGGCTGCTTCACTTGAACCTGTGTTATGGT   | 4440 |
| QY | 1481 | ValIleIleAspAsnPheAsnGluGluLysLysLysPheGlyGlyAspIlePheMet     | 1500 |
| Db | 4441 | GTCACTATAGTAATTAATTCACACGACGAAATAAAGATTTGGAGGTCAACATCTTATG    | 4500 |
| QY | 1501 | ThrGluGluGlnLysLysTrpTrpAsnAlaMetLysLysLeuGlySerLysLysProLis  | 1520 |
| Db | 4501 | ACAGAGAAACAGAAAGAAATACTATAATAGCAATGAAAAAATTGATCGAAAAAACCGCA   | 4560 |
| QY | 1521 | LysProIleProArgProGlyAsnLysPheGluGlyMetValPheAspPheValThrArg  | 1540 |
| Db | 4561 | AAGCTTAATACCTCGACACGAGAAACAATTTCAAGGAATGTCTTGACTTGCATAACAGA   | 4620 |
| QY | 1541 | GlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMetMetVal  | 1560 |
| Db | 4621 | CAAGTTTTTGACAAACATCATCATATCTCATCTGTCTTAACATGGTCAATGTATGGTG    | 4680 |
| QY | 1561 | GluThrAspAspGlnSerGluTrpValThrThrIleLeuSerArgIleAsnLeuValPhe  | 1580 |
| Db | 4681 | GAACAGATGACCGAGAGATATGTACTACCAATTTTGCACGCAATCATGTGGTGTGC      | 4740 |
| QY | 1581 | IleValLeuPheThrGlyLysCysValLeuLysLeuIleSerLeuArgHisTrpLysPhe  | 1600 |
| Db | 4741 | ATTGTGCAATTTACTGGAGAGTGTGTCTGAACCTCATCTCTACGCCCATATATATTT     | 4800 |
| QY | 1601 | ThrIleGlyTrpAsnIlePheAspPheValValIleIleuSerIleValCylMetPhe    | 1620 |
| Db | 4801 | ACCAATGGATGGAATATTTTGATTTGTGTGTGATCTCTCCACTGTAGATATGTT        | 4860 |
| QY | 1621 | LeuIleGluLeuIleGluLysTrpPheValSerProThrLeuPheArgValIleArgLeu  | 1640 |
| Db | 4861 | CTTGCCGAGCGATAGAAAGATATTTGTGTCCCTCCATACCTGTCCGAGTGTACCGCTTT   | 4920 |
| QY | 1641 | AlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLeuLeu  | 1660 |



Db 661 CTCCAGAGATTCAGACATTCAGTCATTCAGGCTCGAAGAACCATGTTGGAGCCCTG 720  
Oy 241 IlegInserValIysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260  
Db 721 ATCCAGCTGTGAGAACAGCTCTCAATGATGAATGATCCTGACTGTGTCTGTGAGCGTA 780  
Oy 261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280  
Db 781 TTTGCTCAATATGGGCTGAGCTGTTCATGAGCAACCTGAGGAATGAATGATACATG 840  
Oy 281 PropThrAsnAlaSerLeuGlnGlnIleuSerIleGlyLysAsnIleThrValAsnTrp 300  
Db 841 CTCCCAACCAATGCTTCTCTTGAGAGAACATGATAGAAAATAATTAATCTGTAATTA 900  
Oy 301 AsnGlyThrIleuIleAsnGlnThrValPheGlnPheAspTrpLysSerTrpIleGlnAsp 320  
Db 901 AATGGTACCTATATAATGAACTGTCTTGTGAGTTGACTGGAAGCATATATCAAGAT 960  
Oy 321 SerArgTrpHisTrpPheLeuGlnGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340  
Db 961 TCAGATATCATTAATTCCTGAGGCTTTTAGATGCACTACTATGTGAAATACCTCT 1020  
Oy 341 AspAlaGlyGlnCysProGlnGlnIleuTrpMetCysValLysAlaGlyArgAsnProAsnTrp 360  
Db 1021 GATGACGGCCAAATGTCAGAGGATATATGTGTGAAAGCTGTGTAAGAAATCCAAATTA 1080  
Oy 361 GlyTrpThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetTrp 380  
Db 1081 GGCTACACAGCTTGTATACCTTCACTTGGCTTTTGTCTCTGTGTGACATATGACT 1140  
Oy 381 GlnAspPheTrpGlnAsnLeuTrpGlnLeuThrLeuArgAlaAlaGlyLysThrTrpMet 400  
Db 1141 CAGGACTTGGGAAATCTTATATCAATGACATGCTGCTGCTGGAAAGCTGACATG 1200  
Oy 401 IlePhePheValLeuValIlePheLeuGlySerPheTrpLeuIleAsnIleLeuAla 420  
Db 1201 AATATTTTGTGTGTGCTATTTCTTGTGGCTCATTTCTACCTAATTAATTTGATCTGGCT 1260  
Oy 421 ValIleAlaMetLeuAlaTrpGlnGlnIleuAsnGlnAlaThrLeuGlnLysAlaGlnLys 440  
Db 1261 GTGGTGCCATGGCTTACAGAGAACATCAGGCCACCTTGGAGAGAGAGAACAGAA 1320  
Oy 441 GlnAlaGlnPheGlnIleMetIleGlnIleuLysLysGlnIleuAlaAlaGlnLys 460  
Db 1321 GAGGCCGAATTCAGCAGATGATTGAACAGCTTAAAGAACAGAGGAGCAGCTCAGCAG 1380  
Oy 461 AlaIleThrAlaThrAlaSerGlnIleuSerArgGlnProSerAlaAlaGlyLeuSer 480  
Db 1381 GCAGCAACGGCACTGCTCAGAACATTCAGAGAGCCAGTCCAGCAGCAGGCTCTCA 1440  
Oy 481 AsnSerSerSerGlnIleuSerLysLeuSerSerLysSerAlaLysGlnIleuArgAsnArg 500  
Db 1441 GACAGCTCATCTAGGCTTAAAGTGAAGTCCAGAGTCTTAAGAAAGAAAGAAATCGG 1500  
Oy 501 ArgLysLysArgLysGlnIleuSerGlyLysGlnIleuLysAspGlnAspGlnPhe 520  
Db 1501 AGGAAGAAAGAAAGAAAGAGAGAGAGTGTGTGGGAGAGAAAGAAAGATGAGATTC 1560  
Oy 521 GlnLysSerGlnSerGlnAspSerIleArgArgLysGlyPheArgPheSerIleGlnLys 540  
Db 1561 CAAAAATCTGAATCTGAGCAGCAGCATCAGAGAGAAAGCTTTCCTCCATTTGAAGGG 1620  
Oy 541 AsnArgLeuThrTrpGlnLysArgTrpSerSerProIleGlnIleuLeuSerIleArg 560  
Db 1621 AACCGATGACATATGAAAGAGAGTACTCTCCCAACACAGCTTGTGTGAGCATCCGT 1680  
Oy 561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580  
Db 1681 GGCTCCATATTTCCACCAAGCCAAATAGCAGAAACAGCTTTTCAGCTTTAGAGGGGCA 1740  
Oy 581 AlaLysAspValGlySerGlnAsnAspPheAlaAspGlnIleuSerThrPheGlnAsp 600

Db 1741 GCAAGAGATGTGGATCTGAGAACAGACTTCGAGATGATGAGACAGCACTTGAAGAT 1800  
Oy 601 AsnGlnSerArgArgAspSerLeuPheValProArgArgHisGlyLysGlnArgAsnSer 620  
Db 1801 AACGAGAGCCGTAGAGATCTCTTGTGTGGCCGAGCAGACAGAGAGAGAACAGCAACAG 1860  
Oy 621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValPheProAlaAsnGlyLys 640  
Db 1861 AACTGATGACAGCAAGAGAGTATCCGAGATGCTGGAGTGTTCACGCAATGGGAG 1920  
Oy 641 MetHisSerThrValAspCysAsnGlyValIleSerLeuValGlyGlyProSerValPro 660  
Db 1921 ATCCACAGACACTGTGATTCGCAATGCTGTCTCTGTGTGTGGTGGAGCTTCAGTTCT 1980  
Oy 661 ThrSerProValGlyLeuLeuLeuProGlnValIleIleAspLysProAlaThrAspAsp 680  
Db 1981 ACATGCTGTGGACAGCTTGTGACAGAG----- 2040  
Oy 681 AsnGlyThrThrGlnGlnGlnMetArgLysArgArgSerSerPheHisValSer 700  
Db 2011 ---GGAACAACCACTGAATCTGAATGAGAAAGAGAGGTCAGATCTTCCACGTTTCC 2067  
Oy 701 MetAspPheLeuGlnAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720  
Db 2068 ATGCACTTTCTAGAAATCTCTCCAAAGCAAGCAATGATAGCAGCATCTA 2127  
Oy 721 ThrAsnThrValGlnGlnLeuGlnIleuSerArgGlnLysCysProProCysTrpTrpLys 740  
Db 2128 ACNAATACAGTACAGAACACTGTAAGAAATCCAGGACAGAAAGCCACCTGTGTGATAAA 2187  
Oy 741 PheSerAsnIlePheLeuIleTrpAspCysSerProTrpTrpLeuLysValLysVal 760  
Db 2188 TTTTCCAACTATCTTAATCTGGAGCTGTCTCCATATTTGTTAAAGTGAACATGTT 2247  
Oy 761 ValAsnLeuValIleMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780  
Db 2248 GTCAACTGTGTGATGAGCAACCATTTGTGACTGGCCATCAGCATGTATGTCTTA 2307  
Oy 781 AsnThrLeuPheMetAlaMetGlnHisTrpPrometThrAspHisPheAsnAsnValLeu 800  
Db 2308 AATACCTTTTCAATGGCCATGAGAGCACTATCAATGACGACCAATTCATTAATAGTCTT 2367  
Oy 801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGlnMetPheLysIleIle 820  
Db 2368 ACAGTAGAAGACTGTGTTTCACTGGGATCTTACACAGAAAGATTTCTGAAATATTT 2427  
Oy 821 AlaMetAspProTrpTrpTrpPheGlnGlnIleuLysTrpAsnIlePheAspGlyPheIleVal 840  
Db 2428 GCCATGATCTTACTATTTATTTCCAGAGAGGCTGGAATATCTTGAAGGTTTATGTG 2487  
Oy 841 ThrLeuSerLeuValGlnLeuGlyLeuAlaAsnValGlnIleuSerValLeuArgSer 860  
Db 2488 ACGCTTAGCTGTGAGAACTTGGACTGCCAATGTGAAAGATTAATCTGCTCCGTTCA 2547  
Oy 861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880  
Db 2548 TTTTGGATTTGTGAGATTTTCAAGTTTGGCAAAATCTTGGCCAAAGTTAAATATGCTATA 2607  
Oy 881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900  
Db 2608 AAGATCATTCGCAATTCCTGGGGGCTGTGGAAATTTAAACCTTCGCTTGGCCATCATC 2667  
Oy 901 ValPheIlePheAlaValAlaGlyMetGlnLeuPheGlyLysSerTrpLysAspCysVal 920  
Db 2668 GTCTTCAATTTTTCGCTGTGTGATGAGCTCTTGTGTAAGATGACAAAGATGTGTC 2727  
Oy 921 CysLysIleAlaSerAspCysGlnLeuProArgTrpPheMetAsnAspPhePheHisSer 940  
Db 2728 TGCAGATATCCGCAATGATTTGCAACTCCACGCTGGCAGCAAGATGACTTTCCACTCC 2787  
Oy 941 PheLeuIleValPheArgValLeuCysGlyLysTrpIleGlnIleuThrAspCysMet 960  
Db 2788 TTCTGTATGTGTCCGCTGCTGTGTGGAGTGGATAGAGACCATGTGGACTGTATG 2847

QY 961 G1uValAlaG1yGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980  
DB 2848 GAGGTGGTGGTCAAGCAGCATGTCCTTACTGCTTCATGATGGTCATGGTATGGAAC 2907  
QY 981 LeuValIleLeuAsnLeuPheLeuAlaLeuLeu\*\*\*SerSerPheSerAlaAspAsnLeu 1000  
DB 2908 CTAGGGGTCGGAACCTCTTCTGGCTGCTTGTAGCTCATTTAGGCAACAACCTT 2967  
QY 1001 AlaAlaThrAspAspAspAsnGlnMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020  
DB 2968 GCAGCAGCTGATGATGATATGAATGAATATCTCCAAATTCGTGTGATGATGATGAC 3027  
QY 1021 LysGlyValAlaArgValLysArgLysIleArgGlnPheIleGlnIleSerPheIleArg 1040  
DB 3028 AAAGAGAGAGCTTATGATGAAAAAATATGATGATTTATCAACAGCTCTTCAATAG 3087  
QY 1041 LysGlnLysIleLeuAsnGlnIleLysProLeuAspAspLeuAsnLysLysAspSer 1060  
DB 3088 AAACAAAAGATTATAGATGAATTAACCACTTGATGATCAAAACACAGAAACAGCT 3147  
QY 1061 CysMetSerAsnHisThr\*\*GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080  
DB 3148 TGTATGTCATCATCATCAACACAAATTTGGAAAGATCTTGACTATCTTAAGATGTAAAT 3207  
QY 1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGlnLysTyrIleIleAspLysSer 1100  
DB 3208 GGAATCTACAGAGGTATAGAACTGGACAGAGTGTGAATAATACATTTATGATGAAAGT 3267  
QY 1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120  
DB 3268 GATTACAGATCATTCATTAACAAACCCAGCTTACTGTGACGTACCAATTCCTGTAGCA 3327  
QY 1121 GluSerAspPheGlnAsnLeuAsnThrGlnAspPheSerSerGlnSerAspLeuGlnIle 1140  
DB 3328 GAATCTGACTTTGAAAAATTTAAACACGACGACATTTAGTAGAATCCGATCTGGAAGA 3387  
QY 1141 SerLysGlnLysLeuAsnGlnLysSerSerSerSerGlnGlySerThrValAspIleGly 1160  
DB 3388 AGCAAAAGAGAACTGAAAGAAAGCAGTACATCAGAAAGTAGACATGTGACATCACTG 3447  
QY 1161 AlaProValGlnGlnGlnProValValGlnProGlnGlnIleGlnIleProGlnLys 1180  
DB 3448 GCACCTGTAGAGAAACACCCGCTAGTGAACCTGGAAGAACTCTGGAACGAAACCTG 3507  
QY 1181 PheThrGlnGlyCysValGlnArgPheLysCysGlnIleAsnValGlnGlnLysArg 1200  
DB 3508 TTCACGTGAAGCTGTGTCAAAAGATTCAGTCTCTCAATCAATGTGGAAGAACGACGA 3567  
QY 1201 GlyLysGlnTyrProAsnLeuArgThrCysPheArgIleValGlnHisAsnTyrPhe 1220  
DB 3568 GGAAGAACATGCTGGAACCTGGAAGAGAGTGTCCGAAATAGTTGAACATPACTGGTTT 3627  
QY 1221 GlnThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGlnAspIle 1240  
DB 3628 GAGACCTTCATGTTTATGATGCTCTTACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3687  
QY 1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGlnTyrAlaAspLysValPheThr 1260  
DB 3688 TATATGATGACGCAAAACAGATTAGACGATGTGGAATATGCTGACAGAGTTTTCCT 3747  
QY 1261 TyrIlePheIleLeuGlnMetLeuLeuLysTyrValAlaTyrGlyTyrGlnThrTyrPhe 1280  
DB 3748 TACATTTTCATTTGGAATAGCTCTTAATAGGCGATGATGCTATCAAAACATATTTTC 3807  
QY 1281 ThrAsnAlaTyrCysTyrPheLysAspPheIleValAspValSerLeuValSerLeuThr 1300  
DB 3808 ACCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3867  
QY 1301 AlaAsnAlaLeuGlyTyrSerGlnLeuGlnValAlaIleLysSerLeuArgThrLeuArgAla 1320  
DB 3868 GCMAATGCTTGGTACTGCAACTGAGCACTTGAGCAATATCTCTCAGAGACCTAGAGCT 3927

QY 1321 LeuArgProLeuArgAlaLeuSerArgPheGlnGlyMetArgValValAlaAsnAlaLeu 1340  
DB 3928 CTGAGACCTCTTAAGAGACCTTATCTCGATTGGAAGGATGAGGGTGTGATGATCCCTT 3987  
QY 1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheThrPheIle 1360  
DB 3988 TTAGAGCAATTCATCCATCATCATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4047  
QY 1361 PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleLeuAsnThr 1380  
DB 4048 TTCACATCATGAGGCTAATATTTGTTGCTGCGAAATTCACACCTGATTTAACCCACA 4107  
QY 1381 ThrGlyAspArgPheAspIleGlnAspValAsnAsnHisThrAspCysLeuLysLeuIle 1400  
DB 4108 ACTGTGACAGGTTTGTGACATCGAAGACGTAATATCATPACTGATGCTGCTAAACTATA 4167  
QY 1401 GluArgAsnGlnThrAlaArgTyrLysAsnValLysValAsnPheAspAsnValGlyPhe 1420  
DB 4168 GAAAGAAATGACACTGCTCGATGAGAAAAATGAAAGTAAACTTTGAAATGATAGGATTT 4227  
QY 1421 GlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTyrPheAspIleMetTyrAla 1440  
DB 4228 GGGTATCTCTCTTCTCTCAAGTCCACATTCANAGATGATGATATATGATGCA 4287  
QY 1441 AlaValAspSerArgAsnValGlnLeuGlnProLysTyrGlnGlnSerLeuTyrMetTyr 1460  
DB 4288 GCAGTGTATCCAGAAATGTGGAATCTCAGCCTAGTGAAGAAAGCTGTACATGAT 4347  
QY 1461 LeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIleGly 1480  
DB 4348 CTTCATCTTGTATTTATTCATCATCTTGTGGTCTTCTTCACTGCAACCTGTATATG 4407  
QY 1481 ValIleIleAspAsnPheAsnGlnGlnLysLysLysPheGlyGlnAspIlePheMet 1500  
DB 4408 GTCATCATGATTAATTTACACGACGAAAGAAAGTTGGAGGCAACATCTTATG 4467  
QY 1501 ThrGlnGlnLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLysProGln 1520  
DB 4468 ACAGAGAAAGAGAAATATCATATGCAATGAAATAATTAAGATGCAAAAAACCGCA 4527  
QY 1521 LysProIleProArgProGlnAsnLysPheGlnGlyMetValPheAspPheValThrArg 1540  
DB 4528 AAGCTTATACCTCGACGAGAAACAAATTTCAAGAAAGGCTTGTGACTGTGTAACCGA 4587  
QY 1541 GlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMetMetVal 1560  
DB 4588 CAAGTTTGTACATGATCATGATGATCTCATCTGTCTTAACTGCTACATGATGCTG 4647  
QY 1561 GlnThrAspAspGlnSerGlnTyrValThrThrIleLeuSerArgIleAsnLeuValPhe 1580  
DB 4648 GAAACAGATGACCAAGAGATATGCTGACTACCATTTTGTCAAGCATCAATCTGCTGCT 4707  
QY 1581 IleValIlePheThrGlyGlnCysValLeuLysLeuIleSerLeuArgHisTyrTyrPhe 1600  
DB 4708 ATTGCTATTTATTCAGAGAGTGTGCTGAAACATCATCTCTACGCAATTAATATTT 4767  
QY 1601 ThrIleGlyTyrProAsnIlePheAspPheValValIleIleSerIleValGlyMetPhe 1620  
DB 4768 ACCATTTGATGGAATATTTTGTATTTGTGTGCTATCTCTCATGTGTGATGATGTT 4827  
QY 1621 LeuAlaGlnLeuIleGlnLysTyrPheValSerProThrLeuPheArgValIleArgLeu 1640  
DB 4828 CTGGCGAGCTGATGAAAGATTTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4887  
QY 1641 AlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLeuLeu 1660  
DB 4888 GCTAGGATTTGGCCGATCTCTACGCTGATCAAAAGAGGAGGAGATCCGACCTGCTC 4947  
QY 1661 PheAlaLeuMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuPheLeuVal 1680  
DB 4948 TTGCTTTGATGATGCTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5007  
QY 1681 MetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgGlnValGly 1700

QY 1601 ThrIleGlyTTPAsnIlePheAspPheValValIleLeuSerIleValGlyMetPhe 1620  
 DB 4801 ACCATTGGATGGAATATTTTGGATTGTTGGTTCATCTCTCCATTCATGATGATGTTT 4860  
 QY 1621 LeuAlaGluLeuIleGlyLeuTyrPheValSerProThrLeuPheArgValIleArgLeu 1640  
 DB 4861 CTTCGCGAGCTGATGAGAAATATTTCTGTCCCTACCTGCTTCCAGTATCCGCTTT 4920  
 QY 1641 AlaArgIleGlyArgGlyLeuArgLeuIleLeuGlyAlaValGlyIleArgThrLeuLeu 1660  
 DB 4921 GCTAGATGGCCGAACTCTACGCTGTATCAAGAGAGAAAGGGATCCGACCGCTGCTC 4980  
 QY 1661 PheAlaLeuMetMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuPheLeuVal 1680  
 DB 4981 TTTGCTTGAATGATGCTCCCTTCCTGCTGTTTAAACATGGCGCTCTCTCTCTCTATGC 5040  
 QY 1681 MetHeIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValIleValArgGlyValGly 1700  
 DB 5041 ATGTTCACTACGCACTTGTGGGATGTCACACTTGTCTATGTTAAAGAGGAGGATGGG 5100  
 QY 1701 IleAspMetPheAsnPheGlyThrPheGlyAsnSerMetIleCysLeuPheGlnIle 1720  
 DB 5101 ATCATGACATGTCATCTTGAAGACCTTGGCAACACATGATCTGCTATTCCTCAATT 5160  
 QY 1721 ThrThrSerAlaGlyTTPAspGlyLeuLeuAlaProIleLeuAsnSerLysProPhe 1740  
 DB 5161 ACAACCTCTGCTGGCGATGATGATGCTACACCATTCCTCAACAGTAAACCCACCCGAC 5220  
 QY 1741 CysAspProAsnLysValAsnProGlySerSerValIleGlyAspCysGlyAsnProSer 1760  
 DB 5221 TGTGACCTTAATTAAGTAACTGAGCTGAGCTGAGTAAAGGAGAGCTGAGGAGACCATCT 5280  
 QY 1761 ValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValValAsnMet 1780  
 DB 5281 GTTGGAAATTTCTTTTGTGATGATCATCATCATCTCTCTGCTGCTGCTGATGACATG 5340  
 QY 1781 TyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGluProLeu 1800  
 DB 5341 TACATCGGCTGATCTGAGAACTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5400  
 QY 1801 SerGluAspAspPheGluMetPheTyrGluValIleProGlyAspPheAsnProAlaThr 1820  
 DB 5401 AGTAGAGATGATCTTGAATATCTCATAGATTTGGGAGGATTTGATCCGATGCAACT 5460  
 QY 1821 GlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaLeuGluProProLeuAsn 1840  
 DB 5461 CAGTTCAATGAAATTTGAAAAATATCTCAAGTTGAGCTGGCGCTTGAACCCCTCTCAT 5520  
 QY 1841 LeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSerGlyAsp 1860  
 DB 5521 CTGCGACACCAACCAAACTCCAGCTCATCTCCATGATTTGCCATGCTGATGAGTGCAC 5580  
 QY 1861 ArgIleHisCysIleAspIleLeuPheAlaPheThrLysArgValIleGluGluSerGly 1880  
 DB 5581 CGGATCCACTGCTGATATCTTATTTCTTTCAAAAGCGGGTTCTAGGAGAGAGTGA 5640  
 QY 1881 GluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAspProSerLys 1900  
 DB 5641 GAGATGATGCTCTACGATACATGATGAGAGAGGATTCATGGCTTCCATCTTCCAG 5700  
 QY 1901 ValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGluValSerAlaVal 1920  
 DB 5701 GTTCCTCATGACCAATCATCTACTACTTTAAAGCAAAAGAGAGAGTATGCTGCTGC 5760  
 QY 1921 IleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGlnAlaSerPhe 1940  
 DB 5761 ATTATTCAGCGCTTACAGACGCCACTTTTAAAGCAAGTGTAAAGCAAGCTTCCCTT 5820  
 QY 1941 ThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuIleLysGluAspMetIle 1960  
 DB 5821 ACGTACATTAATAACCAAAATCAAGAGTGGGCTAATCTTCTTATTAAGAGACATGATA 5880

QY 1961 IleAspArgIleAsnGluAsnSerIlePheGluLysThrAspLeuThrMetSerThrAla 1980  
 DB 5881 ATTGACAGAAATTAATGAAACATCTATTACAGAAAAAACTGATCGACATCTCCACGTCA 5940  
 QY 1981 AlaCysProPheSerTyrAspArgValThrLysProIleValGlyLysHisGluGlu 2000  
 DB 5941 GCTTGTCCACCTTCTCTATGACCGGGTGCACAAAGCCATTTGTGAAAAACATGACAGAA 6000  
 QY 2001 GlyLysAspGluLysAlaLysGlyLys 2009  
 DB 6001 GCCAAGATGAAAGAAAGCAAGGAGAA 6027

RESULT 3

AAH5763 standard; cDNA; 8378 BP.

AAH5763;

04-SEP-2001 (first entry)

Human adult form of SCN1A nucleotide sequence SEQ ID NO:1.

Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;

diagnosis; mutation; chromosome 2q23-q31; neurological disorder;

anticonvulsant; neuroprotective; ss.

Homo sapiens.

MO200138564-A2.

31-MAY-2001.

24-NOV-2000; 2000MO-CA01404.

26-NOV-1999; 99US-0167623.

(UTMC-) UNIV MCGILL.

Rouleau GA, LaFreniere RG, Rochefort D, Cossette P, Ragsdale D;

WPI; 2001-355945/37.

P-PSDB: AAB99674.

Determining a predisposition to epilepsy and/or development of epilepsy

comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a

DNA variant, equivalent, or mutation which shows a linkage

disequilibrium -

Disclosure; Page 90-93; 268pp; English.

The present invention describes a method (M1) of determining an

individual's predisposition to epilepsy and/or development of epilepsy,

as well as predicting the individual's response to medication. The

method comprises determining the genotype of at least one gene selected

from SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation

which shows a linkage disequilibrium. SCN1A, SCN2A and SCN3A are all

sodium channel genes located on chromosome 2. The idiopathic generalised

epilepsy (IGE) gene is more specifically localised on chromosome

2q23-q31. Compounds identified as modulators of the biological activity

of SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating

epilepsy or other neurological disorders. They have anticonvulsant and

neuroprotective activities. AAH5763 to AAH56164 and AAH99674 to

AAH99679 represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR

primers, oligonucleotides and proteins given in the exemplification of

the present invention.

Alignment Scores:

Pred. No.: 0 Length: 8378  
 Score: 10367.00 Matches: 2006  
 Percent Similarity: 99.85% Conservative: 0  
 Best Local Similarity: 99.85% Mismatches: 3



|||||  
Db 2581 TTTCATGCTGCTGAGTTTCAAGTTGGCAAAATCTGGCCAAAGTTAAATGCTAAATA 2640  
OY 881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900  
Db 2641 AAGATCATGCGCAATTCGGGGGGGCTCTGGGAAATTTAACTCTGCTTGGCCATCATC 2700  
OY 901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920  
Db 2701 GCTTCATATTTTGGCGTGGCGAGCATGAGCTCTTGTGTAAGATCAAAAGATTGTGTC 2760  
OY 921 CysLysIleAlaSerAspCysGlnLeuProArgTyrPheIleAsnAspPheIleIleSer 940  
Db 2761 TCCAAAGATGCGCAAGTATGTCAAATCCACCGCTGGCAATGAAATGCTTCCACTCC 2820  
OY 941 PheLeuIleValPheArgValLeuCysGlyGluTyrPheIleGluThrMetTyrAspCysMet 960  
Db 2821 TTCCATGATTTGTTCCGCTGCTGTGTGGGAGTGAATGAGACCAATGTGGGAGCTATAG 2880  
OY 961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980  
Db 2881 GAGGTGCTGGTCAAGCATGCTGCTTACTGCTTCATGATGGTCAATGGATTGGAAC 2940  
OY 981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu\*\*SerSerPheSerAlaAspAsnLeu 1000  
Db 2941 CTAGGTGCTCAATCTCTTCTGGCTGCTTCTGAGCTCATTTGTCAGACCAACTT 3000  
OY 1001 AlaAlaThrAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020  
Db 3001 GCAGCCACTGATGATGATATGAAATGAAATCTCCAAATTCCTTGGATGAGATGCAC 3060  
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OY 1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnLysLysAspSer 1060  
Db 3121 AAACAAATAATTTTATGATGAAATTAACCACTGATGATCTAAACAAAGAAAGACAGT 3180  
OY 1061 CysMetSerAsnHisThr\*\*GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080  
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OY 1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGlnLysTyrIleIleAspGluSer 1100  
Db 3241 GGACACTACAAAGTGTATGAAAGTGGACAGACTGTCGAAAATATCTTATGTAAGT 3300  
OY 1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120  
Db 3301 GATTACATGTCATCTAAACCAACCCAGCTTACTGCTGCTACCAATTTGCTGTAGGA 3360  
OY 1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGln 1140  
Db 3361 GAATCTGACTTGAATAATTTAAACAGGAGACTTATGATGTAATGGGATCTGGAGAA 3420  
OY 1141 SerLysGlnLysLeuAsnGluSerSerSerSerSerGlnLysSerThrValAspIleGly 1160  
Db 3421 ACGAAGAGAACTGAAATGAAGACAGTACTCATCAAGAGTACAGCTGGACATCGGC 3480  
OY 1161 AlaProValGluGlnProValValGluProGluGluThrLeuGluProGluAlaCys 1180  
Db 3481 GCACTGTAGAGAAACAGCCCTGAGTGAACCTGGAAGAAACTTTAAACCGAAGCTTGT 3540  
OY 1181 PheThrGluGlyCysValGlnArgPheLysCysGlnIleAsnValGluGluArg 1200  
Db 3541 TTCACGAAAGGTTGTACAAAGATTCAGTGTGTCAAATGCAATGTGGAAGAGGAGA 3600  
OY 1201 GlyLysGlnTyrPheAsnLeuArgArgThrCysPheArgIleValGlnHisAsnTyrPhe 1220  
Db 3601 GGAAGAAAGATGAGTGAACCTGAGAGAGAGACTGTTCCGAATTAATGACATTAATCTGTTT 3660  
OY 1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240  
|||||

Db 3661 GAGACCTTATGTTTTCATGATTCCTCTAGTACGGTGTCTGGCATTTGACATATA 3720  
OY 1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr 1260  
Db 3721 TATATGATCAGAGAAAGACATTAAGACAGATGTTGAAATATGCTGACAAAGTTTCACT 3780  
OY 1261 TyrIlePheIleLeuGlnMetLeuLeuLysTyrValAlaTyrGlyTyrGlnThrTyrPhe 1280  
Db 3781 TACATTTTATCTTGGAAATGCTTCTTAAATAGGGTGGCATATGAGCTATCAACATATTTTC 3840  
OY 1281 ThrAsnAlaTyrCysThrPheAsnPheLeuIleValAspValSerLeuValSerLeuThr 1300  
Db 3841 ACCAATGCTGGGTGGCTGGAGCTTCTTAAATGTGATGATTTCAATGGCTCACTTAACA 3900  
OY 1301 AlaAsnAlaLeuGlnTyrSerGlnLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320  
Db 3901 GCAAAATGCTTGGGTATACAGAACTGAGACATCAAAATCTCTGAGACATGAAGCT 3960  
OY 1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValAsnAlaLeu 1340  
Db 3961 CTGAGACCTCTAAGACCTTATCTCGATTTGAAGGATGAGGTACTGTGTAATGCCCTT 4020  
OY 1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheThrPheIle 1360  
Db 4021 TTAGAGCAATTCATCATCATGAAATGTGCTTGTGCTTATATTCGCTAAAT 4080  
OY 1361 PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThr 1380  
Db 4081 TTCAGCATCATGGGCTTAATTTGTTGCTGGCAATTTACACAGCTATTAACACACA 4140  
OY 1381 ThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIle 1400  
Db 4141 ACTGGTACAGAGTTTGATGATCGAAAGCTGAATTAATCATACATGATGCTTAAACATATA 4200  
OY 1401 GluArgAsnGluThrAlaArgTyrLysAsnValLysValAspPheAspAsnValGlyPhe 1420  
Db 4201 GAAAGAAATGAGACTGCTGATGAGAAAATGTCAAAAGTAACTTGAATATGAGATTT 4260  
OY 1421 GlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTyrPheLysPheMetCysTyrAla 1440  
Db 4261 GGGTATCTCTCTTGTCTTCAAGTGGCACATTCAAAGATGATGATATATATGATGCA 4320  
OY 1441 AlaValAspSerArgAsnValGluLeuGlnProLysTyrGluGlnSerLeuTyrMetTyr 1460  
Db 4321 GCAGTGAATTCAGAAATATGAAATCCAGCTTAATGAAAGAAAGTCTGTACATGAT 4380  
OY 1461 LeuTyrPheAlaIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIleGly 1480  
Db 4381 CTTTACTTGTATTTTCATCATCTTGGGTCTTCTTCACTTGAACCTGTTATTTGT 4440  
OY 1481 ValIleIleAspAsnPheAsnGlnGlnLysLysPheGlyGlyGlnAspIlePheMet 1500  
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OY 1501 ThrGluGlnLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysProGln 1520  
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OY 1521 LysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheValThrArg 1540  
Db 4561 AACCTTATCTCTGACAGCAAGAAACAAATTTCAAGATGCTTCTTGAACCTGTAACACAGA 4620  
OY 1541 GluValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMetMetVal 1560  
Db 4621 CAAATTTTACATTAAGCATCATGATTCATCTGTCTTAACTATGCTCAAAATGATGCTG 4680  
OY 1561 GluThrAspAspGlnSerGluTyrValThrThrIleLeuSerArgIleAsnLeuValPhe 1580  
Db 4681 GAAACAGATACCAAGATGAAATATGTGACTACCATTTTGCACGATCAATCATGTGGTTC 4740  
OY 1581 IleValLeuPheThrGlyGlyCysValLeuLysLeuIleSerLeuArgHisTyrTyrPhe 1600  
Db 4741 ATTGTCTATTAATCTGAGAGTGTGATGAAATCATCATCTCTTACGCCATTAATATTTT 4800  
|||||



141 AsnGlyValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160  
1421 AACTGCTGTTTATGACAAAGAGTAACCCCTGATGGAGAAAGATGTAAGATTAACC 480  
161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgLysPheCysLeu 180  
1621 TTCCAGGAATATATCTTTGATCATCTTATATAAATTTATGCAAGGGATTCGTGTTA 540  
181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200  
541 GAAGATTTACTTCTTCGGGATCCATGAACTGGCTGCATTCACGTGATCATTAATTT 600  
201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220  
601 GCGTACCTCAGAGATTGTGGACCTGGCAATCTCGGCAATTGAGAAACATTCAGAGTT 660  
221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240  
661 CTCGAGCATTTGAAGAGATTTCAAGTATCCAGGCTGAAACCATTTGAGGAGCCCTG 720  
241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260  
721 ATCCAGCTGTGAAGAGCTCTCAGATGATATGATCCGATGCTGCTGCTGAGGCTA 780  
261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280  
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281 ProProThrAsnAlaSerLeuGluGluIleHisSerIleGluLysAsnIleThrValAsnTyr 300  
841 CTCGCCACCAATGCTTCTCTGGAGAACATAGTATAGAAAGATATATACGTGATTTAT 900  
301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320  
901 AATGTCACCTTAATAAATAAAGTCTGTTGAGTTGACTGGAATCATATATCAAGAT 960  
321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLysCysGlyAsnSerSer 340  
961 TCAGGATATCAATATATTTCTGGAGGCTTTTAAATGACATCATATGTGAAATAGCTCT 1020  
341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaArgAspProAsnTyr 360  
1021 GATTCAGAGGCAATCTCCAGAGGATATATGTGTGAAAGCTGGTGAAGATCCCAATTTAT 1080  
361 GlyTyrThrSerPheAspTrpPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380  
1081 GGGTACACAAAGCTTGATACCTCAGTTGGGCTTTTGTCTGTTGCGACTATGACT 1140  
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1141 CAGGACTTCTGGGAAATCTTATCACTGACATTACGCTGCTGGGAAACGATACATG 1200  
401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420  
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421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440  
1261 GTGTGGCCATGGCTCAGAGAAAGAAAGATCAGGCACTTGGAAGAAAGCAAGAA 1320  
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481 AspSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500  
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521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540  
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561 GlySerLeuPheSerProArgArgAsnSerArgHisSerLeuPheSerPheArgGlyArg 580  
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641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660  
1921 ATGCACAGCACTGTGATGTCGAATGTGTGTCTTGTGTTGAGACCTTCAGTCT 1980  
661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680  
1981 ACATGCGCTGTGGACAGCTTCTCCAGAGGTGATATAGTAAAGCCAGCTACGATGAC 2040  
681 AsnGlyThrThrGluThrGluMetArgLysArgArgSerSerPheHisValSer 700  
2041 AATGAAACACCTGTAACATGAAATGAGAAAGAGTCAATCTTTCACAGTTC 2100  
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2161 ACAATACAGTAGAAGAACTTGAAGAATCCAGCAGAAATCCACCTGTTGCTATAAA 2220  
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2221 TTTTCCAAATATTTCTTAATCTGGAGCTGTCTCCATATGCTTAAAAAGTCAACATGTT 2280  
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2281 GTCAACTGCTGTGATGAGACCACTTGTGTACCTGGCCATACCACTGTATGTCTTA 2340  
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2401 ACAGTAGAAGAACTTGATTCACGTGAGTCTTACACAGAAAGTTCATAAATATTT 2460  
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2461 GCCATGATCTTACTATATTTCCAGAAAGCTGGATATCTTTGAGGTTTATTTGTG 2500  
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2521 ACCTTAGCTGCTGATGAACTTGACCTGCCAATGTGGAAGATATATCTGTTCCGTTCA 2580  
861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880

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Db 5581 CGGATCCAGCTGCTGATATCTATTGCTTTACAAAGGGGCTTCAGAGAGAGTGGG 5640
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Db 5641 GAGATGGATGCTCTACGATACAGATGGAAGGCGATTCATGCTCCAAATCCTTCAAG 5700
Qy 1901 ValSerTyrGluProIleThrThrLeuLysArgIleGlnGluIuAlaSerAlaVal 1920
Db 5701 GTCTCTATACGCAATCACTACTACTTAAACGAAACAGAGAGATATCTGCTGTC 5760
Qy 1921 IleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGlnAlaSerPhe 1940
Db 5761 ATTATTCACGCGCTTACAGACCCCACTTTAAACGAACTTAAACAAGCTTCCTTT 5820
Qy 1941 ThrTyrAsnLysAsnLysIleLysGlyAlaAsnLeuLeuLysGlnAspMetIle 1960
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Db 5881 ATTGACAGATTAATTAATAAAGCTTATACGAAAAAGTGAATGACATGCTCACTGCA 5940
Qy 1981 AlaCysProProSerTyrAspArgValThrLysProIleValGluLysHisGluGlnIu 2000
Db 5941 GCTTGCCACCTTCTCATGACGCGTGACAAAGCCAAATTTGTGAAAAACATGACAGAA 6000
Qy 2001 GlyLysAspGluLysAlaLysGlyLys 2009
Db 6001 GGCAAAAGATGAAAAACCAAGGAGAA 6027

RESULT 2
AAD27266
ID AAD27266 standard; cDNA: 6027 BP.
AC AAD27266;
XX
DT 09-APR-2002 (first entry)
DE Human transporter and ion channel-13 (TRICH-13) cDNA.
XX
KW Human; transporter and ion channel-13; TRICH-13; neuroprotective; asthma;
KW nocotropic; cytoskeletal; cardiovascular; immunosuppressive; cardiomyopathy;
KW antiinflammatory; protein therapy; akinesia; cystic fibrosis; leukaemia;
KW Bell's palsy; amyotrophic lateral sclerosis; Alzheimer's disease; cancer;
KW amnesia; dementia; myocardiitis; Duchenne's muscular dystrophy; AIDS;
KW Acquired Immune Deficiency Syndrome; Addison's disease; allergy; angina;
KW cell proliferative disorder; psoriasis; cardiac disease; hypertension;
KW bradyarrhythmia; gene expression; drug screening; ss.
XX
OS Homo sapiens.
XX
FH Key 1.6027 Location/Qualifiers
FT CDS
FT /tag= a
FT /product= "Human TRICH-13 protein"
FT /note= "CDS does not include stop codon"
FT /partial
XX
MO200192304-AZ.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US17065.
XX
PR 26-MAY-2000; 2000US-20842AP.
XX
PR 01-JUN-2000; 2000US-209001P.
XX
PR 08-JUN-2000; 2000US-210588P.
XX
PR 16-JUN-2000; 2000US-212335P.
XX
PR 22-JUN-2000; 2000US-213747P.
XX
PR 29-JUN-2000; 2000US-215391P.
XX
PA (INCY-) INCYTE GENOMICS INC.

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XX
PI Thornton M, Walla NK, Yue H, Nguyen DB, Lai P, Gandhi AR;
PI Trihoulley CM, Yao MG, Rankumar J, Au-Yang J, Lu Y, Tang YF;
PI Azimzai Y, Bruns CM, Griffin JA, Yang J, Sanjavalva MS;
PI Raumann BE, Lee EA, Hatalia A, Baughn MR, Green BD, Khan FA;
PI Keaneey L, Elliott VS, Seilhamer JJ, Policky JL, Borowsky ML;
PI Burford N, Ding L, Lu DAM, Hillman JL;
DR WPI: 2002-122055/16.
DR P-PSDB: AAE16776.
XX
PT New human transporters and ion channels (TRICH) polypeptides useful for
PT diagnosing, treating or preventing disorders associated with aberrant
PT expression of TRICH
XX
PS Claim 11: Page 196-197; 210pp; English.
XX
CC The invention relates to human transporters and ion channels (TRICH)
CC polypeptides and their cDNA molecules. The nucleic acid and polypeptide
CC sequences are useful in the diagnosis, treatment, and prevention of
CC disorders associated with transport (akinesia, cystic fibrosis, Bell's
CC palsy, amyotrophic lateral sclerosis); neurological (Alzheimer's disease,
CC amnesia, dementia); muscle (cardiomyopathy, myocardiitis, Duchenne's
CC muscular dystrophy); immunological (AIDS, Addison's disease, allergies,
CC asthma); cell proliferative disorders (cancers, leukaemia, psoriasis);
CC cardiac disease (angina, hypertension, or bradyarrhythmia) and in the
CC assessment of the effects of exogenous compounds on the expression of
CC nucleic acid and amino acid sequences of transporters and ion channels.
CC The polynucleotides may be used to detect and quantify gene expression
CC in biopet tissues in which TRICH expression may be correlated with a
CC disease, to generate hybridization probes for mapping naturally occurring
CC genomic sequence, and in drug screening. The present sequence is human
CC TRICH-13 cDNA.
XX
SQ Sequence 6027 BP; 1785 A; 1189 C; 1348 G; 1705 T; 0 other;
SQ
XX
Alignment Scores:
Pred. No.: 0 Length: 6027
Score: 10376.00 Matches: 2004
Percent Similarity: 99.80% Conservative: 1
Best Local Similarity: 99.75% Mismatches: 4
Query Match: 99.80% Indels: 0
DB: 24 Gaps: 0
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Qy 21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
Db 61 TCTCTGCGGCTATGTAAGAGACCATTTGACAGAAAGCAAGATCCCAACAGAC 120
Qy 41 LysLysAspAspAspGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 60
Db 121 AAAAAAGATGACACAGAAATGGCCCAAGCCAAATAGTACTTGGAAAGTGGAAAGAC 180
Qy 61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
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Qy 81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
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Qy 101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
Db 301 CGGTCAGTGCACCTCGCCCTGACATTTTAATCCCTTCAATCCCTTGAAGAAATA 360
Qy 121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
Db 361 GCTATTATGAATTTGGTACATTCATTAATTCAGCATCTAATTAATGACACTATTTTGACA 420

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QY 1161 AlaProValglugluInProValgluProglugluThrLeuGluprogluLacys 1180  
DB 3481 GCACCTGTAGAGAACACCCGTAAGTGAACCTGAGAACCTGTGAAACACAGCTTCT 3540  
QY 1181 PheThrIuglucysValgluThrPheThyScysCysgluInleasnValgluLacys 1200  
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QY 1201 GlylysglnTrpTrpAsnLeuArgThrCysPheArgIleValgluHisAsnTrpPhe 1220  
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DB 3661 GAGACCTTCATTTCTTCATGATTCCTTGTAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3720  
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QY 1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaIleTyrGlyThrTyrPhe 1280  
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QY 1281 ThrAsnIleTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300  
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QY 1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320  
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QY 1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValAlaValAsnAlaLeu 1340  
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QY 1461 LeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIleGly 1480  
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QY 1481 ValIleIleAspAsnPheAsnGluInLysLysLysPheGlyGlyValAspIlePheMet 1500  
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QY 1521 LysProIleProArgProGlyLysAsnLysPheGlnGlyMetValPheAspPheValThrArg 1540  
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XX      21-FEB-2002.
XX      15-AUG-2001; 2001MO-US25650.
XX      16-AUG-2000; 2000US-225989P.
XX      (LEXI-) LEXICON GENETICS INC.
XX      Turner CA, Mathur B, Mathur D;
XX      WPI: 2002-280757/32.
XX      P-PSDB; MAE20515.
XX      Novel polynucleotides encoding human sodium channel proteins,
XX      particularly voltage-gated sodium channel proteins useful for drug
XX      screening, diagnosis and in gene therapy of biological disorders
XX      Claim 2: Page 55-57; 83pp: English.
XX
XX      The present sequence is a cDNA encoding novel human protein (NHP), ion
XX      channel protein. NHP share structural similarity with mammalian sodium
XX      channel proteins particularly voltage-gated sodium channel proteins.
XX      NHP oligonucleotides are useful as hybridisation probes for screening
XX      libraries and assessing gene expression patterns. Sequences derived
XX      from regions adjacent to the intron/exon boundaries of NHP gene can be
XX      used to design primers for use in amplification assays to detect
XX      mutations within the exons, splice sites, introns that can be used in
XX      diagnostics and pharmacogenomics. NHP nucleotide sequences are useful
XX      for drug screening effective in the treatment of symptomatic or
XX      phenotypic manifestations of perturbing the normal function of NHP in
XX      the body, and nucleotide constructs encoding NHP products are useful to
XX      genetically engineer host cells to express NHP products in vivo. These
XX      genetically engineered cells function as bioreactors in the body
XX      delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion
XX      protein to the body. Nucleotide construct encoding NHP products are
XX      also useful in gene therapy for modulating NHP expression and to
XX      produce genetically engineered host cells to express NHP products in
XX      vivo. NHP nucleotide sequences may also be used as part of ribozyme
XX      and/or triple helix sequences that are useful for NHP gene regulation.
XX      The NHP polypeptides are useful for generating antibodies, as
XX      reagents in diagnostic assays, for identifying other cellular gene
XX      products related to NHP and as reagents in assays for screening for
XX      compounds that are useful in the treatment of mental, biological or
XX      medical disorders and diseases.
XX
XX      Sequence 6030 BP; 1786 A; 1190 C; 1345 G; 1706 T; 3 other:
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XX      Percent Similarity: 100.00% Conservative: 0
XX      Best Local Similarity: 100.00% Mismatches: 0
XX      Query Match: 99.96% Indels: 0
XX      DB: 24 Gaps: 0
XX
XX      US-09-930-871-12 (1-2009) x AAD32844 (1-6030)
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DB      1 ATGGAGCAAAACAGTGTCTGACCAACAGGACCTGACAGCTTCACTTCCACAGAGAA 60
OY      21 SerLeuAlaIleAlaIleGluArgArgIleAlaGluGluValAlaIleAsnProGlyProAsp 40
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DB      181 CTTCATTATTATTATGAGACATTCCTCCAGAGATGGTGTGACAGCCCTCGAGACCTG 240
OY      81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyAlaIlePhe 100
DB      241 GACCCCTACTATATCAATTAAGAAACCTTTATAGATGATTAAGAAAGGAGCCATCTTC 300
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DB      301 CGGTTCAGTGCACCTCTGCCCCCTTACATTTTAACTCCCTCAATCCCTTAGAGAAATA 360
OY      121 AlaIleLysIleLeuValIleSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
DB      361 GCTATTAAAGNTTTGGTACATTCATATTCAGCATGCTAATATATGTCACATTTTGGACA 420
OY      141 AsnCysValPheMetThrMetSerAsnProProAspTyrThrLysAsnValGluTyrThr 160
DB      421 AACTGTGTATTATGACAATGATGATACCCCTCGATTGGACAAAGAAATGTGAATACACC 480
OY      161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgLysPheCysLeu 180
DB      481 TTCACAGGAATATATACCTTTGGAATCACTTAAATAATATGCAAGGCGATGTGTTTA 540
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DB      541 GAAGATTTTACTTCTCTCGGGATCCATGACATGCTGCTGATTCACATCTGATTAACATT 600
OY      201 AlaTyrValThrGluPheValAspLeuLysAsnValSerAlaLeuArgThrPheArgVal 220
DB      601 GCGTACGTCACAGAGTTTGTGGACCTGGCAATGCTCGGCAATTGAGAAACATTCAGAGTT 660
OY      221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
DB      661 CTCGACCATTTGAAGAGATTCAGTCAATCCAGCGCTGAAACCATTCCTGGGAGCCCTG 720
OY      241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
DB      721 ATCCAGTGTGAAAGAGCTCTCAGATGTAAATGATCCGACTGTGTCTGTCAAGCGTA 780
OY      261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGluTyr 280
DB      781 TTTCCTTAATTTGGCTGACGCTTTCATGCGCAACCTGAGCAATTAATGATATCAATGG 840
OY      281 ProProThrAsnAlaSerLeuGluGluHisSerIleGlyLysAsnIleThrValAsnTyr 300
DB      841 CTTCCACCAATGCTTCTCTGAGCAACATGATATGAAAGAAATATTAACGTGAATATAT 900
OY      301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTyrLysSerTyrIleGluAsp 320
DB      901 AATGTACACTTATTAATTAAGAACTGTCTTGAAGTTGACTGGAAGTCAATATATCAAGAT 960
OY      321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyLysSerSer 340
DB      961 TCAAGATATATATTTTTCCTGAGAGGTTTATAGATGACACACATGTGGAATAGCTCT 1020
OY      341 AspAlaGlyLeuCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360
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DB      1141 CAGAGCTTTCGGGAAATCTTTATCAACTGACATTTACCTGCTGCGGAAACGTTACATG 1200
OY      401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420

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GenCore version 5.1.4.p5.4578  
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OM protein - nucleic search, using frame\_plus.p2n model

Run on: April 22, 2003, 18:36:20 ; Search time 568 Seconds

(without alignments)  
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Searched: 2185239 segs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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| 1          | 10393   | 100.0       | 6030   | 24    | Human ion channel  |
| 2          | 10376   | 99.8        | 6027   | 24    | Human transporter  |
| 3          | 10367   | 99.7        | 8378   | 22    | Human adult form o |
| 4          | 10321   | 99.3        | 8378   | 22    | Human neonatal for |
| 5          | 10320.5 | 99.3        | 5997   | 24    | Human ion channel  |
| 6          | 10273   | 98.8        | 8131   | 24    | Human sodium chann |
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| 12         | 8468.5  | 81.5        | 9112   | 22    | Human adult form o |
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| 16         | 7861.5  | 75.6        | 6371   | 17    | Human adult form o |
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| 18         | 7735.5  | 74.6        | 6007   | 19    | Human adult form o |
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## ALIGNMENTS

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ID: AAD32844  
Standard: CDNA: 6030 BP.  
AAD32844:  
01-JUL-2002 (first entry)  
Human ion channel cDNA #6.  
Human; novel human protein; NRP; voltage-gated sodium channel;  
gene therapy; bioelectro; mental disorder; biological disorder;  
gene; medical disorder; ss.  
Homo sapiens.  
Key: Location/Qualifiers  
CDS 1..6030



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 DEFINITION Sequence 33 from Patent WO0138564.  
 ACCESSION AX164203  
 VERSION AX164203.1 GI:14545141  
 KEYWORDS  
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 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1 (bases 1 to 8349)  
 AUTHORS Rouleau,G.A., Lafreniere,R.G., Rochefort,D., Cossette,P. and  
 Ragsdale,D.

TITLE Loci for idiopathic generalized epilepsy, mutations thereof and  
 method using same to assess, diagnose, prognosis or treat epilepsy  
 JOURNAL Patent: WO 0138564-A 33 31-May-2001;  
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 Location/Qualifiers  
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 Best Local Similarity: 87.04% Mismatches: 114  
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| OY | 280  | TrpProPThrAsnAlaSerLeuGlnIleHisSerIleGluAspIleThr-----             | 297  |
| Db | 946  | TGGCGTCAGATATATCT-----TCTTTGAATAAATGATCTACCTCTTC                   | 990  |
| OY | 298  | -----ValAsnTYrAsnGlyThrLeuIleAsnGlnThrValPheGluPheAsp              | 313  |
| Db | 991  | TTTAAACATTCAATGGATGGGAATGGTACTACTTTCAATAGGACAGTGGCATATTATAC        | 1050 |
| OY | 314  | TrpIysSerTYrIleGlnIleAspSerActgTYrHisTYrPheLeuGlnGlyPheLeuAspAla   | 333  |
| Db | 1051 | TGGGATGAATATATATGAGGATTAAGTCACTTTATTTTGTAGAGGGCAAAATGATCT          | 1110 |
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| Db | 1111 | CTGCTTTGTGGCAACAGCTCAGATGCAAGGCACTGTCCTGAAGGATACATCTGTGTGAG        | 1170 |
| OY | 354  | AlaGlyArgAsnProAsnTYrGlyTYrThrSerPheAspThrPheSerTrpAlaPheLeu       | 373  |
| Db | 1171 | GCTGCTGAAGAACCCCACTATGGCTACAGAGCTTTCAGACCTTTAGTTGGGCTTTTGG         | 1230 |
| OY | 374  | SerLeuPheArgLeuMetThrGlnAsnPheTrpGlnAsnLeuTYrGlnLeuThrLeuArg       | 393  |
| Db | 1231 | TCTTATTTGCTCTCACTCACTCAAGCTTGTGGGAAACCTTTATCTCACTGCACTTACTG        | 1290 |
| OY | 394  | AlaAlaGlyIysThrTYrMetIlePhePheValLeuValIlePheLeuGlySerPheTYr       | 413  |
| Db | 1291 | GCTGCTGGGAAACCTCAATGATATTTTTCGTCTGTCATTTTCTGTGGCCTCATTCAT          | 1350 |
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| OY | 434  | LeuGluGlnIleGluGlnIlyAsnGluAlaGlnPheGlnGlnMetIleGlnIleuIysIys      | 453  |
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| OY | 454  | GlnGlnGlnIleAlaAlaGlnGlnAlaAlaThrAlaThrAlaSerGluHisSerArgLeuPro    | 473  |
| Db | 1471 | CAACAGAGAGAGCT---CAGCGCGGACGCTCGACGCCGATCTGCTGAATCAAGACACTTC       | 1527 |
| OY | 474  | SerAlaAlaGlyArgLeu-----SerAspSerSerSerGluAlaSerIysLeuSer           | 490  |
| Db | 1528 | AGTGGTCTGCTGGAGTAGAGAGTTTTCAGAGACTTCTTCAGTACACTTAAGTTGAGC          | 1587 |
| OY | 491  | SerIysSerAlaIysGluArgArgAsnArgArgIlyIysArgIlyGlnIysGlnIleuSer      | 510  |
| Db | 1588 | TCCAAAAGTGAAGAAAGCTGAAGAAACAGAGAGAAAGAAAGAAACAGAAACACAGCTT         | 1647 |
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| OY | 551  | SerProHisGlnSerLeuLeuSerIleArgGlySerLeuPheSerProArgArgAsnSer       | 570  |
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| Db | 1825 | AGGGCGACCTTTCACCTTCAGAGGCTGAGCAAGAGCAATGGGCTCTGAGATATACCTT         | 1884 |
| OY | 591  | AlaAspArgGluHisSerThrPheGluAspAsnGluSerArgArgAspSerLeuPheVal       | 610  |
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| OY | 611  | ProArgArgHisGlyIleuArgArgAsnSerAsnLeuSerGlnThrSerArgSerSerArg      | 630  |

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| Db | 1945 | CCGCACACACATGTGAGAAACGGCGGCACAGACATGTCAAGCCAGCGCGTCCACAG       | 2004 |
| Qy | 631  | MetLeuAlaValPheProAlaAsnGlyLysMetHisSerThrValAspCysAsnGlyVal   | 650  |
| Db | 2005 | GTGCTCCCAACCTCCGACCAATGAATGAGAAATGATCATAGCGCTGTGACATGATGTGTG   | 2064 |
| Qy | 651  | ValSerLeuValGlyLysProSerValProThrSerProValGlyIleuLeuProGlu     | 670  |
| Db | 2065 | GTCTCCCTGGTGGGGGCGCTCTTACCTCCACATCT---GCTGGGAGCTCTCTACCAGAG    | 2121 |
| Qy | 671  | ValIleIleAspLysProAlaThrAspAspAsnGlyThrThrThrGluThrGluLeuArg   | 690  |
| Db | 2122 | -----GGCACAACTACTAAACAAATAATAGA                                | 2148 |
| Qy | 691  | LysArgArgSerSerSerPheHisValSerMetAspPheLeuGluAspProSerGlnArg   | 710  |
| Db | 2149 | AAGAGACGGTCCACTGTCTTATCATCTTCCATGGATTTATTTGGAACATCTCTACATCAAG  | 2208 |
| Qy | 711  | GlnArgAlaMetSerIleAlaSerIleLeuThrAsnThrValGluGluLeuGluLysSer   | 730  |
| Db | 2209 | CAAAAGAGAAAGATATATAGCCAGATTTTATACCAACACCATGGAAACACTTAAANAATCC  | 2268 |
| Qy | 731  | ArgGlnLysCysProProCysTyrTyrLysPheSerAsnIlePheLeuIleTyrAspCys   | 750  |
| Db | 2269 | AGACAGAAATCCCAACCATGCTGATATAAATTTGCTATATATGTGTTGATTTGGACACT    | 2328 |
| Qy | 751  | SerProTyrTyrPheLysValLysHisValValAsnLeuValValMetAspProPheVal   | 770  |
| Db | 2329 | TGTAAACCATGTTAAAGTGAAACACTTGTCAACCTGGTGTATATGAGACCATTTGTT      | 2388 |
| Qy | 771  | AspLeuAlaIleThrIleCysIleValLeuAsnThrLeuPheMetAlaMetGluHisTyr   | 790  |
| Db | 2389 | GACCTGGCCATCACCATCTGATGTGTTAAATACCTTCTCATGTGCTATGAGACATAT      | 2448 |
| Qy | 791  | PrometThrAspHisPheAsnAsnValLeuThrValGlyAsnLeuValPheThrGlyIle   | 810  |
| Db | 2449 | CCCATGAGAGAGACAGTTCACAGAGTGTACTGTCTTGGAACCTGGTCTTCACAGAGATC    | 2508 |
| Qy | 811  | PheThrAlaGluMetPheLeuLysIleIleAlaMetAspProTyrTyrTyrPheGlnGlu   | 830  |
| Db | 2509 | TTCACAGCAGAAATGTTTCTCAACATATATGGCATGGATCCATATATTACTTTCACAGA    | 2568 |
| Qy | 831  | GlyTyrAsnIlePheAspGlyPheIleValThrLeuSerLeuValGluLeuGlyLeuAla   | 850  |
| Db | 2569 | GGCTGGATATTTTGTGATGATTTATTTGTATGTCAGCCCTAGTTAAATGGAACCTGGTGGCA | 2628 |
| Qy | 851  | AsnValGluGlyLeuSerValLeuArgSerPheArgLeuLeuArgValPheLysLeuAla   | 870  |
| Db | 2629 | AATGTGGAAAGATTTCTCAGTTCTCCGATCATTCGCGCTGCTCGGAATTTTCAAGTTGGCA  | 2688 |
| Qy | 871  | LysSerTyrProThrLeuAsnMetLeuIleLysIleIleGlyAsnSerValGlyAlaLeu   | 890  |
| Db | 2689 | AAATCTTGCCACACTCTAATATATCTAATTAAGTATCTATGGCAATTCGTGGGGCGCTCA   | 2748 |
| Qy | 891  | GlyAsnLeuThrLeuValLeuAlaIleIleValPheIlePheAlaValAlaGlyMetGln   | 910  |
| Db | 2749 | GGAAACCTCACCTGGTATGTGGCATATGCTCTTCTATTTTCTGTGGTGGCATGACAG      | 2808 |
| Qy | 911  | LeuPheGlyLysSerTyrLysAspCysValCysLysIleAlaSerAspCysGlnLeuPro   | 930  |
| Db | 2809 | CTCTTTGGTAAAGCTACAAAGAAATGTCTGCAAGATTTTTCAAATATGTTGAACTCCCA    | 2868 |
| Qy | 931  | ArgTyrPheIleMetAsnAspPhePheHisSerPheLeuIleValPheArgValLeuGly   | 950  |
| Db | 2869 | CGCTGGCACATGACATGACTTTTTCACCTCTCTCTATCTGTGTTCCGCGTGTGTGTGGA    | 2928 |
| Qy | 951  | GluTyrPheGluThrMetTyrAspCysMetGluValAlaGlyGlnAlaMetCysLeuThr   | 970  |
| Db | 2929 | GAGTGGATATGAGACATGTGGAGCTGATATGGAGGTGCTGGCAAAACATGTGGCTTACT    | 2988 |
| Qy | 971  | ValPheMetMetValMetValIleGlyAsnLeuValValLeuAsnLeuPheLeuAlaLeu   | 990  |

Dh 2989 GTCCTCATGATGTCATGATGATGGAATCTAGTGGTTCTGAACTCTTCTGCGCTTG 3048  
Qy 991 Leu\*\*\*SerSerPheSerAlaAspAsnLeuAlaIthrAspAspAsnGluMetAsn 1010  
Dh 3049 CTTTGAATCTCTTCAGTGTGACATCTCTGCTGACTGATGATGAAACCAATGAT 3108  
Qy 1011 AsnLeuGlnIleAlaValAspArgMetHisLysGlyValAlaIthrValLysArgLysIle 1030  
Dh 3109 AATCTCCAGATGCTGCTGGGAGATGCGAAGAAAGATCGATTTTGTAAAAAGAAATA 3168  
Qy 1031 TyrGluPheIleGlnInSerPheIleArgLysGlnLysIleLeuAspGluIleLysPro 1050  
Dh 3169 CGTGAATTTATTCAGAAAGCCTTTGTTAGGAAGCAAGAGCTTTGATGAAATTAACCG 3228  
Qy 1051 LeuAspAspLeuAsnAsnLysLysAspSerCysMetSerAsnHisThr\*\*\*GluIle 1069  
Dh 3229 CTTGAGAGTCTAAATTAATAAAAAGACAGCTGATTTCCAACTACCACTAACAATA 3288  
Qy 1070 GilyAspAspLeuAspTyrLeuLysAspValAsnGlyThrThrSerGlyIleGlyThrGly 1089  
Dh 3289 GCGCAAGACCTCAATATATCTCAAGACGGAATGGAAGTACTAGTGCATA----GCG 3342  
Qy 1090 SerSerValGluLysTyrIleIleAspGluSerAspTyrMetSerPheIleAsnAsnPro 1109  
Dh 3343 AGCAGTGAAGAAAAATATGCTGTGATGAAGTGAATTCATGCTATTATTAACAACCT 3402  
Qy 1110 SerLeuThrValIThrValProIleAlaValGlyLysAspPheGluAsnLeuAsnThr 1129  
Dh 3403 AGCCTCACTGAGACAGTACCAATGCTGCTGTGAGAAATCTGATTTGAAATTAATTAAT 3462  
Qy 1130 GilyAspPheSerSerGluSerAspLeuGluInSerLysGluLysLeuAsnGluSerSer 1149  
Dh 3463 GAAAGATTCACACGACGATCTCAATATGAGAAAGCAAGAAAGCACTAAAT---GCAACT 3519  
Qy 1150 SerSerSerGluLysSerThrValAspIleGlyAlaProValGlu---GluGlnProVal 1168  
Dh 3520 AGTTCATCTGAAGGAGCAGCGTGTGATGTGAGCTCCCGCGAGGAGCAACAGCTGAG 3579  
Qy 1169 ValGluProGluGluThrLeuGluProGluAlaCysPheThrGluGlyCysValGlnArg 1188  
Dh 3580 GTTGACCTGGAGATCCCTGGAACCTGAAACCTGTTTACAGAAAGCTGTGACGGAAG 3639  
Qy 1189 PheLysCysGlyGlnIleAsnValGluGluGluArgGlyLysGlnIleThrAspAsnLeuArg 1208  
Dh 3640 TTCAAGTGTGTGATAGATAGCATAGAAAGCAAGGAAAGCACTGTGTGAAATTTGAGG 3699  
Qy 1209 ArgThrCysPheArgIleValAlaHisAsnTrpPheGluThrPheIleValPheMetIle 1228  
Dh 3700 AAAACATGCTATAGATAGTGTGAGACAAATGCTTGAACCTTCAATGTCTTCAATGAT 3759  
Qy 1229 LeuLeuSerSerGlyAlaLeuAlaPheGluAspIleTyrIleAspGlnArgLysThrIle 1248  
Dh 3760 CTGCTGAGACATGGGGGCTCTGCGCTTGAATATATATGATGACAGCAAGAAACCAAT 3819  
Qy 1249 LysThrMetLeuGluIThrAlaAspLysValPheThrTyrIlePheIleLeuGluMetIle 1268  
Dh 3820 AAGACCATGATAGATAGTGTGACAGAGTTTCACTACATATTCATTTCTGGAATATGCTG 3879  
Qy 1269 LeuLysTrpValAlaTyrGlyTyrGlnIleThrTyrPheThrAsnAlaTrpCysTrpLeuAsp 1288  
Dh 3880 CTAAGTGGTGTGATATGCTTTCACAGTGTATTTTACCAATGCTGTGTGTGCTGATAGC 3939  
Qy 1289 PheLeuIleValAspValSerLeuValSerLeuThrAlaAsnAlaLeuGlyTyrSerGlu 1308  
Dh 3940 TTCTGATGTTGATGTCTCACTGCTGTTAGCTTAATCTGCAAAATGCTTGGTACTACANA 3999  
Qy 1309 LeuGlyAlaIleLysSerLeuArgThrLeuArgAlaLeuArgProLeuArgAlaLeuSer 1328  
Dh 4000 CTTGCTGCACCAATTCCTAGAACACTAGAGCTGTGAGGCCACTAGAGCTTTGTCC 4059  
Qy 1329 ArgPheGluGlyMetArgValAlaValAsnAlaLeuLeuGlyAlaIleProSerIleMet 1348  
Dh 4060 CGGTTTGAAGGAATGAGGCGCTTTGTAATGCTCTTTTGAAGGACCATTCATCTATCATG 4119

Qy 1349 AsnValLeuLeuValCysLeuIlePheThrPheIlePheSerIleMetClyAlaAsnLeu 1368  
Dh 4120 AATGATCTCTGCTGTGTGTGATCTTGTGCTAAATATGATATCATGTGGAGATGATTC 4179  
Qy 1369 PheAlaGlyLysPheThrHisCysIleAsnThrThrGlyAspArgPheAspIleGlu 1388  
Dh 4180 TTTCGCGCAAGTTTATTCATTTGTATTAATACACCACTGAGAGATGTTGATGTATAC 4239  
Qy 1389 AspValAsnAsnHisThrAspCysLeuLysLeuIleGluArgAsnGluThrAlaArgTrp 1408  
Dh 4240 GTGGTCAACACATGACAGTGTGACAAAGCTTCATTTGAGAGCAATCAACATGCGACGTGG 4299  
Qy 1409 LysAsnValLysValAsnPheAspAsnValGlyPheGlyTyrLeuSerLeuGlnVal 1428  
Dh 4300 AAAAATGTAAAGTAAATCTTATTAACAGTGTGATCTGTCTCTCTACTTCAAGTA 4359  
Qy 1429 AlaThrPheLysGlyTyrPheAspIleMetTyrAlaIleAlaValAspSerArgAsnValGlu 1448  
Dh 4360 GCGACGTTTAAAGGATGATGATATTAATATGACAGCTGTGATTCACGAATGTAGAA 4419  
Qy 1449 LeuGlnProLysTyrGluGluInSerLeuTyrMetTyrLeuTyrPheValIlePheIleIle 1468  
Dh 4420 TTACAACCCAGATAGAACACAACTGTACATGATCTTATTTGTCAATCTTATAT 4479  
Qy 1469 PheGlySerPhePheThrLeuAsnLeuPheIleGlyValIleIleAspAsnPheAsnGln 1488  
Dh 4480 TTTGGTCAATCTTTTACCTTGAATCTTTTCAATGATGTCATATGATATCAACCA 4539  
Qy 1489 GilyLysLysPheGlyGlyGlnAspIlePheMetThrGluGluGlnLysTyrTyr 1508  
Dh 4540 CAGAAAAAAGTTTGGAGAGTCAAGCATTTTATGACGAAAGAACGAAAGAAATATCTAC 4599  
Qy 1509 AsnAlaMetLysLysLeuGlySerLysLysProGlnLysProIleProArgProGlyAsn 1528  
Dh 4600 AATGCAATGAAAAAATCTGGCTTCAAGAAACCAAAACCAATACCTGACCTGTATAC 4659  
Qy 1529 LysPheGlnGlyMetValPheAspPheValIThrArgGlnValPheAspIleSerIleMet 1548  
Dh 4660 AATTTCCAAAGGATGTCTTTGATTTGTATTTGACCAAAAGCTTGTGATATGACATATG 4719  
Qy 1549 IleLeuIleCysLeuAsnMetValIThrMetMetValGluThrAspAspIleSerGlyTyr 1568  
Dh 4720 ATCTCATCTGCTTATACATGTGTACCATGATGATGTGGAAGCAAGTACCAAGTCAAGAA 4779  
Qy 1569 ValIThrThrIleLeuSerArgIleAsnLeuValPheIleValLeuPheThrGlyLysCys 1588  
Dh 4780 ATGACAAACATTTCTGATGATTAATCTGTGTTATTTGTTCTGTCTGACATGAGATCT 4839  
Qy 1589 ValLeuLysLeuIleSerLeuArgHisTyrTyrPheThrIleGlyTyrPAsnIlePheAsp 1608  
Dh 4840 GTGCTGAACATGATCTCTCTGTTACTACTTATTCACATATGATGAAATATTTTGTAT 4899  
Qy 1609 PheValIleValIleLeuSerIleValGlyMetPheLeuAlaGluLeuIleGlyLysTyr 1628  
Dh 4900 TTGTGTGTGTATCTCTCAATGTAGGAATGTTGTGCGTCACTGATTAAGAAAGTAT 4959  
Qy 1629 PheValSerProThrLeuPheArgValIleArgIleAlaAlaArgIleGlyArgIleLeuArg 1648  
Dh 4960 TTGTGTGCTCCATACCTGTGTCGAGATGATCGCTTTCGACAGATTTGCCGATTCCTACT 5019  
Qy 1649 LeuIleLysGlyAlaLysGlyIleArgThrLeuLeuPheAlaLeuMetSerLeuPro 1668  
Dh 5020 CTGATCAAAAGGAGCAAGAGGATCCGACGCTGCTTGTGATATGATGTGCCCTTCT 5079  
Qy 1669 AlaLeuPheAsnIleGlyLeuLeuLeuPheLeuValMetPheIleTyrAlaIlePheGly 1688  
Dh 5080 GCGTGTATTAACATGCGCTCTCTTCTTTCCTGTGTCATGTTATCTACGCCATTTTGGG 5139  
Qy 1689 MetSerAsnPheAlaTyrValLysArgGluValAlaGlyIleAspAspMetPheAsnPheGlu 1708  
Dh 5140 ATGTCATATTTTGCCTATGTTAAGAGGAAAGTGGGATGATGATGATGATGATGATGATG 5199



OY 240 LeuIleGlnSerValIlySlyIleuSerAspValMetIleuThrValPheCysIleuSer 259  
 |||||  
 DB 826 CTGATCCAGTCATGAGAGAGCTTTCTGATGTAATGATCTTGCTGTTCTGTCTAAGC 885  
 OY 260 ValPheAlaLeuIleGlyLeuGlnIleuPheMetGlyAsnLeuArgAsnIlyCysIleGln 279  
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 DB 886 GTGCTTGGCTATATAGATTTGCAGTTGTTCTATGGGCACTAGGAATATAATTTTGCA 945  
 OY 280 TrpProThrAsnAlaSerLeuGlnIleuSerIleGluIlyAsnIleThr----- 297  
 |||||  
 DB 946 TGCCCTCCAGATATCT-----TCCCTTGAATATAATATCACTTCTCTTC 990  
 OY 298 -----ValAsnTrpAsnGlyThrLeuIleAsnGlnThrValPheGluPheAsp 313  
 |||||  
 DB 991 TTTTAAACAATTCATGAGATGGGAAATGGTACTACTTTCATAGACATGACCATATTTAAC 1050  
 OY 314 TrpIlySerSerTrpIleGlnAspSerArgTrpHisTrpPheLeuGlnIlyPheLeuAspAla 333  
 |||||  
 DB 1051 TGGGATGAATATATTGAGATATAAGTCACTTTATTTTATAGAGGGCAAAATGATGCT 1110  
 OY 334 LeuLeuCysGlyAsnSerSerAspAlaGlyIleCysProGlnIlyTrpMetCysValIlyS 353  
 |||||  
 DB 1111 CTGCTTGTGGCAACAGCTCAGATGACAGCCAGTGTCTGTAAGATACATCTGTGGAAG 1170  
 OY 354 AlaGlyArgAsnProAsnTrpGlyTrpThrSerPheAspThrPheSerTrpAlaPheLeu 373  
 |||||  
 DB 1171 GCGGTGAGAAACCCCAACTATGGCTACACAGCTTTGACACCTTATGTTGGGCTTTTTC 1230.  
 OY 374 SerLeuPheArgLeuMetThrGlnAspPheTrpGlyAsnLeuTrpGlnLeuThrLeuArg 393  
 |||||  
 DB 1231 TCTTTATTTTGTCTCATGATCAAGACTTCTGGGAAACCTTTATCACTGACACACTACG 1290  
 OY 394 AlaAlaGlyIlySlyThrTrpMetIlePhePheValLeuValIlePheLeuGlySerPheTrp 413  
 |||||  
 DB 1291 GCGCTGGGAAACAGTACATGATATTTTGTCTGTCTGCTATTTCTTCTGGGCTCATCTAT 1350  
 OY 414 LeuIleAsnLeuIleLeuAlaValAlaMetAlaTrpGlnIleGlnIleAsnGlnAlaThr 433  
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 DB 1351 CTATATAATTTGATTTGGTGTGGTGGCCATGGCCATGAGAGACAAATTCAGGCCACA 1410  
 OY 434 LeuGlnGlnIleAlaGlnIlySlyGlnIleAlaPheGlnIleMetIleGlnIleuIlySlyS 453  
 |||||  
 DB 1411 TTGGAGAGGCTGACAGAGAGAGAGATTTTCAAGACTGTCTGACAGCTTGGAAGAAAG 1470  
 OY 454 GlnGlnGlnIleAlaGlnIleAlaIleThrAlaThrAlaSerGlnIleSerArgIlePro 473  
 |||||  
 DB 1471 CAACAAGAGAGAGACT---CAGGCGGAGCTGACCGCATCTGCTGAATCAAGAGACTTC 1527  
 OY 474 SerAlaAlaGlyArgLeu-----SerAspSerSerSerGlnIleAspIlySleuSer 490  
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 DB 1528 AGTGTGCTGTGGTGGATAGAGATTTTTCAGAGAGTTCTTCACTAGCATCTAAGTTGAGC 1587  
 OY 491 SerIlySerAlaIlySlyGlnArgArgAsnArgIlySlyArgIlySlyGlnIlySlyIleuSer 510  
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 DB 1588 TCCAAAGATGAAAAGAGCTGGAAGAAAACAGAGAAAAGAAAAGAAAAGAAAGAAAGCTCT 1647  
 OY 511 GlyIlyGlnIleuIlySlySpgIleuPheGlnIlySerIleuSerGlnIlySlySerIleArg 530  
 |||||  
 DB 1648 GGAGAGAGAGAGAAAAT---GACAGAGTCTTAATAATCGAATCTGAGACACATTAAGA 1704  
 OY 531 ArgIlyGlyPheArgPheSerIleGlnIlyAsnArgLeuThrTrpGluIlySlyArgIlySer 550  
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 DB 1705 AGAAAAAGTTTCCGTTTTCCTTGGAGAGAGAGTGTGACATATATAAAGAGATTTTCT 1764  
 OY 551 SerProHisGlnSerLeuSerIleArgGlySerLeuPheSerProArgArgAsnSer 570  
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 DB 1765 TCTCCACACCAAGCTTCTACTGACATCCGTGGTCCCTTTTCTCTCAAGACCAACAGT 1824  
 OY 571 ArgThrSerLeuPheSerPheArgGlyArgAlaIlyAspValGlySerGlnAsnAspPhe 590  
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 DB 1825 AGGCGAGAGCTTTTCAAGCTTCAGAGGTGAGAGAAAGAGACATTTGGCTGTGAGATGACTTT 1884

OY 591 AlaAspAspGlnIleHisSerThrPheGlnIleAspAsnGlnSerArgTrpAspSerLeuPheVal 610  
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 DB 1885 GCTGATGATAGACACACACCTTTGAGGACATACACCCGAAAGACCTCTCTGTCTG 1944  
 OY 611 ProArgArgHisGlyIleuArgArgAsnSerAsnLeuSerGlnThrSerArgSerSerArg 630  
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 DB 1945 CCGCAGACAGATGAGAGAAAGCGCCACAGCAATGTCAAGCAGGCGACCGTCCAGG 2004  
 OY 631 MetLeuAlaValPheProAlaAsnGlyIlyMetHisSerThrValAspCysAsnGlyVal 650  
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 DB 2005 GTCTCCCTCCATCTCCCTGCAATGGAGATGATGATGCTGTGAGCTGTGCAATGGTGTG 2064  
 OY 651 ValSerLeuValGlyIlyProSerValProThrSerProValGlyIleuLeuProGln 670  
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 DB 2065 GTCTCCCTGTGGGGGCGCCCTTCACTCACATCT---GCTGGGAGCTCTTACAGAG 2121  
 OY 671 ValIleIleAspIlySproAlaThrAspAspAsnGlyThrThrThrGlnThrGluMetArg 690  
 |||||  
 DB 2122 -----GGCAACAATCTGAAACAGAAATTAAGA 2148  
 OY 691 LysArgArgSerSerSerPheHisValSerMetAspPheLeuGlnIleuProSerGlnArg 710  
 |||||  
 DB 2149 AAGAGAGGTCAGTCTTATATATGTTTCCATGATTTATGGAAGATCCTACATCAAG 2208  
 OY 711 GlnArgAlaMetSerIleAlaSerIleLeuThrAspThrValGlnIleuGlnIleuSer 730  
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 DB 2209 CAAGAGCAATGAGATATAGCAGATATTTTACCAACACCATGAGAAAGATTTGAAGATCC 2268  
 OY 731 ArgGlnIlySlyCysProProCysTrpTrpIlySlyPheSerAsnIlePheLeuIleTrpAspCys 750  
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 DB 2269 AGACAGAAATGCCACCATCTCTGTATTAATTTGCTTAATATGCTTTGATTTGGACACTGT 2328  
 OY 751 SerProTrpTrpLeuIlySlyValIlyHisValValAsnLeuValIleMetAspProPheVal 770  
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 DB 2329 TGTAAACCATGTTAAAGGTGAACACCTTCACACCTGTGTGAAGGACCCATTTGTT 2388  
 OY 771 AspLeuAlaIleThrIleCysIleValLeuAsnThrIleuPheMetAlaMetGlnIleThr 790  
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 DB 2389 GACCTGGCCTACACCATCTCATTTCTTAAATACACTTTCATGCTATGCTATGAGACACTAT 2448  
 OY 791 ProMetThrAspHisPheAsnAsnValLeuThrValGlyIlyAsnLeuValIlePheThrGlyIle 810  
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 DB 2449 CCATGACGAGAGAGTTCACACAGATGATCTGTCTGTGGAACCTGCTTCACAGGGATC 2508  
 OY 811 PheThrAlaGlnMetPheLeuIlySlyIleIleAlaMetAspProTrpTrpTrpPheGlnIle 830  
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 DB 2509 TTCACAGCAGAAATGTTTCCAGATATATGCCATGATCCATATATATATATCAAGAA 2568  
 OY 831 GlyTrpAsnIlePheAspGlyPheIleValThrLeuSerLeuValGlnIleuGlyLeuAla 850  
 |||||  
 DB 2569 GCGTGAATAATTTTGAATGATTTTATGATGAGCTTAAATGAAACCTTGTGTTGCA 2628  
 OY 851 AsnValGlnIlyLeuSerValIleuArgSerPheArgLeuLeuArgValIlePheIlyLeuAla 870  
 |||||  
 DB 2629 AATGTGGAAGATGTGACATGATTCCTGATTCCTGCGGTGCTCCGATGTTTCAAGTTGCA 2688  
 OY 871 LysSerTrpProThrLeuAsnMetLeuIleIlySlyIleIleGlyAsnSerValGlyAlaLeu 890  
 |||||  
 DB 2689 AATCTTGGCCACATCTAATATATGCTAATTAAGATCATGTGCAATTCGTGGGGGCTCTA 2748  
 OY 891 GlyAsnLeuThrIleuValLeuAlaIleIleValPheIlePheAlaValIleGlyMetGln 910  
 |||||  
 DB 2749 GGAACCTCACTTGTGATTTGGCCATCATGCTCTCAATTTTGTGTGGTGGCGATCAG 2808  
 OY 911 LeuPheGlyLysSerTrpIlySasPysValIlySlyIleAlaSerAspCysGlnIleuPro 930  
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 DB 2809 CTCTTTGGTGAAGCTACAAAGATGTGTCTGCAAGATTTTCCATGATTTGTGAATCTCCA 2868  
 OY 931 ArgTrpHisMetAsnAspPhePheHisSerPheLeuIleValPheArgValIleuCysGly 950  
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 DB 2869 CGCTGACACATGATGACTTTTCCACTCTCTGTGATGTGTTCGGCGTGTGTGGA 2928  
 OY 951 GluTrpIleGlnIleuThrAspCysMetGlnValAlaIleGlyIleAlaMetCysLeuThr 970









QY 671 ValIleIleAspLysProAlaThrAspAsnGlyThrThrThrGluThrGluMetArg 690  
DB 2122 -----GGCACAACTACTGAAACACAAATAAACA 2148  
QY LysArgArgSerSerPheHisValSerMetAspPheLeuGluAspProSerGlnArg 710  
DB 2149 AAGAGACGGTCCAGTCTTATCATCTTTCACATGATTTATTTGGAAGATCTCAATCACAAG 2208  
QY GlnArgAlaMetSerIleAlaSerIleLeuThrAsnThrValGluGluLeuGluSer 730  
DB 2209 CAAGAGCAATGATGATAGCCAGTATTTGACCAACACATGGAAGAACTTGAAGATCC 2268  
QY ArgGlnLysCysProProCysTrpTyrLysPheSerAsnIlePheLeuIleTrpAspCys 750  
DB 2269 AGACAGAAATGCCCACTGCTGATTAATTTGCAATATGCTTTGATTTGGAGACTGT 2328  
QY SerProTyrTrpLeuLysValLysHisValAlaAsnLeuValValMetAspProPheVal 770  
DB 2329 TGTAAACCATGGTTAAAGGTGAAACACCTGTCAACCTGGTGTGAATGACCATTTGTT 2388  
QY AspLeuAlaIleThrIleCysIleValLeuAsnThrIlePheMetAlaMetGluHisTyr 790  
DB 2389 GACCTGGCCATCACCATCTGCATCTCTTAATATACACTCTTCATGGCTATGAGCAGCAT 2448  
QY ProMetThrAspHisPheAsnAsnValLeuThrValGlyAsnLeuValPheThrGlyIle 810  
DB 2449 CCCATGACGAGCAGTTCAGCAGTACTGCTGTGTGAACCTGGCTTCACAGGAGCAT 2508  
QY PheThrIleGluMetPheLeuLysIleIleAlaMetAspProTyrTyrTyrPheGlnGlu 830  
DB 2509 TTCACAGCAAAATGTTCTCAAGATTAATGGCATGATCCATTAATTAATTAACGAA 2568  
QY GlnTyrAsnIlePheAspGlyPheIleValThrLeuSerLeuValGluLeuGlyLeuAla 850  
DB 2569 GCGTGAATATTTTGAAGGTTTATGTGAGCCTTACTGTTAATGAACTGGTTGGCA 2628  
QY AsnValGluGlyLeuSerValLeuArgSerPheArgLeuLeuArgValPheLysLeuAla 870  
DB 2629 AATGGGAGAGATGTCTGCTTCCGATCATCCGCTGCTCCGAGTTTCAAGTTGGCA 2688  
QY LysSerTrpProThrLeuAsnMetLeuIleLysIleIleGlyAsnSerValGlyAlaLeu 890  
DB 2689 AAATCTGGCCAACTCAATATGCTAATTAAGATCATTTGGCAATTCGTGGGGCTCTCA 2748  
QY GlnAsnLeuThrLeuValLeuAlaIleIleValPheIlePheAlaValValGlyMetGln 910  
DB 2749 GGAACCTCACCCTTGATTTGGCCATCATCGCTTCATTTTGGCTGGCTGGCA 2808  
QY LeuPheGlyLysSerTyrLysAspCysValCysLysIleAlaSerAspCysGlnLeuPro 930  
DB 2809 CTTCTTGGTAAAGCTCAAAAGATGTCTGCAAGATTTCCAAATGATGTGAACCTCCA 2868  
QY ArgTrpHisMetAsnAspPhePheHisSerPheLeuIleValPheArgValLeuGlyGly 950  
DB 2869 CGCTGGCAGATGATGATCTTTTCCATCTTCGATCGATCGTTCGGGTGCTGTGTGA 2928  
QY GlnTrpIleGluThrMetTrpAspCysMetGluValAlaGlyGlnAlaMetCysLeuThr 970  
DB 2929 GAGTGGATAGACCATATGGGAGCTGTATGAGAGTGGCTGGCCAAACCATGAGCTTACT 2988  
QY ValPheMetValMetValIleGlyAsnLeuValValLeuAsnIlePheLeuAlaLeu 990  
DB 2989 GTCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3048  
QY Leu\*\*\*SerSerPheSerAlaAspAsnLeuAlaAlaThrAspAspAsnGluMetAsn 1010  
DB 3049 CTTTGAATCTCTTCACTTCTGACATCTTCTGCTGCTGATGATGATGATGATGATGAT 3108  
QY AsnLeuGlnIleAlaValAspArgMetHisLysGlyValAlaIleTyrValLysArgLysIle 1030  
DB 3109 AATCTCCAGATGCTGTGTGGAAAGATGCAAGAAAGATGATTTGTGTTAAAGAAATAA 3168

QY 1031 TyrGluPheIleGlnGlnSerPheIleArgLysGlnLysIleLeuAspGluIleLysPro 1050  
DB 3169 CGTGAATTTATTCAGAAACCCCTTGTAGCAAGCAGAAAGCTTTATGATGAATTAACCG 3228  
QY 1051 LeuAspAspLeuAsnLysLysAspSerCysMetSerAsnHisThr\*\*\*-GluIle 1069  
DB 3228 CTTGAGATCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3288  
QY GlnLysAspLeuAspTyrIleLeuLysAspValAlaGlyThrThrSerGlyIleGlyThrGly 1089  
DB 3289 GGCAAGACCTCAATTAATTCAAAGACGGAATGCACTACTAGTGGCAATA-----GCC 3342  
QY 1090 SerSerValGluLysTyrIleIleAspGluSerAspTyrMetSerPheIleAsnAsnPro 1109  
DB 3343 AGCATGTGAAATAATATCTGCTGATGAAAGTGAATGATATCATCTTATTAACAACCT 3402  
QY 1110 SerLeuThrValThrValProIleAlaValGlyLysUserAspPheGluAsnLeuAsnThr 1129  
DB 3403 ACCCTCACTGTAACAGTACCAATTCCTGTGAGAAATCGACTTGAATAATTAATACT 3462  
QY 1130 GluAspPheSerSerGluSerAspLeuGluGluSerLysGluLysLeuAsnGluSerSer 1149  
DB 3463 GAGAATTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 3519  
QY 1150 SerSerSerGluGlySerThrValAspIleGlyAlaProValGlu--GluGlnProVal 1168  
DB 3520 AGTTCATCTGAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 3579  
QY 1169 ValGluProGluGluThrLeuGluProGluAlaCysPheThrGluGlyCysValGlnArg 1188  
DB 3580 GTTGAACCTGAGAGAAATCCCTTAACCTGAAAGCTTTTACGAAAGACTGTACGAGAG 3639  
QY 1189 PheLysCysCysGlnIleAsnValGluGluGluGlyArgGlyLysGlnTrpTrpAsnLeuArg 1208  
DB 3640 TTCAGTGTGTGACATTAATAGCTACAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 3699  
QY 1209 ArgThrCysPheArgIleValGluHisAsnTrpPheGluThrPheIleValPheMetIle 1228  
DB 3700 AAACATCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3759  
QY 1229 LeuLeuSerSerGlyValAlaLeuAlaPheGluAspIleTyrIleAspGlnArgLysThrIle 1248  
DB 3760 CTGCTGACGAGTGGGGCTGTGGCTTTGAAAGTAAATTAATTAATTAATTAATTAAT 3819  
QY 1249 LysThrMetLeuGluTyrValAlaAspLysValPheThrTyrIlePheIleLeuGluMetLeu 1268  
DB 3820 AAGACCATCTTGATTAATGCTACAAAGCTTTTCACTTCAATTAATTAATTAATTAAT 3879  
QY 1269 LeuLysTrpValAlaTyrGlyTyrGlnThrTyrPheThrAsnAlaTrpCysTrpLeuAsp 1288  
DB 3880 CTAAGTGGGTTGCATATAGTGTTCACAGTATTTTACCAGTCCGTGGCTGCTAGAC 3939  
QY 1289 PheLeuIleValAspValSerLeuValSerLeuThrAlaAsnAlaLeuGlyTyrSerGlu 1308  
DB 3940 TTCCGATTTGTTGATGCTCACTGCTTAACTGAAATGCTTGGTGTACACAAA 3999  
QY 1309 LeuGlyAlaIleLysSerLeuArgThrLeuArgAlaLeuArgProLeuArgAlaLeuSer 1328  
DB 4000 CTTGGTGCATCAAAATCCCTCAAGAACTAGAGCTGTGAGGCCCTGAGACCTTTGTCC 4059  
QY 1329 ArgPheGluGlyMetArgValValValAlaAsnAlaLeuLeuGlyAlaIleProSerIleMet 1348  
DB 4060 CGGTGTGAAGAAATGAGGGCTGTCTTAATGCTCTTTTAAAGAGCCATTCATCTATCTG 4119  
QY 1349 AsnValLeuLeuValCysLeuIlePheThrLeuIlePheSerIleMetGlyValAsnLeu 1368  
DB 4120 AATGATCTTCTGTTGTCTGATCTTTTGGCTAAATTAATCAATATCATGAGATGAGATCT 4179  
QY 1369 PheAlaGlyLysPheTyrHisCysIleAsnThrThrPheGlyAspArgPheAspIleGlu 1388  
DB 4180 TTTGCTGGCAAGTTTACCATGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4239  
QY 1389 AspValAsnAsnHisThrAspCysLeuLysLeuIleGluArgAsnGluThrAlaArgTrp 1408

|    |      |  |      |
|----|------|--|------|
| Db | 4240 | GTGTCACACACACACAGTACGTGACCAAGCTCATTGAGACGAATCAACACTGCCAGGTGCG    | 1299 |
| Qy | 1409 | LysAsnValIysValAsnPheAspAsnValGlyPheGlyTYRLeuSerLeuLeuGlnVal     | 1428 |
| Db | 4300 | AAAAATGTGAAATAAACTTTCATCTTAACAGTAGACCTTGATATCTGCTCTCAAGTA        | 4359 |
| Qy | 1429 | AlaThrPheIysGlyIrrPheMetAspIleMetTYRAlaIvalAspSerArgAsnValGlu    | 1448 |
| Db | 4360 | GCCACGCTTAAAGGATGAGATGATATATAGTAVGACGTGTGATTCACGAAATGTGAA        | 4419 |
| Qy | 1449 | LeuGlnProIlystTYRGlusIleSerLeuTYRMetTYRLeuTYRPhaValIlePheIle     | 1468 |
| Db | 4420 | TTACACCCCAAGATGATAGACCAACCGTACATGATCTTTATTTTGTGATCTTTATAT        | 4479 |
| Qy | 1469 | PheGlySerPhePheThrLeuAsnLeuPheIleGlyValIleIleAspAsnPheAsnGln     | 1488 |
| Db | 4480 | TTTGGTTCATCTTTACCTTGAAATCTTTTCATTTGGTGCATCATGATGATTAACCTCA       | 4539 |
| Qy | 1489 | GlnIlystIysIysPheGlyGlyGlnAspIlePheMetThrGlnGlnIlystTYR          | 1508 |
| Db | 4540 | CAGAAAAAGAGATTGGAGGTCAAGCATTATTATGACAGAAAGAACAAATAATCTAC         | 4599 |
| Qy | 1509 | AsnIleMetIysIysIleuGlySerIlystIysProGlnIysProIleProArgProGlyAsn  | 1528 |
| Db | 4600 | AATGCATGAAAAAACTGGGTTCAAGCAACCAACCAAAACCATCTCGACCTGCTAAC         | 4659 |
| Qy | 1529 | LysPheGlnIlyMetValPheAspPheValThrArgIvalPheAspIleSerIleMet       | 1548 |
| Db | 4660 | AAATTCACAGAAATGGCTTGATTTGTAACCAAAAGCTCTTGATACAGATCATCG           | 4719 |
| Qy | 1549 | IleLeuIleGlyLeuAsnMetValThrMetMetValGlnThrAspAspGlnSerGlyIlyr    | 1568 |
| Db | 4720 | ATTCCTCATCTGCTTAAACAGTGACACCAATGATGGTGGAAACCGAATGACCAAGTCA       | 4779 |
| Qy | 1569 | ValThrThrIleLeuSerArgIleAsnLeuValPheIleValLeuPheThcGlyGlnCys     | 1588 |
| Db | 4780 | ATGCACAACATTCTGATCTGATGATTAATCTGCTGCTTATTTGTTCTTCACTGGAAGAT      | 4839 |
| Qy | 1589 | ValLeuIysLeuIleSerLeuArgHisTYRTYRPhaThrIleGlyTYRAsnIlePheAsp     | 1608 |
| Db | 4840 | GTGCTGAACATGATCTCTCTCTTCTACTCATATTCATATTCAGATGAGAAATATTTTCAT     | 4899 |
| Qy | 1609 | PheValIvalIvalIleLeuSerIleValGlyMetPheLeuAlaGlnLeuIleGlyIlystYr  | 1628 |
| Db | 4900 | TTTGTGTGTGATCTCTCTCCATTATGAGAAATGTTCTGGCGGAACATATGAAAAATAT       | 4959 |
| Qy | 1629 | PheAlaSerProThrIleuPheArgValIleIleArgLeuAlaArgIleGlyArgIleLeuArg | 1648 |
| Db | 4960 | TTTTGTGCCCCCTACCCGTGTCGAGATGATCCGCTTGGCCAGGATTTGGCGGAATCTTACGT   | 5019 |
| Qy | 1649 | LeuIleIysGlyAlaIysGlyIleArgThrLeuLeuPheAlaIleuMetSerLeuPro       | 1668 |
| Db | 5020 | CTGATCAAGAGACGAAGGGGATCCGACCGCTCTCTTGGCTTGATATGATGCCCTTCTCT      | 5079 |
| Db | 5080 | GGCTGTGTTAAACATCGGCCCTCTTCTTTCCTGTCATGTTCACTACCATCTTTGGG         | 5139 |
| Qy | 1689 | MetSerAsnPheAlaTYRValIysArgGluValGlyIleAspAspMetPheAsnPheGlu     | 1708 |
| Db | 5140 | ATGTCACAATTTTGGCTATGTTAAAGAGGAAAGTTGGGATGATGATGATGTCACACTTTGAG   | 5199 |
| Qy | 1709 | ThrPheGlyAsnSerMetIleGlySerLeuPheGlnIleThrThhSerAlaGlyTYRAspGly  | 1728 |
| Db | 5200 | ACCTTTGGCACAACATGATCTGCTGCTTCCAAATTAACAACCTCTGCTGCGTGGGATGGA     | 5259 |
| Qy | 1729 | LeuLeuAlaProIleLeuAsnSerIysProProAspCysAspProAsnIysValAsnPro     | 1748 |
| Db | 5260 | TTGTGAGACCTATTTTATATATGAGCCGTCAGACATGAGACCGTCGACAAAGATCACCT      | 5319 |
| Qy | 1749 | GlySerSerValIysGlyAspCysGlyAsnProSerValGlyIlePhePhePheValSer     | 1768 |

[illegible]







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|----|------|---|------|
| Dh | 3034 | GAGTGGATATAGACACCATGTGGACATGCAATGAGAGTGGCGGCGACACCATGTGGCTTACT  | 3093 |
| Oy | 971  | ValPheMetLeuValMetValIleGlyAsnLeuValValLeuAsnLeuPheLeuValLeu    | 990  |
| Dh | 3094 | GCTTCATCATGATGCTCATGCTGATTTGGGAACCTGTGTCTCTGAACTCTTCTTGGCCCTTG  | 3153 |
| Oy | 991  | Leu***SerSerPheSerAlaAspAsnLeuAlaAlaThrAspAspAspAsnGluMetLsn    | 1010 |
| Dh | 3154 | CTCTCGAGTCTCTTCACCTCGACACCAACCTGGCTGCCACAGATGACGAAATGAAATGAC    | 3213 |
| Oy | 1011 | AsnLeuGlnIleAlaValAspArgMetHisGlyValAlaValIleValLysArgLysIle    | 1030 |
| Dh | 3214 | AACCTCCAGATAGCCCGTGGAGAGATGCAAGAAAGGAATTTGATTTGTTAAAGCAATGA     | 3273 |
| Oy | 1031 | TyrGlnPheIleGlnInSerPheIleArgLysGlnLysIleLeuAspGluIleLysPro     | 1050 |
| Dh | 3274 | CGTGAATTCATTCAGAAAGCCTTTGTACAGAAAGCAAGAAAGCTTTAGATGAATCAAAACG   | 3333 |
| Oy | 1051 | LeuAspAspLeuAsnAsnLysLysAspSerCysMetSerAsnHisThr***GluIle       | 1069 |
| Dh | 3334 | CTGGAAATCTGGAATTAACAAGAAAGACAGTGTATCTCCAAACACACACCATAGAAATA     | 3393 |
| Oy | 1070 | GlyLysAspLeuAspTyrLeuLysAspValAsnGlyThrThrSerGlyIleGlyThrGly    | 1089 |
| Dh | 3394 | GGCAAGACCTCAATTAATCTCCAAAGATGGAAGCGGACGACCACTGGGATA-----GGC     | 3447 |
| Oy | 1090 | SerSerValGluLysTyrIleIleAspGluSerAspTyrMetSerPheIleAsnAspPro    | 1109 |
| Dh | 3448 | AGCAGTGTGGAGAACTATGTGTGATGAGAGATTAATATGCTTCATTAACAACACCC        | 3507 |
| Oy | 1110 | SerLeuThrValIhrValProIleAlaValGlyGluSerAspPheGluAsnLeuAsnThr    | 1129 |
| Dh | 3508 | AGCCTCACCGTGAAGTGTGCCATCGCCCTTGGAGAGTGTGACTTTGAACACTTAACACG     | 3567 |
| Oy | 1130 | GluAspPheSerSerGluSerAspLeuGlnGluSerLysGlnLysLeuAsnGluSerSer    | 1149 |
| Dh | 3568 | GAAACATTCAGTACTGTGTGAGATATGGAAGAGCAAGCAAGCAAAATTTGAT---GCAACT   | 3624 |
| Oy | 1150 | SerSerSerGluGlySerThrValAspIleGlyAlaProValGlu---GluGlnProVal    | 1168 |
| Dh | 3625 | AGCTCATCTGAGGGCAGTACGTTGATATAGCGCTCCGCGAGAGGAGAGACGACCAAG       | 3684 |
| Oy | 1169 | ValGluProGluGluThrLeuGluProGluAlaCysPheThrGluGlyCysValGlnArg    | 1188 |
| Dh | 3685 | GCCCAACCGGAAGAAATGCTTTGAACCGGAAGCGTGTTCACGAAGACTGTGTGAGAAAG     | 3744 |
| Oy | 1189 | PheLysCysCysGlnIleAsnValGlnGluArgLysArgLysGlnIleThrPheAsnLeuArg | 1208 |
| Dh | 3745 | TTCAAGTGTGTCTGATGAACATATGAAGAGAGGCAAGGCAACCTGTGGGAACTTGAGG      | 3804 |
| Oy | 1209 | ArgThrCysPheArgIleValGlnLysAsnThrPheGluThrPheIleValPheMetIle    | 1228 |
| Dh | 3805 | AAAACGTGCTCAAGATATGATAGACATTAACGTGTTGAACCTTCATGTGTTTATGATT      | 3864 |
| Oy | 1229 | LeuLeuSerSerGlyAlaLeuAlaPheGluAspIleTyrIleAspGlnArgLysThrIle    | 1248 |
| Dh | 3865 | CTGCTCAGCAGTGTGTCTGTGGCTTTGAAGACATTTATATGACACGAAAGCACATC        | 3924 |
| Oy | 1249 | LysThrMetLeuGluTyrAlaAspLysValPheThrTyrIlePheThrIleGlnLysMetLeu | 1268 |
| Dh | 3925 | AAGACCATGTGGAGATGTGTGAACAGGTTTCACTTAATCTTAATCTCGACATGCTT        | 3984 |
| Oy | 1269 | LeuLysTrpValAlaTyrGlyTyrGlnThrTyrPheThrAsnAlaTrpCysTrpLeuAsp    | 1288 |
| Dh | 3985 | CTTAAGTGGGTGGCTATGTGTTTCCAAATGATATTTCACCAATGCTGGTGTGGCTGAC      | 4044 |
| Oy | 1289 | PheLeuIleValAspValSerLeuValSerLeuThrAlaAsnAlaLeuGlyTyrSerGlu    | 1308 |
| Dh | 4045 | TTCTCGATCGTGTATGTCTCTTGTTAGATTAACTGCAAAATGCTGGGCTATTCGGAA       | 4104 |
| Oy | 1309 | LeuGlyAlaIleLysSerLeuArgThrLeuArgAlaLeuArgProLeuArgAlaLeuSer    | 1328 |
| Dh | 4105 | CTTGGTGGCAATCAAGTCCCTCCGAAGCTTAAAGACTGTGAAGACTCTTACGAGCCCTTATCC | 4164 |

|    |      |  |      |
|----|------|--|------|
| QY | 1329 | ATPheGluGlyMetArgValValAlaAsnAlaLeuGlyValAlaIleProSerLLeMet      | 1348 |
| Db | 4165 | CGATTGGAAGGAATGAAGGGTGTGTGTAAGCGCTCTTGAAGGCCATCTCCCTCCATTAATG    | 4224 |
| QY | 1349 | AsnValIleuLeuValCysLeuIlePheTrpLeuIlePheSerLLeMetGlyAlaAsnLeu    | 1368 |
| Db | 4225 | AACGTAACCTTCGGCTCGCTCGATGATCTTTGGCTAAATATACATATCAATGGGGGTGAATCTC | 4284 |
| QY | 1369 | PheAlaGlyLysPheTrpHisCysIleAsnThrThrThrGlyAspArgPheAspIleGlu     | 1388 |
| Db | 4285 | TTTGGTCGCAAGTCTACATTCATTCATCACTACACACGCGGGGAATCTTGTATGTGAGC      | 4344 |
| QY | 1389 | AspValAsnAsnThrAspCysLeuLysLeuIleGluArgAsnGluThrAlaArgTrp        | 1408 |
| Db | 4345 | GTGGTCACACACTACAGTGAATGGCAAGCTCTCATTTGAGACATACAGCGCCAGGTGG       | 4404 |
| QY | 1409 | LysAsnValLysValAsnPheAspAsnValGlyPheGlyTrpLeuSerLeuGluVal        | 1428 |
| Db | 4405 | AAGAACGTGAAGGTCAACTTCGATTAACGTGGGACTGGATACCTTCTCGCTCCAACTGA      | 4464 |
| QY | 1429 | AlaTrpPheLysGlyTrpMetAspIleMetTrpAlaAlaValAspSerArgAsnValGlu     | 1448 |
| Db | 4465 | GCCACCTTTAAAGATGGAATGGAATCATATATGACAGCTGTGCATCAAGAAATGTACAA      | 4524 |
| QY | 1449 | LeuGlnProLysTrpGluGluSerLeuTrpMetTrpLeuTrpPheValIlePheIleLe      | 1468 |
| Db | 4525 | CTGCAGGCCAAATAGCAAGAACATCTCATATCTACTTACTTCTGCTCATCTTCATATC       | 4584 |
| QY | 1469 | PheGlySerPhePheThrLeuAsnLeuPheIleGlyValIleIleAspAsnPheAsnGln     | 1488 |
| Db | 4585 | TTTCGGCTCATCTTCACCCGTGAACCTGTCATTTGGTGCATCTAGACAACTTCAACGAG      | 4644 |
| QY | 1489 | GlnLysLysLysPheGlyGlyGlnAspIlePheMetThrGluGlnGlnLysTrpTrp        | 1508 |
| Db | 4645 | CAGAAGAAGAGTTTGGAGGTCAAGACATCTTTATGACAGACAGACAGAAATACTAC         | 4704 |
| QY | 1509 | AsnAlaMetLysLysLeuGlySerLysLysProGlnLysProIleProArgProGlyAsn     | 1528 |
| Db | 4705 | AATGCATAGAGAAGACTCGGCTCCAAAGAACCCGACAAAGCCCATTCCTCGGCTCCAAAC     | 4764 |
| QY | 1529 | LysPheGlnGlyMetValPheAspPheValThrArgGlnValPheAspIleSerIleMet     | 1548 |
| Db | 4765 | AAATTTCAAGGATGAGTCTTGTGATTTGTGAACCAAGATCTTTGACATCCAGCATCAG       | 4824 |
| QY | 1549 | IleLeuIleCysLeuAsnMetValThrMetLeuValGlyThrAspAspIleSerLLeuTrp    | 1568 |
| Db | 4825 | ATCCCATCTCGCTCAACATGATGATGACCATGATGTTGAAGCGACGACCATGACGAG        | 4884 |
| QY | 1569 | ValThrThrIleLeuSerArgIleAsnLeuValPheIleValLeuPheThrGlyGluCys     | 1588 |
| Db | 4885 | ATGACCAACATCCGTACCTGATATCACTGTGTTCAATGTCTCTGTTCAAGGCGCAAGT       | 4944 |
| QY | 1589 | ValLeuLysLeuIleSerLeuArgHisTrpTrpPheThrIleGlyTrpAsnIlePheAsp     | 1608 |
| Db | 4945 | GTGGCGAAGCTCATCTCCCTCGGCATTAATTAATTCACATCGCGTGGAAATTTTGTAT       | 5004 |
| QY | 1609 | PheValValValIleLeuSerIleValGlyMetPheLeuAlaGluLeuIleGlyLysTrp     | 1628 |
| Db | 5005 | TTTGTGTAGTACATCCCTCATTTGTAGCAATGTTCGTGCGGAGCTGATAGAGAATAT        | 5064 |
| QY | 1629 | PheValSerProThrIleuPheArgValIleArgLeuAlaArgIleGlyArgIleLeuArg    | 1648 |
| Db | 5065 | TTTCGTGCTCCCTACCCGTTCCTCGAGTATCCGCTCGCCAGGATTTGGAGAAATCCTACGC    | 5124 |
| QY | 1649 | LeuIleLysGlyAlaLysGlyIleArgThrLeuLeuPheAlaLeuMetMetSerLeuPro     | 1668 |
| Db | 5125 | CTGATCAAAAGCGGCAAGGGGATCCGACATCTGCTCTTGGCTGTATATATGCTCCCTTCT     | 5184 |
| QY | 1669 | AlaLeuPheAsnIleGlyLeuLeuLeuPheLeuValMetPheIleTrpAlaIlePheGly     | 1688 |
| Db | 5185 | GCGCGTTTCAACATCGGCTCTCCGCTTTCTGCTGATGTATCATAGCCCATCTTTGGG        | 5244 |

QY 1689 MetSerAspPheAlaTyrValLysArgGluValGlyIleAspPheMetPheAsnPheGlu 1708  
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 Db 5245 ATGTCCACACTTGGCTTACGTTAGAGGGAAGTGGATTGATGACATTTCACTTGGAG 5304  
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 Db 5365 CTCTGCGCCCTTACTAAATATAGGAGGACCTCTCTACCTGTGACCTGAAAAAGACACCT 5424  
 QY 1749 GlySerSerValLysGlyAspCysGlyAsnProSerValGlyIlePhePheValSer 1768  
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 Db 5665 TCTGACTTTCACAGCTGCGCTGGATCTCCCTCTCTCATCGCAAAAGCCAAACCAAGTCCAG 5724  
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 ACCESSION M22254

VERSION M22254.1 GI:1041090  
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 SOURCE Rattus norvegicus cDNA to mRNA.  
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 Rattus.  
 REFERENCE 1 (bases 1 to 8552)  
 AUTHORS Noda, M. and Numa, S.  
 TITLE Structure and function of sodium channel  
 JOURNAL J. Recept. Res. 7 (1-4), 467-497 (1987)  
 MEDLINE 87311395  
 PUBMED 2442385  
 COMMENT On Oct 27, 1995 this sequence version replaced gi:340712.  
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 QY 21 SerLeuAlaAlaIleGluArgGlnAlaGluLysAlaLysAsnProLysProAsp 40  
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 Db 271 TCCCTTCTGCTATCGACAGACGCTTGCAGAGAAAGATTAAGAACCCAAACAGAA 330  
 QY 41 LysLysAsp---AspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLys 59  
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 QY 60 AsnLeuProPheIleIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAsp 79  
 |||||  
 Db 391 TCCCTTCTTATTTATGAGACATTCCTCCAGAGATGTGTGAGAAACCACTGAGAGAC 450  
 QY 80 LeuAspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIle 99  
 |||||  
 Db 451 CTGAGACCCCTACTATATCAATTAAGAAACCTTATATGATTAAGGAGGAAAGCAATC 510  
 QY 100 PheArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLys 119  
 |||||  
 Db 511 TCGGGGTTCAGCGCCACTCTGCGCTGTACTTTAATCTCCCTTCAACCCCATTAAGAAA 570  
 QY 120 IleAlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeu 139  
 |||||  
 Db 571 TTACCTATTAAGATTGTGTCATCTTATTAATCAATGCTTATCANTGTGCAAAATCTT 630  
 QY 140 ThrAsnCysValPheMetThrMetSerAspProProAspTyrPheLysAsnValGluTyr 159  
 |||||  
 Db 631 ACCAAGTGTGTATGACCATGATGATCCCTCAACATGAGAAAGAAAGATGAGATAT 690  
 QY 160 ThrPheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCys 179  
 |||||  
 Db 691 ACTTTTACAGGAATTTATCTTTGATCACTATTTAAATCCCTGCAAGGCGCTTTGT 750  
 QY 180 LeuGluAspPheThrPheLeuArgAspProTyrPheAsnThrLeuAspPheThrValIleThr 199

Db 751 CTAGAGATTTCACATTTCTACGAAATCCGTAATTCGTTGATTCACAGTCACTACT 810  
 QY 200 PheAlaIyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArg 219  
 Db 811 TTTCGGATGATGAAGAAATTTGTAACTCAGCAATGTTTCAAGCTTCTGCAACTTTCGA 870  
 QY 220 ValLeuArgAlaLeuGlyThrIleSerValIleProGlyLeuGlyThrIleValGlyVala 239  
 Db 871 GCTCTGAGAGCTTGAAACATTTCTGTAAATCCAGGCTGGAAGACTATGCTGGGGCC 930  
 QY 240 LeuIleGlnSerValIlyLysIleuSerAspValMetIleLeuThrValPheCysLeuSer 259  
 Db 931 CTGATCCAGTCAGTGAAGAACTCTCTGAGCTCATGATCCGACAGGCTGCTGCTGCTGCT 990  
 QY 260 ValPheAlaLeuIleGlyLeuGlnLeuPheMetCylAsnLeuArgAsnLysCysIleGln 279  
 Db 991 GCTCTTCTCTAAATCGGCTGCTGCTCTCTCATGAGCAACTGAGGAATTAATGCTGTCAG 1050  
 QY 280 TrpProThrAsnAlaSerLeuGlnIleHisSerIleGlyAsnIleThr----- 297  
 Db 1051 TGGCCCCACAGCAATTC-----ACCTTGAAATTAATATCATCTTCTTC 1095  
 QY 298 -----ValAsnTyrAsnGlyThrLeuIleAsnGluThrValPheGluPheAsp 313  
 Db 1096 TTATATACATTCATGATGGAATGATGATGCTCTCAATAGAGGCTGAACATGTTTAC 1155  
 QY 314 TrpLysSerTyrIleGlnAspSerArgTyrHisTyrPheLeuGlnGlyPheLeuAspAla 333  
 Db 1156 TGGGACCAATATATGAAGAAAGTCACTTTATTTTGGAAAGCAAAAGCATGCTCT 1215  
 QY 334 LeuLeuGlyAsnSerSerAspAlaGlyGlnCysProGluGlyTyrMetCysValLys 353  
 Db 1216 CTGCTTTGTGGAAACAGCTGCGATGCTGAGACAGTCCAGAGGATCATCTGTGTGAG 1275  
 QY 354 AlaGlyArgAsnProAsnTyrGlyTyrThrSerPheAspThrPheSerTrpAlaPheLeu 373  
 Db 1276 GCTGGGAAACCCCACTAGGCTACACAGTTTGTGACACTTCACTGAGCTGCTCTG 1335  
 QY 374 SerLeuPheArgLeuMetThrGlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArg 393  
 Db 1336 TCTTATTTGCTCATGACTCAAGACTTCTGGGAAACCTTATACACTGCTGCTGCT 1395  
 QY 394 AlaAlaGlyLysThrTyrMetIlePhePheValLeuValIlePheLeuGlySerPheTyr 413  
 Db 1396 GCTGCCGGGAAACATCATATATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1455  
 QY 414 LeuIleAsnLeuIleLeuAlaValAlaMetAlaTyrGlnGlnAsnGlnAlaThr 433  
 Db 1456 CTGATTAATTTGATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1515  
 QY 434 LeuGlnGlnAlaGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 453  
 Db 1516 CTGAGAGAGGCTGAAAG 1575  
 QY 454 GlnGlnGlnAlaAlaGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 473  
 Db 1576 CAGAGAGAGAGAGCT---CAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1632  
 QY 474 SerAlaAlaGlyArgLeu-----SerAspSerSerSerGlnAlaSerIleLeuSer 490  
 Db 1633 AGCGGGGAG 1692  
 QY 491 SerLysSerAlaLysGlnArgArgAsnArgTyrLysArgLysGlnLysGlnLysGlnLys 510  
 Db 1693 TCCAAAGATGAAG 1752  
 QY 511 GlyGlyGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 530  
 Db 1753 GGGGAGAGAGAGAGAG---GAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1809  
 QY 531 ArgLysGlnPheArgPheSerIleGlnGlnLysAsnArgLeuThrTyrGlnLysArgTyrSer 550  
 Db -----

Db 1810 AAGAAGGCTTCAGATTTCCCTGGAGAGAGATGATGACCTACGAGAGAGATTTCC 1869  
 QY 551 SerProHisGlnSerLeuLeuSerIleArgGlySerLeuPheSerProArgArgAsnSer 570  
 Db 1870 TCTCCGACACAGCTCTCTCTTGAAGATCCGAGGCTCCCTATTTTTCACAGAGCAACAGT 1929  
 QY 571 ArgThrSerLeuPheSerPheArgGlyArgAlaLysAspValGlySerGluAsnAspPhe 590  
 Db 1930 AGACCAACCTTTTCACTTCAAAAGTGCAGTGAAGAGATTTGGTTCGCAAAATGACTTT 1989  
 QY 591 AlaAspAspGlnHisSerThrPheGluAspAsnGlnSerArgArgAspSerLeuPheVal 610  
 Db 1990 GCAGACGATGAACACAGACATTTGAGGACACAGACAGACAGAGAGACTCTCTATTGTA 2049  
 QY 611 ProArgArgHisGlyGlnArgArgAsnSerAsnLeuSerGlnThrSerArgSerSerArg 630  
 Db 2050 CCACACAGACATGAG 2109  
 QY 631 MetLeuAlaValPheProAlaAsnGlyLysMetHisSerThrValAspCysAsnGlyVal 650  
 Db 2110 GGGATACCCACTCTAACCATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2169  
 QY 651 ValSerLeuValGlyGlyProSerValProThrSerProValGlyGlnLeuLeuProGlu 670  
 Db 2170 GTCGCCCTGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2229  
 QY 671 ValIleIleAspLysProAlaThrAspAspAsnGlyThrThrGluThrGluMetArg 690  
 Db 2230 -----GCCACACTAGACAGCAAGAAATAGG 2256  
 QY 691 LysArgArgSerSerSerPheHisValSerMetAspPheLeuGluAsnProSerGlnArg 710  
 Db 2257 AAGAGAGATCCAGTCTTACACGCTCTATGAGCTGTGGAAGAGAGGAGGAGGAGGAGGAG 2313  
 QY 711 GlnArgAlaMetSerIleAlaSerIleLeuThrAsnThrValGluGlnLeuGlnLeuSer 730  
 Db 2314 CAAGGGGAAATGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2373  
 QY 731 ArgGlnLysCysProProCysTyrTyrLysPheSerAsnIlePheLeuIleTrpAspCys 750  
 Db 2374 AGACAGAAATCCCACTGCTGATTAATTTGCTATATGCTGCTGCTGCTGCTGCTGCTGCT 2433  
 QY 751 SerProTyrTrpLeuLysValLysHisValAlaAsnLeuValAlaMetAspProPheVal 770  
 Db 2434 TGTAAAGCATGCTTAAGATGAAGAAACGCTGTCAATCGGATGATGATGATGATGATGAT 2493  
 QY 771 AspLeuAlaIleThrIleCysIleValLeuAsnThrLeuPheMetAlaMetGluHisTyr 790  
 Db 2494 GACCTGGCATCACCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2553  
 QY 791 ProMetThrAspHisPheAsnAsnValLeuThrValGlyAsnLeuValPheThrGlyIle 810  
 Db 2554 CCCATGACTGAGCACTGACAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2613  
 QY 811 PheThrAlaGlnMetPheLeuLysIleIleAlaMetAspProTyrTyrTyrPheGlnGln 830  
 Db 2614 TTCAGGCGAGAAATGTTCTCAAGATTAATACCATGATGATGATGATGATGATGATGATGAT 2673  
 QY 831 GlyTyrAsnIlePheAspGlyPheIleValThrLeuSerLeuValGlnLeuGlyLeuAla 850  
 Db 2674 GCGTGGATATCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2733  
 QY 851 AsnValGlnGlyLeuSerValLeuArgSerPheArgLeuLeuArgValPheLysLeuAla 870  
 Db 2734 AATGTGAAGATGTCAGTCTCCGATCATTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2793  
 QY 871 LysSerTrpProThrLeuAsnMetLeuIleLysIleIleGlyAsnSerValGlyAlaLeu 890  
 Db 2794 AAGTCTGGGCCACACGAAATGCTCATTAAGATCAATCGCAACTGCTGCTGCTGCTGCTGCT 2853  
 QY 891 GlyAsnLeuThrLeuValLeuAlaIleIleValPheIlePheAlaValAlaGlyMetGln 910  
 Db 2854 GGCACCTGACCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2913

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|----|------|--|------|
| QY | 911  | LeuphegIyLSerTyrItyrAspCysValCysIyIleAlaSerAspCysGluLeuPro       | 930  |
| Db | 2914 | CTGTTTGGAG--AGCTACCAAGGAGTGTGTGTGAATATTTCATATATGTGAGCTCCG        | 2872 |
| QY | 931  | ArgTPHLSMeTAsnAspPhePheHisSerPheLeuIleValAPheArgValLeuCysGly     | 950  |
| Db | 2973 | CGCTGGACATGACAGACACTTCTCCACCTCCTTCATGCTGTTCAGAGCGCTGTGGG         | 3032 |
| QY | 951  | GluTPPIleGluThrMetTrpAspCysMetGluValAlaGlyGlnAlaMetCysLeuThr     | 970  |
| Db | 3033 | GAGTGGATAGAACCATGTGGGACTGCAGAGAGGTGCGGGCCAGACCATGTGCTTACT        | 3092 |
| QY | 971  | ValPheMetMetValMetAlaIleGlyAsnIleValValLeuAsnLeuPheLeuAlaLeu     | 990  |
| Db | 3093 | GCTTCATCATGTGCTCATGTGTGATGGGAACCTGTGTGCTGTGAACCTCTTCTGGCCCTG     | 3152 |
| QY | 991  | Leu***SerSerPheSerIleAspAsnLeuAlaAlaThrAspAspAsnGluMetAsn        | 1010 |
| Db | 3153 | CTCCACAGTCTTTCAGCTCCAGACCAACCTGGCTGCCACAGATGACATTAACGAATGAC      | 3212 |
| QY | 1011 | AsnLeuGlnIleAlaValAspArgMetHisIysGlyValAlaTyrValIysArgIysIle     | 1030 |
| Db | 3213 | AACCTCCAGATAGCCGTGGGAAGGATGCAGAAAGGAAATGATTGTGTAAAGGAAGATA       | 3272 |
| QY | 1031 | TyrGluPheIleGlnIleSerPheIleArgIysGlnIysIleLeuAspGluIleIysPro     | 1050 |
| Db | 3273 | CGTGAATTCATTCAGAAACCCCTTGTGCAGAAACCAAAAGCCTTTAATGAAATCAAAACG     | 3332 |
| QY | 1051 | LeuAspAspLeuAsnAsnIysIysAspSerCysMetSerAsnHisThr***-GluIle       | 1069 |
| Db | 3333 | CTGGAAAGATCTGAATTACCAAGAAAGACAGTTGTATCTCCACCAACGACCATAGAAATA     | 3392 |
| QY | 1070 | GlyIysAspLeuAspTyrIleuIysAspValAsnGlyThrThrSerGlyIleGlyThrGly    | 1089 |
| Db | 3393 | GGCAAGAGACTCAATTACTCAAAAGATGGAAGAGGGACGACAGTGGCATATA-----GGC     | 3446 |
| QY | 1090 | SerSerValGluIuIyIyIleIleAspGluSerAspTyrMetSerPheIleAsnAsnPro     | 1109 |
| Db | 3447 | AGCAGGTGTGAGAGATGATGGTGGAGATGAGAGAGATTAACGTGTCATTAACCAACCCC      | 3506 |
| QY | 1110 | SerLeuThrValThrValProIleAlaValAlaGlyIleSerAspPheGluAsnLeuAsnThr  | 1129 |
| Db | 3507 | AGCTCAACCTGACGTGGCCATCGGCCCTTGGAGAGCTGACCTTGAATAACTTAACACG       | 3566 |
| QY | 1130 | GluAspPheSerSerGluSerAspLeuGluGluSerIysGluIysLeuAsnGluSerSer     | 1149 |
| Db | 3567 | GAAAGATTCAGTAGTAGTGCAGATATGGAAGAAAGCAAGAGAAATGATAT---GCANCT      | 3623 |
| QY | 1150 | SerSerSerGluIuIySerThrValAspIleGlyAlaIleProValGlu---GluGlnProVal | 1168 |
| Db | 3624 | AGCTCATCTGAGGCGAGTACGGTGTGATATGAGCACTCGGCAAGGGAGGAGGCCACAG       | 3683 |
| QY | 1169 | ValGluProGluIuIyThrLeuGluProGluAlaCysPheThrGluIyCysValGlnArg     | 1188 |
| Db | 3684 | GCCGAACCGGAAGAAATCGCTTGAAACCGGAAGCGCTGTTTCACAGAAAGCTGTGTGAGAAAG  | 3743 |
| QY | 1189 | PheIysCysGlnIleAsnValGluGluGlyIArgGlyIysGlnTyrTPAsnLeuArg        | 1208 |
| Db | 3744 | TTCAAGTGTGTGACAGATTAACCATAGAAGAGGCGCAAGCAAGCTGTGTGAACTTGAGG      | 3803 |
| QY | 1209 | ArgThrCysPheArgIleValAlaGluHisAsnTPheGluThrPheIleValPheMetIle    | 1228 |
| Db | 3804 | AAACATGTCACACAGATAGTAGAGCATTAACCTGTTTGAACCTTCATCCGTTTTATATAT     | 3863 |
| QY | 1229 | LeuLeuSerSerGlyAlaLeuAlaPheGluAspIleTyrIleAspGlnArgIysThrIle     | 1248 |
| Db | 3864 | CTGCTAGCAGGTGTGTCTGTGGCTTGAAGACATTTATATATGAGCAGCGCAAGAACCATC     | 3923 |
| QY | 1249 | LysThrMetLeuGluIyrrAlaAspIysValAPheThrTyrIlePheIleLeuGluMetLeu   | 1268 |
| Db | 3924 | AAAGCATGCTGAGATATGCTGACAAAGTTTTCATTAATCTTCATCCCTGGAGATGCTT       | 3963 |

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|----|------|---|------|
| OY | 1269 | LelysTPRValAlaIyrgLYTYrGLInThTyPheThrAsnAlATrPCysTrpLeuAsp    | 1288 |
| Dd | 3984 | CTAAAGTGGGTGGCCCTTAGTGTTTCCAAATGTAATTACCAATGCCGTGGCTGGCGAC    | 4043 |
| OY | 1289 | PheLeuIleValAspValSerLeuValSerLeuThrAlaAsnAlaLeuGIYTrpSerGIu  | 1308 |
| Dd | 4044 | TTCGCATCGTGTGATGTGCTCCTTGAGTTAGCTTAATGCAAATGGCTGGGCTAATCGGA   | 4103 |
| OY | 1309 | LeuGIyAlaAlIeLysSerLeuAtgThrLeuArgAlaLeuArgProLeuArgAlaLeuSer | 1328 |
| Dd | 4104 | CTTGCTGGCAACAAGTCCCTCCGACAGTTTAAGAGCTCTGACACTCTACGACCCTTAACC  | 4163 |
| OY | 1329 | ArgPheGIuLysMetArgValAlaValAsnAlaLeuLeuGIYAlaIleProSerIleMet  | 1348 |
| Dd | 4164 | CGATTTGAAGAATAAGAGGGTGTGTGTAAGCGCTCTTAAAGGGCCATCCCCTCCATAATG  | 4223 |
| OY | 1349 | AsnValLeuLeuValCysLeuAlIephTrpLeuIlePheSerIleMetGIYValAsnLeu  | 1368 |
| Dd | 4224 | AACGACTTCCTGGTCTGCGCATGACTTTTGCTAATATCAATACATATGAGGGGTAACTTC  | 4283 |
| OY | 1369 | PheAlaGIYLysPheTrpHisCysIleasnThrThrThGIYAspArgPheAspIleGIu   | 1388 |
| Dd | 4284 | TTTTGCTGGCAAGTCTACATGCATTCACATCACACACGGGGAAATGTTGATCTGTGAC    | 4343 |
| OY | 1389 | AspValIAsnAsnHISThrAspCysLeuLysLeuIleGIuArgAspGIuThraIaArgTrp | 1408 |
| Dd | 4344 | GTTGGTCAACAACATACAGATGATGCAAGCTCTCATTTGAAGCAATACAGACGCCAGGTGG | 4403 |
| OY | 1409 | LysAsnValIlysValAsnPheAspAsnValGIYPheGIYTrpLeuSerLeuLeuGIuVal | 1428 |
| Dd | 4404 | AAGAACGTGAAGGTCAACTTCGATTAACGTGGAGCTGGATACCTTCTCTGCTCCAAGTA   | 4463 |
| OY | 1429 | AlaThrPheLysGIYTrpMetAspIleMetTrpAlaAlaValAspSerArgAsnValGIu  | 1448 |
| Dd | 4464 | GCCACCTTTAAAGATGGATGGAATCATGATATGACAGCTGTGACACAGAATGTAAAG     | 4523 |
| OY | 1449 | LeuGIuNPolySTyrGIuLysSerLeuTrpMetTrpLeuTrpPheValIlePheIleIle  | 1468 |
| Dd | 4524 | CTGACGCCCAATACGAGACAACTCTACATGTACCTTACTTTGTCACTTTCATCATC      | 4583 |
| OY | 1469 | PheGIYSerPhePheThrLeuAsnLeuPheIleGIYValIleIleAspAsnPheAsnGIu  | 1488 |
| Dd | 4584 | TTCGGCTCATTTCTCACCCCTGAACCTGTCAATTGGTGTATCATTAACAACCTTCAACAG  | 4643 |
| OY | 1489 | GIuLysLysLysPheGIyGIyGIuAspIlePheMetThrGIuGIuLysLysTrpTrp     | 1508 |
| Dd | 4644 | CAGAAAGAAGATTGGAGGTCAAGACATCTTATATGACAGAAAGACAGAAAATACAC      | 4703 |
| OY | 1509 | AsnAlaMetLysLysLeuGIYSerLysLysProGIuLysProIleArgProGIuLysN    | 1528 |
| Dd | 4704 | AATGCAATGAAGAAGCTCGCTCCAAATAAACCGAGAAGGCCATTCCTCGGCTCGCAAC    | 4766 |
| OY | 1529 | LysPheGIuGIyMetValPheAspPheValThrArgGIuValPheAspIleSerIleMet  | 1548 |
| Dd | 4764 | AAATTTCAAGGAGATGCTTTGATTTTGTAACCAAAACAACTTTTACATCAGCATCATG    | 4822 |
| OY | 1549 | IleLeuAlIecysLeuAsnMetValThrMetMetValGIuThraspaspInsercIuyTr  | 1566 |
| Dd | 4824 | AATCCATCTGCTCCATCATGTGATCATGTATGATGTGAAGACGACAGCAGATCAGGAG    | 4883 |
| OY | 1569 | ValThrThrIleLeuSerArgIIeAsnLeuValPheIleValLeuPheThrGIyGIuLys  | 1588 |
| Dd | 4884 | ATGCAACCAATCTCTACTGATGAACCTGGTGTCTTGTCTGTTCACGGGCGAGTGT       | 4943 |
| OY | 1589 | ValIleuLysLeuIleSerLeuArgHISTyrTrpPheThrIleGIYTrpAsnIlePheAsp | 1608 |
| Dd | 4944 | GTTGCTGAAGCTCATCTCCCTCCGCATTAATATTTCACCATGGCTGGATATTTTGAT     | 5003 |
| OY | 1609 | PheValAlaValAlIeLeuSerIleValGIYMetPheLeuAlaLeuLeuIleGIuLysTrp | 1628 |
| Dd | 5004 | TTTTGGTGAATGATCATCTCTCCATTTGTAGGAATGTTTTCTCGCGAGCTGATAGGAAGAT | 5063 |
| OY | 1629 | PheValSerProThrLeuPheArgValAlIeArgLeuAlaArgIleGIYArgIleLeuArg | 1648 |

Db 5064 TTCGTCCTCCACCGCTGTCGAGTCATCGCCCTGGCCAGGATTTGGAGATTCCTACGC 5123  
QY 1649 LeuIleuysGlyAlaLysGlyIleArgThrLeuLeuPheAlaLeuMetSerLeuPro 1668  
Db 5124 CTGATCAAGAGGCGCAAGGAGTCCGCACTGCTCTTGTGATGATGTCCTCTCT 5183  
QY 1669 AlaLeuPheAlaLeuLeuLeuLeuPheLeuValMetPheIleTyrAlaIlePheGly 1688  
Db 5184 GCGCTGTCACATCGGCTCTGCTTTCCTGTCATGTCATCTACGCCATCTTGGG 5243  
QY 1689 MetSerAnPheAlaTyrValLysArgGluValGlyIleAspAspMetPheAnPheGlu 1708  
Db 5244 ATGTCCAACTTGGCTTACGTTAAGAGGAGTGGAAATGATGATGATGATGATGATG 5303  
QY 1709 ThrPheGlyAsnSerMetIleCysLeuPheGlnIleThrPheSerAlaGlyTyrPaspGly 1728  
Db 5304 ACTTTGGCAACAGCATGATGCTGCTGTCCTCAATCACCACCTGCGGCTGGGCGGA 5363  
QY 1729 LeuLeuAlaProIleLeuAnSerLysProProAspCysAspProAnLysValAnPro 1748  
Db 5364 CTGCTGGCCCTTATATCAATTAAGCGACCTCTGACTGTGACCTGAAATAAGATCACCT 5423  
QY 1749 GlySerSerValLysGlyAspCysGlyAsnProSerValGlyIlePhePhePheValSer 1768  
Db 5424 GGAAGCTCGGTGAAGGAGGAGTGGAGTGGAAATGATGATGATGATGATGATGATG 5483  
QY 1769 TyrIleIleIleSerPheLeuValValValAsnMetTyrIleAlaValIleLeuGlnAn 1788  
Db 5484 TACATCATCATATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5543  
QY 1789 PheSerValAlaThrGlnGlnSerAlaGluProLeuSerGluAspAspPheGluMetPhe 1808  
Db 5544 TTCAGCGTCGCGCAGGAAAGTGCAGAGCTCTGAGTGAAGAGACACTTGAAGATGTT 5603  
QY 1809 TyrGluValTyrPglLysPheAspProAspAlaThrGlnPheMetGluPheGluLysLeu 1828  
Db 5604 TACGAGCTCGGTGAAGGAGTGGAGTGGAAATGATGATGATGATGATGATGATG 5663  
QY 1829 SerGlnPheAlaAlaAlaLeuGlnProProLeuAnSerLysProGlnProAnLysLeuGln 1848  
Db 5664 TCTGACTTGGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5723  
QY 1849 LeuIleAlaMetAspLeuProMetValSerGlyAspArgIleHisCysLeuAnspIleLeu 1868  
Db 5724 CTGATTCGCAAGGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5783  
QY 1869 PheAlaPheThrLysArgValLeuGlnLysSerGlyLysMetAspAlaLeuArgIleGln 1888  
Db 5784 TTTGCTTTTACAAAGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5843  
QY 1889 MetGlnGluArgPheMetAlaSerAnProSerLysValSerTyrGlnProIleThrThr 1908  
Db 5844 ATGGAAGAAAGTTCATGCTTCCAAACCTCTCAAGGCTCTTATGAGCCATTTACACC 5903  
QY 1909 ThrLeuLysArgLysGlnGlnGlnValSerAlaValIleIleGlnArgAlaTyrArgArg 1928  
Db 5904 ACCCTGAACGGAACAAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5963  
QY 1929 HisLeuLeuLysArgThrValLysGlnAlaSerPheThrTyrAsnLysAsnLysIleLys 1948  
Db 5964 TATCTCCTGAAGCAAGATTAAAGAAATTTCTGCTATCTATATAAAAGACAAAGTAA 6023  
QY 1949 GlyGlyAlaAsnLeuLeuIleLysGlnLysPheMetIleIleAspArgIleAsnGlnAnSer 1968  
Db 6024 GAAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 6083  
QY 1969 IleThrGlnLysThrAspLeuThrMetSerThrAlaAlaCysProProSerTyrAspArg 1988  
Db 6084 ACTCCAGAGAGAGTGCATGCTTCCACACTTCT---CCACCTTCCACATGATG 6140  
QY 1989 ValThrLysProIleValGlnLysHisGlnGlnLysLysAspGluLysAlaLysGly 2008  
|||||

Db 6141 GTGACGAAGCGAG 6200  
QY 2009 Lys 2009  
Db 6201 AAA 6203

Search completed: April 23, 2003, 01:44:23  
Job time : 8079 secs

Query Match: 99.71% Indels: 1  
 DB: 22 Gaps: 0  
 US-09-930-871-12 (1-2009) x AAH55763 (1-8378)

QY 1 MetGIuGlnThrValLeuValProProGlyProAspSerPheAsnPhetHrArgGlu 20  
 DB 266 ATGGAGCAACAAGAGTGGTGTACACAGACCTGACAGCTCAACTCTTCACCAAGAA 325  
 QY 21 SerLeuAlaAlaIleGluArgArgIleAglGluGluLysAlaLysAnProLysProAsp 40  
 DB 326 TCTCTGGCGCTATTAAAGACCATTCGAGAAAGAAAGCAAGATCCCAACCAAGAC 385  
 QY 41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuAglLysAsn 60  
 DB 386 AAAAAAGATGACGACGAAATGCCCCAAAGCCAAATAGTACTGTGAGACTGGAAGAAC 445  
 QY 61 LeuProPheIleThrGlyLysPheProGluMetValSerGluProLeuGluAspLeu 80  
 DB 446 CTTCCTATTATTATGAGACATCTCTCCAGAGATGCTGACAGCCCTGAGAGACTG 505  
 QY 81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100  
 DB 506 GACCCCTACTATATCAATAAGAAACTTTATATGATATGATAAAGAGAGGCACTCTTC 565  
 QY 101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120  
 DB 566 CGGTCAGTGGCCACTCTGGCCCTGTACATTTTAACTCCCTTCAATCCTCTTACGAAATA 625  
 QY 121 AlaIleLysIleLeuValIleSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140  
 DB 626 GCTATTAAAGATTTGGTACATTCATTATTCAGCATCTAATTATGTGCACTATTGAC 685  
 QY 141 AsnCysValPheMetHrMetSerAsnProProAspTyrPheLysAnValGluTyrThr 160  
 DB 686 AACTGTGTATATGCAATGAGTAAACCTCTCGATTGGCAAGATGTAGATACACC 745  
 QY 161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgLysPheCysLeu 180  
 DB 746 TTCACAGGAATATATCTTTTGAATCACTATAAAATATTCAGAGGCACTCTGTGTA 805  
 QY 181 GluAspPheThrPheLeuArgAspProTyrPheAsnTyrLeuAspPheThrValIleThrPhe 200  
 DB 806 GAGAGATTTACTTCTCTCGGAGTCAATGAGACCTGCTCATTTCACTGCAATTAACATTT 865  
 QY 201 AlaTyrValThrGluPheValAspLeuGluAsnValSerAlaLeuArgTyrPheArgVal 220  
 DB 866 GCTACGCTACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTTGAGAACATTCAGAGTT 925  
 QY 221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240  
 DB 926 CTCGAGCAATGAAAGCAATTCAGTATCCAGGCTGAAACCAATGTGGAGAGCCGCTG 985  
 QY 241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260  
 DB 986 ATCCAACTCTGTGAAGAGCTCTCAGATGATATCATCTGCTGTCTGTCTGAGAGGTA 1045  
 QY 261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTyr 280  
 DB 1046 TTGTGCTATATGGCTGTGGAGCTGTTCATAGGGCACTGAGAAATAATATATACATGG 1105  
 QY 281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAnIleThrValAspTyr 300  
 DB 1106 CCTCCACCAATCTCTCTCTGGAGAAATAGATATAGAAATAATTAATCTGCAATTAAT 1165  
 QY 301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTyrLysSerTyrIleGlnAsp 320  
 DB 1166 AATGTACACTTATTAATGAAATGCTCTTGAATTTGACGAGAAATATATATTAATCAAGAT 1225  
 QY 321 SerArgTyrHisTyrPheLeuGluGluPheLeuAspAlaLeuLeuGlySerGlyAsnSer 340  
 DB 1226 TCAAGATATCATTAATTTCTGTGAGGGGTTTTTTTATGATGCACTACTATGTGAAATATGCTCT 1285

QY 341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360  
 DB 1286 GATGACAGGCCAAATGCTCAAGAGGATATATGTGTCAAAAGCTGTGTAATCCCAATTAAT 1345  
 QY 361 GlyTyrThrSerPheAspThrPheSerTyrPalaPheLeuSerLeuPheArgLeuMetThr 380  
 DB 1346 GGTCTACACAGCTTATATACCTTCATGAGTTGGCTTTTGTCTCTGTTTGCATTAATGACT 1405  
 QY 381 GlnAspPheThrPalaLeuAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400  
 DB 1406 CAGGACTCTGGGAAATATCTTATATCAATGACATTAACGTCTGCTGGAAATGTAACATG 1465  
 QY 401 IlePhePheValLeuValIlePheLeuGlySerPheTyrIleLeuIleAsnLeuIleAla 420  
 DB 1466 ATATTTTGTATTTGTGCTATTTCTTGGGCTCATTCCTACTAATTAATTTGATCCCTGGCT 1525  
 QY 421 ValValAlaMetValThrGluGluGluGluAsnGlnAlaThrLeuGluGluLysGluGln 440  
 DB 1526 GTGGTGGCCATGGCTTACAGACAGAACATTCAGGCCACTTGGAGAGACAGAACAGAA 1585  
 QY 441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysGlnGlnGluAlaGlnGln 460  
 DB 1586 GAGCGCGAATTTGACAGATGATTAACAGCTTAAAGCAACAGAGGCGAGCTGACGAC 1645  
 QY 461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480  
 DB 1646 GCAGCAACGGCACTCCCTCAGAACATTCACAGACCCCACTGACAGGACGAGCTCTCA 1705  
 QY 481 AspSerSerSerGluLysLeuSerLysSerSerLysSerAlaLysGluArgAsnArg 500  
 DB 1706 GACAGCTCATCTGAACCTCTTAAGTGTAGTCCAAAGAGTCTAAGAAAGAAATAATCCG 1765  
 QY 501 ArgLysLysArgLysGlnLysGlnSerGlyGlyGluLysAspGluAspGluPhe 520  
 DB 1766 AGGAGAAAGAAAGAAAGAAAGAGAGCTCTGGGGGAGAGAAAGATGAGATGCAATTC 1825  
 QY 521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGlyLys 540  
 DB 1826 CAAAAATCTGAATCTGAGGACAGCATCAGAGAGAAAGTTTGCCTTCTCAATGAAAGG 1885  
 QY 541 AsnArgLeuThrTyrGluArgTyrSerSerProHisGlnSerLeuSerIleArg 560  
 DB 1886 AACCGATGCAATATGAAAGAGAGTCTCTCCACACAGCTCTTGTGTGACATCTCGT 1945  
 QY 561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580  
 DB 1946 GGTCTCCTATTTTCCACCAAGGCAATATGAGAAACAAGCTTTTCACTTAAAGGGCGA 2005  
 QY 581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600  
 DB 2006 GCAAGAGATGCGATCTGAGACAGCACTTCGAGATGATGACACAGCACCTTTGAGAGAT 2065  
 QY 601 AsnGluSerArgArgAspSerLeuPheValProArgArgIleGlyGluArgAsnSer 620  
 DB 2066 AACGAGAGCCGTGAAGATTCCTGTGTGTGCCCCGAGACAGAGAGAGAACCCACAGC 2125  
 QY 621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValPheProAlaAsnGlyLys 640  
 DB 2126 AACCTGAGTACAGCACTAGTATCCCGGATCTGCGCACTGTTTCCAGCGAATGGGAG 2185  
 QY 641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyLysProSerValPro 660  
 DB 2186 ATGCACAGCACTGTGATTCATATGTTGTCTTCTGTGTGTGAGCACTTCAATGCTCT 2245  
 QY 661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680  
 DB 2246 ACATTCCTCTGTGTGAGAGCTTGTGCGAGAGTATATATATAGCCAGCTACTGTATGAC 2305  
 QY 681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerPheHisValSer 700  
 DB 2306 AATGGAACACCACTGAATGTAATGAGAAAGAGGTCAAGTTCTTTCACGTTTCC 2365  
 QY 701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720



|||||  
Db 2366 ATGGACTTCTGAGAGATCCCTCCCAAGCAACGAGCATATGATATAGCCAGCATCTCA 2425  
Oy 721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProCysTrpTyrLys 740  
Db 2426 ACAAAATACAGTGAAGAACTTGAAGATCCAGGCAAGAAATGCCCACTGTTGATATAA 2485  
Oy 741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760  
Db 2486 TTTCCCAACATATCTTAAATCTGGAGAGCTGTTCCATATGTTGTTAAAGTGAACATGTT 2545  
Oy 761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780  
Db 2546 GTCAACGCTGTTGATGAGCAACCATTTGTTGACCTGGCCATCACCATCTGTTTGTCTTA 2605  
Oy 781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800  
Db 2606 AATACCTCTTTCATGGCCATGAGGACATATCCATAGCAGCACCATTTTCAATATGTCCT 2665  
Oy 801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820  
Db 2666 ACAGTAGGAACCTGGTTTCACTGGAGCTTTACAGCAGAAATGTTCTGAAAAATATAT 2725  
Oy 821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTyrPasnIlePheAspGlyPheIleVal 840  
Db 2726 GCCATGAGATCCTTACTATTTATTTCCAAAGAGCTGGAATATCTTGACGGTTTATTTGTC 2785  
Oy 841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860  
Db 2786 ACGCTTAGCCTGGTAGAAGCTTGACCTCCCAATGAGAAAGATATATCTGTTCCGTTCA 2845  
Oy 861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880  
Db 2846 TTTGATATGCTGCGAGTTTCAAGTTGGAAAAATCTGGCAGACGTAAATATGCTAATA 2905  
Oy 881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900  
Db 2906 AAGATCATGCGCAATTCCTGGGGGCTCGGGAATTTAACCTCGTCTGGCCATCATC 2965  
Oy 901 ValPheIlePheAlaValAlaGlyMetGluLeuPheGlyLysSerTyrLysAspCysVal 920  
Db 2966 GTCCTCATTTTGGCGGTGGCGCATGAGCTCTTGGTAAAGCTACAAAGATTTGTCGC 3025  
Oy 921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPheHisSer 940  
Db 3026 TGCAGATGCGCAATGATGTCACCTCCACCTGGCACATGAATGACTCTTCCACATCC 3085  
Oy 941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960  
Db 3086 TTCCTGATTTGTTCCGGCTGCTGTGTGGGAGTGGATAGACCATGCGGACCTGTATG 3145  
Oy 961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980  
Db 3146 GAGGTGTGCTGCAAGCCATGTCCTTACTGCTCATGATGCTGATGGTGAATGGAAC 3205  
Oy 981 LeuValIleValLeuAsnLeuPheLeuAlaLeuLeu\*\*\*SerSerPheSerAlaAspAsnLeu 1000  
Db 3206 CTAGAGGTGCTGAATCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3265  
Oy 1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020  
Db 3266 GCAGCAGCATGATGATATGAATGAATATATCTCCAAATTCGCTGATAGATGACAC 3325  
Oy 1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040  
Db 3326 AAAGAGAGAGCTTATGTGTAAGAAAAATATATGATTTATTCACACATCTCCCTTCATAGG 3385  
Oy 1041 LysGlnLysIleLeuAspGlnIleLysProLeuAspAspLeuAsnLysLysAspSer 1060  
Db 3386 AAACAAAGATTTAGATGAATTAACACACTGATGATCTAAACACACAGAAACAGT 3445  
Oy 1061 CysMetSerAsnHisThr\*\*GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080  
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Db 3446 TGTATGTCATCATACAGCAGAAATTTGGAAAGATCTTGACTATCTTAAAGTGAAT 3505  
Oy 1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100  
Db 3506 GGAAGTACAGATGATAGAGACCTGACAGCAGTGTGAATAATATATATGATGAAGT 3565  
Oy 1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValIleThrValProIleAlaValGly 1120  
Db 3566 GATTACATGTCATTCATTAACAAACCCAGCTTACTGTCATGTCATGTCATGTCATGTCATG 3625  
Oy 1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerSerLeuGluGlu 1140  
Db 3626 GAATCTGACTTTGAAAATTTTAAACACGGAAGCTTTAGTAGTGAATCGATCTGGAGAA 3685  
Oy 1141 SerLysGluLysLeuAsnGluSerSerSerSerGluGlySerThrValAspIleGly 1160  
Db 3686 AGCAAGAGAACTCATATGAAGAGAGTACTCATGAGAGATAGACATCTGGACATCGGG 3745  
Oy 1161 AlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCys 1180  
Db 3746 GCACCTGTAGAAAGAACAGCCCTAGTGAACCTGAAGAACTTGAACAGAACGCTTGT 3805  
Oy 1181 PheThrGluGlyCysValGlnArgPheLysCysGlnIleAsnValGluGluGlyArg 1200  
Db 3806 TTCATGTAAGCTGTGTCACAAAGATTCAGTGTGTCAATATCAATGTGAAGAGAGCAGA 3865  
Oy 1201 GlyLysGlnTrpTrpAsnLeuArgArgTrpCysPheArgIleValGluHisAsnTrpPhe 1220  
Db 3866 GGAAGAAATAGTGTGACACTGAGAAAGAGAGCTGTTCCGAATGTTGAACATATAGTGT 3925  
Oy 1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240  
Db 3926 GAGACCTCATTTGTTTATGATGATTCCTTACTAGTGGTGGCG -GCATTTGAAGTATA 3984  
Oy 1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr 1260  
Db 3985 TATATGATCAGCGAAAGACGATTAAGACGATCTTGGAATATGCTGACAAAGTTTCACT 4044  
Oy 1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPhe 1280  
Db 4045 TACATTTTCATCTGGAAGTCTTCAAAATGGGGCATATAGGCTATCAAAACATATTTC 4104  
Oy 1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300  
Db 4105 ACCAATGCTGTGTGTGGCTGACCTTTAATGTTGAATGTTCAATGCTGATTAACA 4164  
Oy 1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320  
Db 4165 GCAAATGCTTGCTGATCTCAGAACTTGAAGCCATCAAAATCTCTCAGCACCTAAGAGCT 4224  
Oy 1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValAlaAsnAlaLeu 1340  
Db 4225 CTGAGACCTCTTAAGACCTTATCTGATTTGAAGGATGAGGTGGTGTGATGCCCT 4284  
Oy 1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheThrPheIle 1360  
Db 4285 TTAGAGCAATTCATCATCATGATGATGCTTGGTTTGTCTTATATCTGCGCTAAAT 4344  
Oy 1361 PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThr 1380  
Db 4345 TTCACATCATGAGGCTGAATTTTGTTCCTGCGCAAAATTCACACCTGTTTAACACACA 4404  
Oy 1381 ThrGlyAspArgPheAspIleGluLysValAsnAsnHisThrAspCysLeuLysLeuIle 1400  
Db 4405 ACTGCTGACAGGTTTGAATGAGAGAGCTGATATCATCATGATGCTGCTTAAACATAA 4464  
Oy 1401 GluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnAspAsnValGlyPhe 1420  
Db 4465 GAAGAAATAGAGACTGCTGAGTGAAGAAATGGAAGTAACTTGAATATGTAGGATTT 4524  
Oy 1421 GlyTyrLeuSerLeuGluGlnValAlaThrPheLysGlyTrpMetAspIleMetTyrAla 1440  
Db 4525 GGGTATCTCTCTTCTTCAAGTTGCCACATTCAAAGATGATGATATATGATGCA 4584

QY 1441 AlaValAspSerArgAsnValGluLeuGlnProLysTyrGluGlnSerLeuTyrMetTyr 1460  
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 Db 4585 GCAGTTGATTCAGAAATGAGAACTCCAGCTTAAGATGAAAGAACTGTGATCAT 4644  
 QY 1461 LeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIleGly 1480  
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 Db 4645 CTTTACTTGTGTATTTTTCATCATCTTTGGTCTCTTCACTGACCTGTAACCTGTTATTTGCT 4704  
 QY 1481 ValIleIleAspAsnPheAsnGlnGlnLeuLysTyrPheGlyGlyGlnAspIlePheMet 1500  
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 Db 4705 GTCAATCATATATATTTCAACACAGCAAGAAAGAGTTTGAGAGCTCAAGACATCTTATG 4764  
 QY 1501 ThrGluGlnGlnLysTyrTyrTyrAsnAlaMetLysLysLeuGlySerLysLysProGln 1520  
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 Db 4765 ACAGAGACAGAAAGAAATCTATATATGCAATGAAATAATAGATGAAATAACCCGAA 4824  
 QY 1521 LysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheValThrArg 1540  
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 Db 4825 AACCTATACCTCGACAGCAAGAAACAAATTCAGGAATGGCTTTGACTTCGTAAACAGA 4884  
 QY 1541 GluValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMetMetVal 1560  
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 Db 4885 CAAGTTTTCATATACATACATATGATTCATCTCTTACATGTCACATATATATGCTG 4944  
 QY 1561 GluThrAspAspGlnSerGluTyrValThrThrIleLeuSerArgIleAsnLeuValPhe 1580  
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 Db 4945 GAAACAGATGACAGATGAAATATGTCATACATTTTGGACAGCAATATCTGCTGTC 5004  
 QY 1581 IleValLeuPheThrGlyGlyCysValLeuLysLeuIleSerLeuArgHisTyrTyrPhe 1600  
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 Db 5005 ATTGTCTATTACTGAGAGGTGTACTAAACTCATCTCTACCCCATATATATTTT 5064  
 QY 1601 ThrIleGlyTrpAsnIlePheAspPheValValIleLeuSerIleValGlyMetPhe 1620  
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 Db 5065 AACATGAGATGAAATATTTTGTATTTGTGTGTCTATCTCTCATTTGATGATGATGTT 5124  
 QY 1621 LeuAlaGluLeuIleGlyLysTyrPheValSerProThrLeuPheAspValIleArgLeu 1640  
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 Db 5125 CTGGCGAGCTGATAGAAAGATTTTGTGTCCTCCCTACCCGTTCGAGATGATCGCTT 5184  
 QY 1641 AlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLeuLeu 1660  
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 Db 5185 GCTAGGATGCGCGAAATCTACGTCATCAAGAGCAAGGCGATCCGACCTGCTC 5244  
 QY 1661 PheAlaLeuMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuPheLeuVal 1680  
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 Db 5245 TTTCCTTGAATGATGCTCCCTCTGCGTGTGTTTACATCGGCTCTGCTCTTCTATGTC 5304  
 QY 1681 MetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgGluValGly 1700  
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 Db 5305 ATGTTCATCTACGCCATCTTTGGATGTCACAACTTTCCTATGTTAAGAGGAAGTTGGG 5364  
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 Db 5365 ATCGATACACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTCCATATTCCAATT 5424  
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 Db 5425 ACAACCTCTCTGCTGGAGTGTCTACACCCATCTCAACACAGTAAACCCAGCCAGC 5484  
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 Db 5545 GTTGGAATTTTCTTTTGTGACAGTACATCATATCTCTCCGTTGTGGTGAACATG 5604  
 QY 1781 TyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGlnSerAlaGluProLeu 1800  
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 Db 5605 TACATCGCGGTCTCTCGAGAACTTCAAGTGTCTACTGAAGAAAGTGCAGAGCCCTCTG 5664

QY 1801 SerGluAspAspPheGluMetPheTyrGluValIleProGlyLysPheAspProAspAlaThr 1820  
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 Db 5665 AGTGGAGTGTACTTGAATGATCTTCATGAGGTTTGGGAGATTTGATGATCCGATCACT 5724  
 QY 1821 GlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaIleGluGlnProLeuAsn 1840  
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 Db 5725 CAGTTCATGATTTGAAATAATTAATCTCAGTTTGAGCTGGCTGGAACCGCTCTCAT 5784  
 QY 1841 LeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSerGlyAsp 1860  
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 Db 5785 CTGCCACACCAACAACTCAGCTCATTCGATGATTTGCCATGCTAGTGTGCTAC 5844  
 QY 1861 ArgIleHisCysLysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGlnSerGly 1880  
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 Db 5845 CGGATCCACTGCTGATATATCTTATTTGCTTTACAAAGCGGTTCTAGAGAGAGTGA 5904  
 QY 1881 GluMetAspAlaLeuArgIleGluMetGlnGluArgPheMetAlaSerAspProSerLys 1900  
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 Db 5905 GAGATGAGTGTCTACGATACAGATGAGAGAGCAATTCATGCTTCAATCTTCCAAAG 5964  
 QY 1901 ValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGluValSerAlaVal 1920  
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 Db 5965 GTCTCTATCAGCCATACATCTCTTAAACGAAACAGAGAGATCTGCTGTC 6024  
 QY 1921 IleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGlnAlaSerPhe 1940  
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 Db 6025 ATTATTCAGCTGCTTACAGAGCCACTTTAAAGCAAGCTGTAACAAAGCTTCTT 6084  
 QY 1941 ThrTyrAsnLysAsnLysIleLysGlyLysAlaAsnLeuLeuIleLysGluAspMetIle 1960  
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 Db 6085 ACGTACAAATTAACAAATTAACAAATTAACAAATTAACAAATTAACAAATTAACAAATTA 6144  
 QY 1961 IleAspArgIleAsnGluAsnSerIleThrGluLysThrAspLeuThrMetSerThrAla 1980  
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 Db 6145 ATTGACAAATTAACAAATTAACAAATTAACAAATTAACAAATTAACAAATTAACAAATTA 6204  
 QY 1981 AlaCysProProSerTyrAspArgValThrLysProIleValGluLysHisGlnGlnGlu 2000  
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 Db 6205 GCTTCTCCACCTCTCTATGACCGGCTGACAAAGCAATTTGGAAACATGACGACAA 6264  
 QY 2001 GlyLysAspGluLysAlaLysGlyLys 2009  
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 Db 6265 GGCAGAGATGAAAAAGCCCAAGGAAA 6291  
 RESULT 4  
 AAH55764  
 ID AAH55764 standard; cDNA: 8378 BP.  
 AC AAH5764;  
 DT 04-SEP-2001 (first entry)  
 XX  
 DE Human neonatal form of SCN1A nucleotide sequence SEQ ID NO:2.  
 XX Human; epilepsy; chromosome 2; SCN1A; SCN2A; identification;  
 KW diagnosis; mutation; chromosome 2q23-q31; neurological disorder;  
 KW anticonvulsant; neuroprotective; ss.  
 OS Homo sapiens.  
 XX  
 PN MO200138564-A2.  
 XX  
 PD 31-MAY-2001.  
 XX  
 PF 24-NOV-2000; 2000WO-CA01404.  
 XX  
 PR 26-NOV-1999; 99US-0167623.  
 XX  
 PA (UWMC-) UNIV MCGILL.  
 XX  
 FI Rouleau GA, Lafreniere RG, Rochefort D, Cossette P, Ragsdale D;  
 XX MPI; 2001-355945/37.

DR P-PSDB: AAB99675.

XX Determining a predisposition to epilepsy and/or development of epilepsy  
 PT comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a  
 PT DNA variant, equivalent, or mutation which shows a linkage  
 PT disequilibrium

PS Disclosure: Page 93-96; 268bp; English.

XX The present invention describes a method (M1) of determining an  
 CC individual's predisposition to epilepsy and/or development of epilepsy,  
 CC as well as predicting the individual's response to medication. The  
 CC method comprises determining the genotype of at least one gene selected  
 CC from SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation  
 CC which shows a linkage disequilibrium. SCN1A, SCN2A and SCN3A are all  
 CC sodium channel genes located on chromosome 2. The idiopathic generalised  
 CC epilepsy (IGE) gene is more specifically localised on chromosome  
 CC 2q23-q31. Compounds identified as modulators of the biological activity  
 CC of SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating  
 CC epilepsy or other neurological disorders. They have anticonvulsant and  
 CC neuroprotective activities. AAB55763 to AAB56164 and AAB99674 to  
 CC AAB99679 represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR  
 CC primers, oligonucleotides and proteins given in the exemplification of  
 CC the present invention.

SO Sequence 8378 BP; 2498 A; 1571 C; 1775 G; 2534 T; 0 other;

Alignment Scores:

Pred. No.: 0 Length: 8378  
 Score: 10321.00 Matches: 2002  
 Percent Similarity: 99.75% Conservative: 2  
 Best Local Similarity: 99.65% Mismatches: 5  
 Query Match: 99.27% Indels: 2  
 Gaps: 0

US-09-930-871-12 (1-2009) x AAB55764 (1-8378)

QY 1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhenThrArgGlu 20  
 Db ATGGAGCAACAGCTCTGTACACAGAGACCTGACAGCTTCAACTCTTCCACAGAGAA 325  
 QY 21 SerLeuAlaIleAlaGluArgGluIleAlaGluIleAlaGluIleAlaGluIleAlaGlu 40  
 Db TCTCTGGGGCTATGAAAGACGCAATGCGAAGAAAGCAAGATCCCAACCAAGAC 385  
 QY 41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluIleAlaGlyLysAsn 60  
 Db AAAAAAGATGACGACGAAATGCGCCCAAGCAATAGTACTGGAAGCTGGAAAGAAC 445  
 QY 61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80  
 Db CTTCAATTATTATTAGGACATTCCTCCAGAGATGCTGACAGCCCTCGAGGACCTG 505  
 QY 81 AspProTyrTyrIleAsnLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100  
 Db GACCCCTCATATCAATCAAGAACTTTATAGATTGAATTAAGGAGGACCATCTTC 565  
 QY 101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120  
 Db CGGTCACTGCACCTGCGCCCTGACATTTAATCCCTTCAATCCCTTGAAGAAATA 625  
 QY 121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140  
 Db GCTATTAGATTGGTGGTACATTATTCACAGCTAATATATGACACTATTTTGACA 685  
 QY 141 AsnCysValPheMetThrMetSerAsnProProAspTyrThrLysAsnValGluTyrThr 160  
 Db AACTGTGTTTATGACATGATGATACCTCTGATGGACAAAGATGTAAATACAC 745  
 QY 161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180  
 Db TTCACAGGAATATATACCTTTTGAATCATTATATAAAATTAATTGCAAGGGAATTCGTTTA 805

QY 181 GluAspPheThrPheLeuArgAspProTyrAsnThrLeuAsnPhenThrValIleThrPhe 200  
 Db GAGGATTTACTCTTCCCTGGAGATCATGAACTGCTGATTTCACTGCAATACATT 865  
 QY 201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220  
 Db GCGTTTGTAAACAAATTTTAAACCTAGGCAATTTTCAGCTCTTGCACCTTCAAGATC 925  
 QY 221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240  
 Db TTGAGAGCTTTGAAACATTTTCGTAATTCAGGCTGAAACCATTTGGAGGCCCTG 985  
 QY 241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260  
 Db ATCCATCTGTGAAAGAGCTTCAGATGATATCATCTGCTGCTGTGACCGTA 1045  
 QY 261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnThr 280  
 Db TTTGCTTATTTGGCTGCACTGTTTCATGCGCACTGAGCAATGATTAATACATG 1105  
 QY 281 ProProThrAsnAlaSerLeuGluGluIleSerIleGluLysAsnIleThrValAsnTyr 300  
 Db CTTCCCAACCAATGCTCTTGGAGAAATATGATGAAAGATTAATCTGATTTAT 1165  
 QY 301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTyrLysSerTyrIleGlnAsp 320  
 Db AATGGTACACTTATTAATTAATCACTGCTTGTGATTTGACTGGAATCATATATTCAGAT 1225  
 QY 321 SerArgTyrHisTyrPheLeuGluGluIlePheLeuAspAlaLeuLysGlyAsnSerSer 340  
 Db TCAAGATATCATATTTATCTGAGGGCTTTTATGATGCACTACTATGTAATACCTCT 1285  
 QY 341 AspAlaGlyGlnCysProGluGluIleTyrMetCysValIleAlaGlyArgAsnProAsnTyr 360  
 Db GATGACAGGCCAATGTCACAGAGGATATGTGTGTGAAGGCTGTGAATCCATTTAT 1345  
 QY 361 GlyTyrThrSerPheAspThrPheSerTyrPheLeuSerLeuPheArgLeuMetThr 380  
 Db GGTACACAAAGCTTTATACCTTCACTGAGCTTTTCTCTTCTGTTGCACTAAATGACT 1405  
 QY 381 GluAspPheThrGluAsnLeuTyrGluIleThrLeuArgAlaIleAlaGlyLysThrTyrMet 400  
 Db GAGGACTTTGGGAAATTTTATATCACTGACATTAACGCTGCTGGAAGCAATGACATG 1465  
 QY 401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleAla 420  
 Db ATATTTTGTATTTGTGCTATTTTCTGGGCTCATTTCTACTAATTAATTTGATCCGCT 1525  
 QY 421 ValValAlaMetAlaTyrGluGluIleAsnGlnAlaThrLeuGluIleAlaGluIleLys 440  
 Db GTGTGTGGCCATGGCTACAGAGACAGATCAAGGCCACTTGGAAAGCAAGACAGAA 1585  
 QY 441 GluAlaGluPheGluGlnMetIleGluGluIleLysGlyGlnGluIleAlaGlnGlu 460  
 Db GAGGCCGAATTTTCAGAGATGATGACAGCTTAATAAACCAACAGGAGCAGCTGACAG 1645  
 QY 461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaIleAlaGlyArgLeuSer 480  
 Db GCAGCAGAGGCACTGCTCCAGAACATTTCCAGAGACCAGAGGCAAGCAGGCTCTCA 1705  
 QY 481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500  
 Db GACAGTCAATCTGAAGCCCTCAAGTTGAATTCACAGAGCTCAAGAGAAAGAAATCGG 1765  
 QY 501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlnGluIleLysAspLysGluPhe 520  
 Db AGGAAAGAAAGAAAGAAAGAGAGAGCTGTGGGGGAGAGAGAAATGAGATGATGATTC 1825  
 QY 521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540  
 Db CAATAATCTGAATCTGAGAGACATCAAGAGGAAAGGTTTCCGCTTCCATTTGAAGG 1885  
 QY 541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560

1886 AACCGATTACATATGAAAAAGAGTACTCCCTCCCAACACAGTCTTTGTTGACATCCGT 1945  
 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580  
 1946 GGGTCCCTATTTTCCACAGGCGAAATAGAGAACAAAGCTTTTCAAGCTTTACAGGGCGA 2005  
 AlaLysAspValIglySerGluAsnAspPheAlaAspSpGluHisSerThrPheGluAsp 600  
 2006 GCAAAGATGTGGATCTGTGAAGAGACTTCGCAGATGATAGGCC -AGCACTTTGAGAT 2064  
 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgAsnSer 620  
 2065 AACGAGAGCGGTAGAGATCTCTGTTGTCGCCGAGACGACGAGAGAGACCAACAGC 2124  
 AsnLeuSerGluThrSerArgSerArgMetLeuAlaValPheProAlaAsnGlyLys 640  
 2125 AACCTAGTCAGACCGAGTAGAGTCCCGATCCGAGTCTGGCACTTTTCCAGCGAATGGGAG 2184  
 MetHisSerThrValAspCysAsnGlyValValSerLeuValIglyLysProSerValPro 660  
 2185 ATGCACAGACACTGTGATGTCATGTTGTTCTTGGTTGGTGGACCTTCAGTCTCT 2244  
 ThrSerProValIglyLysLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680  
 2245 ACATCCCTGTGGACAGCTTGTCCAGAGGTATATATAGATTAAGCCAGCTACTGAGAAC 2304  
 AsnGlyThrThrThrcGluThrGluMetArgLysArgArgSerSerPheHisValSer 700  
 2305 AATGGAACACCACTGAACCTGAATGAGAAAGAAAGGTCACAGTCTTTCCAGCTTCC 2364  
 MetAspPheLeuGluAspProSerGluArgGluArgAlaMetSerIleAlaSerIleLeu 720  
 2365 ATGAGATTCTTAAGATATCTTCCCAAGGCAACGACATGATAGTATAGCCAGCATCTTA 2424  
 ThrAsnThrValIgluLysGluGluGluSerArgGluLysCysProProCysTTPtyLys 740  
 2425 ACAAAATACAGTAGAAGAACTGTAAGAAATCCAGGACAGAAAGCCCACTTGTGTATAAA 2484  
 PheSerAsnIlePheLeuIleThrPAspCysSerProTyrTrpLeuLysValHisVal 760  
 2485 TTTTCCACATATTTCTTAATCTGGACTGTTCCCATATTTGTTAAAGAAAGCAATGTT 2544  
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 2545 GTCACCTGGTGTGATGAGCCCATTTGTTGACCTGGCCATCAACATCTGATGTCTTA 2604  
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 2605 AATACCTCTTTCATGGCCATGAGCACTATCCAAATGACGACCAATTAATAGTCTCT 2664  
 ThrValIgluAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuValIle 820  
 2665 ACAGTAGAAGAACTGTGTTTCACTGGCATCTTTACAGCAAAATGTTTCTGAAAATATTT 2724  
 AlaMetAspProTyrTyrTyrPheGluGluGlyTyrPAsnIlePheAspGlyPheIleVal 840  
 2725 GCCATGGATCTTACTATATTTTCCAAAGAGCGTGAATATCTTTGACGGTTTATGTGT 2784  
 ThrLeuSerLeuValIgluLeuGlyLeuAlaAsnValIgluLysLeuSerValLeuArgSer 860  
 2785 ACCCTTAGCTGTAGAACTGAGACTGCGCAATGTGAGAGATTAATGTGTTCCGTTCA 2844  
 PheArgLeuLeuArgValPheLysIleuAlaLysSerTrpProThrLeuAsnMetLeuIle 880  
 2845 TTTTCGATGCTGTGAGTTTCAAGTTGCGAAATCTTGGCCACGTTAAATATCTTATA 2904  
 LysIleIleGlyAsnSerValIgluAlaLeuGlyAsnLeuThrLeuValIleuAlaIleIle 900  
 2905 AAGATCATCGCAATTCGCGGGGCTCTGGAAATTAACCCCTGCTGGCCATCATC 2964  
 ValPheIlePheAlaValIgluMetGluLeuPheGlyLysSerTyrLysAspCysVal 920

2965 GTCTCATTTTGGCCGTGGCATGCACCTCTTTGTAAAGCTACAAAGATGTGTTC 3024  
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 GluValAlaGlyGluAlaMetCysLeuThrValPheMetIleValIleGlyAsn 980  
 3145 GAGCTTCTGTGTAAGCCATGCTTACTCTTCTTCAATGATGATGATGATGGAAC 3204  
 LeuValAlaLeuAsnLeuPheLeuAlaLeuLeu\*\*\*SerSerPheSerAlaAspAsnLeu 1000  
 3205 CTACTGTCTGTAATCTTCTTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 3264  
 AlaAlaThrAspAspAspAsnGluMetAsnLeuGluIleAlaValAspArgMetHis 1020  
 3265 GCACCCACTGATGATGATTAATGAAATGAAATCTCCAAATCTGTGTGATGATGATGAT 3324  
 LysGlyValAlaThrValLysArgLysIleTyrGluPheIleGluGlnSerPheIleArg 1040  
 3325 AAGGAGTAGCTTATGTAAGAAAGAAATATATGAAATTAATCAACAGTCTTCAATAGG 3384  
 LysGluLysIleLeuAspGluIleLysProLeuAspAspLeuAsnLysLysAspSer 1060  
 3385 AAGCAAAAGATTTAGATGAAATTAACCACTGATGATGATTAACCAAGAAAGACAGT 3444  
 CysMetSerAsnHisThr\*\*\*GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080  
 3445 TGTATGTCATATCATACAGCAAGAAATGGGAATCTTACATCTTAAGATGATTAAT 3504  
 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100  
 3505 GGAACCTACAGGTATAGGACTGGCAGAGTGTTAATAAATATATATGATGATGAT 3564  
 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValIglu 1120  
 3565 GATTACATGTCATTAACCAACCCAGCTTCTGATGATGATGATGATGATGATGATGAT 3624  
 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140  
 3625 GAATCTGACTTTGAAATTAACCAAGCAAGTATGATGATGATGATGATGATGATGAT 3684  
 SerLysGluLysLeuAsnGluSerSerSerSerSerGlySerThrValAspIleGly 1160  
 3685 AGCAAGAGAACTGAATGAAAGCAAGTACATCAAGAGATGACACTGTGACATGAGC 3744  
 AlaProValIgluGluGluProValIgluProGluLysLeuGluLysLeuGluLys 1180  
 3745 GCACCTGTAGAAAGAAAGCCGCTGTGAACTGTAAGAACTGTGAAAGCAAGCTGT 3804  
 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValIgluGlyArg 1200  
 3805 TTCACTGAGGCTGTGTACAAAGATTAAGATGATGATGATGATGATGATGATGATGAT 3864  
 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValIgluHisAsnTrpPhe 1220  
 3865 GGAAGAACATGTGAAAGCTGAGAGAGACGTTTCCGAATGATGATGATGATGATGATGAT 3924  
 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240  
 3925 GAGACCTCATGTTTTCATGATCTCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3984  
 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluLysValAspLysValPheThr 1260  
 3985 TATATGATGATGCAAGAAAGCAATTAAGATGATGATGATGATGATGATGATGATGAT 4044  
 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPhe 1280  
 4045 TACATTTTCATTTGAAATGCTTCTTAAGATGATGATGATGATGATGATGATGATGAT 4103



DB 6264 GGCAGAGATGAAAAAGCCAAAGGAAA 6290

|||||

RESULT 5  
AAD32839  
ID AAD32839 standard; cDNA: 5997 BP.  
XX AAD32839;  
AC AAD32839;  
XX 01-JUL-2002 (first entry)  
DE Human ion channel cDNA #1.  
XX  
XX Human; novel human protein; NHP; voltage-gated sodium channel;  
KW gene therapy; bioreactor; mental disorder; biological disorder;  
RV gene; medical disorder; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX Key Location/Qualifiers  
FT CDS 1..5997  
FT /tag- a  
FT /product= "Human ion channel protein #1"  
FT /transl\_except= (pos:2941..2943, aa:Xaa)  
FT /transl\_except= (pos:3166..3168, aa:Xaa)  
FT /note= "Xaa = any amino acid"  
XX  
XX MO200214498-A2.  
XX  
XX 21-FEB-2002.  
XX  
XX 15-AUG-2001; 2001WO-US25650.  
XX  
XX 16-AUG-2000; 2000US-225989P.  
XX  
XX (LEXI-) LEXICON GENETICS INC.  
XX  
XX Turner CA, Mathur B, Mathur D;  
XX  
XX WPI; 2002-280757/32.  
XX  
XX P-PSDB; AAE20510.  
XX  
XX Novel polynucleotides encoding human sodium channel proteins,  
XX particularly voltage-gated sodium channel proteins useful for drug  
XX screening, diagnosis and in gene therapy of biological disorders  
XX  
XX Claim 1; Page 28-30; 83pp; English.  
XX  
XX The present sequence is a cDNA encoding novel human protein (NHP), ion  
XX channel protein. NHP share structural similarity with mammalian sodium  
XX channel proteins particularly voltage-gated sodium channel proteins.  
XX NHP oligonucleotides are useful as hybridisation probes for screening  
XX libraries and assessing gene expression patterns. Sequences derived  
XX from regions adjacent to the intron/exon boundaries of NHP gene can be  
XX used to design primers for use in amplification assays to detect  
XX mutations within the exons, splice sites, introns that can be used in  
XX diagnostics and pharmacogenomics. NHP nucleotide sequences are useful  
XX for drug screening effective in the treatment of symptomatic or  
XX phenotypic manifestations of perturbing the normal function of NHP in  
XX the body, and nucleotide constructs encoding NHP products are useful to  
XX genetically engineer host cells to express NHP products in vivo. These  
XX genetically engineered cells function as bioreactors in the body  
XX delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion  
XX protein to the body. Nucleotide construct encoding NHP products are  
XX also useful in gene therapy for modulating NHP expression and to  
XX produce genetically engineered host cells to express NHP products in  
XX vivo. NHP nucleotide sequences may also be used as part of ribozyme  
XX and/or triple helix sequences that are useful for NHP gene regulation.  
XX The NHP polypeptides are useful for generating antibodies, as  
XX reagents in diagnostic assays, for identifying other cellular gene  
XX products related to NHP and as reagents in assays for screening for  
XX compounds that are useful in the treatment of mental, biological or  
XX medical disorders and diseases.

XX  
SQ Sequence 5997 BP; 1773 A; 1185 C; 1338 G; 1698 T; 3 other;

Alignment Scores:

| Pred. No.:             | Score:   | Length: | Matches: | Conservative: | Mismatches: | Indels: | Gaps: |
|------------------------|----------|---------|----------|---------------|-------------|---------|-------|
| 0                      | 10320.50 | 5997    | 1398     | 0             | 0           | 11      | 1     |
| Percent Similarity:    | 99.458   |         |          |               |             |         |       |
| Best Local Similarity: | 99.458   |         |          |               |             |         |       |
| Query Match:           | 99.268   |         |          |               |             |         |       |
| DB:                    | 24       |         |          |               |             |         |       |

US-09-930-871-12 (1-2009) x AAD32839 (1-5997)

QY 1 MetcGlInThrValLeuValProProGlyProAspSerPheAsnPhetherArgGlu 20  
|||||  
DB 1 ATGACCAAAAGAGTGGCTTGACACAGACGCGACAGCTTCAACTCTTCACACAGAA 60  
QY 21 SerLeuAlaAlaIleGluArgGllleAlaGluLysAlaLysAsnProLysProAsp 40  
|||||  
DB 61 TCTCTGGCGGCTATTGAAAGACGCAATTCAGAAAGAAAGCAAGATCCCAACAGAC 120  
QY 41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60  
|||||  
DB 121 AAAAAAGATGACGACCAAAATGGCCCAAGCCAAATATGATGCTTGAAGCTGGAAGAAC 180  
QY 61 LeuProPheIleTyrgLysPileProProGluMetValSerGluProLeuGluAspLeu 80  
|||||  
DB 181 CTTCATTTATTATGAGACATTCCTCCAGAGATGGTGACAGCCCGCGAGACCTG 240  
QY 81 AspProTyrrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100  
|||||  
DB 241 GACCCCTACTATATCAATAGAAACTTTATGATGATGATGATGATGATGATGATGATG 300  
QY 101 ArgPheSerAlaThrSerAlaLeuTyrrIleLeuThrProPheAsnProLeuArgLysIle 120  
|||||  
DB 301 CGGTTAGTGCCACCTGCGCTGATCATTTTAACTCCCTCAATCTCTTAGAANAATA 360  
QY 121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140  
|||||  
DB 361 GGTATTAAGATTTTGGTACATTCATTATTCAGCATGCTATATGTCACACTATTTGACA 420  
QY 141 AsnGlyValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrrThr 160  
|||||  
DB 421 AACTGTGTGTTTATGCAATGAGTAACTCCCTGATTTGGCAAAAGATGTAGATATACCC 480  
QY 161 PheThrGlyIleTyrrThrPheGluSerIleLysIleIleLeuAlaArgGlyPheCysLeu 180  
|||||  
DB 481 TTCACAGATATATATCTTTGAACTATTAATAATTAATGCAAGGAGATCTGTTTA 540  
QY 181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200  
|||||  
DB 541 GAAGATTTTACTTCTCTGGGATTCAGTACGACGCGCATTTCACTGATTCATTAATTT 600  
QY 201 AlaTyrrValIleThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220  
|||||  
DB 601 GGTAGTGTACAGAGTTTGGACCTGGGCAAGTCTCGGCATTCAGAACATTCAGAGTT 660  
QY 221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValAlaLeu 240  
|||||  
DB 661 CTCGAGCATTTGAAAGCATTTTCAGTCATTCAGGCGCTGAAACCATTTGGGGGCGCTG 720  
QY 241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260  
|||||  
DB 721 ATCCAGCTGTGGAAGAGCTCTCAGATGTATGATCTGCTGCTGCTGAGGCTG 780  
QY 261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280  
|||||  
DB 781 TTTGCTCTATTGGCTGACGCTTCATGCGGCAACCTGAGGATTAATATATACATG 840  
QY 281 ProProThrAsnAlaSerLeuGluGluIleSerIleGluLysAsnIleThrValAsnTyrr 300  
|||||  
DB 841 CTTCCCAACCAATGCTCTTGGAGGACATGATGATGAAAGATTAATTAATGATTAAT 900



|    |      |   |      |
|----|------|---|------|
| QY | 301  | ASnGlyThrIleuIleasnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp     | 320  |
| Db | 901  | AAATGGACACTTAATAATGAAGAACTGCTTGGAGTTGACTGGAAAGCAATATTTAAAT        | 960  |
| QY | 321  | SeArGrGlyHisTyrPheLeuGlnGluGlyPheLeuAspAlaGluLeuCysGlyAsnSerSer   | 340  |
| Db | 961  | TCAAGATATATCATTTATTTCCCGAGAGGGTTTTTATGATGACACTACTATGTGGAAATAGCTCT | 1020 |
| QY | 341  | AspAlaGlyLeuCysProGlnGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr      | 360  |
| Db | 1021 | GATCGACAGCCAAATGTCAGAGAGGATATATGTGTGTAAGAAAGCTGTATGAATATCCCAATAT  | 1080 |
| QY | 361  | GlyTyrThrSerPheAspTrpPheSerTrpAlaPheLeuSerLeuPheArgIleuMetThr     | 380  |
| Db | 1081 | GGCTACCAACAAGCTTTGATACCTTCCTGACTGGCTTTTTCCTGTTCCTGACTAATTAAGCT    | 1140 |
| QY | 381  | GlnAspPheTrpGlnAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlySerThrTyrMet      | 400  |
| Db | 1141 | CAGACCTTCGGGAAATCTTTTCAACATTCACATTCACGTCTGCGGGAAAAAGCTACATG       | 1200 |
| QY | 401  | IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleAla         | 420  |
| Db | 1201 | ATATTTTGTGGTGGTCATTTTCTGGGGCTATCTTACCTTAATAATTGATCCTGGCT          | 1260 |
| QY | 421  | ValValAlaMetAlaTyrGlnGluGlnGlnAsnGlnAlaThrLeuGlnGluAlaGluLys      | 440  |
| Db | 1261 | GTGTGTGGCACTGGCTTACGAGGAACGAATACAGGCCACTTGGAAAGACAGAACAGAA        | 1320 |
| QY | 441  | GlnAlaGluPheGlnGlnMetIleGlnGlnLeuLysLysGlnGlnAlaGlnGln            | 460  |
| Db | 1321 | GAGGCCAAATTCACGAGATGATTGAACGCTTAATAAACCAACAGAGAGCACTACAG          | 1380 |
| QY | 461  | AlaAlaThrAlaThrAlaSerGlnHisSerArgGluProSerAlaAlaGlyArgLeuSer      | 480  |
| Db | 1381 | GCACAGACGGCACTGCTCAGAAACATTCACAGAGACCCAGTGCAGAGCGAGCTCTCA         | 1440 |
| QY | 481  | AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg      | 500  |
| Db | 1441 | GACAGCTCACTGMAAGGCTCTAAGTTGAGTTCACAAAGTGTCAAGAAAGAAATACGG         | 1500 |
| QY | 501  | ArgLysLysArgLysGlnLysGlnGlnGlnGlnGlnGlnGlnLysAspGluAspGluPhe      | 520  |
| Db | 1501 | AGGTAAGAAAGAAACAGAAAGACAGCTCGGTGGGGAAAGAAAGATAGAGATTAATTC         | 1560 |
| QY | 521  | GlnLysSerGlnSerGlnAspSerIleArgArgLysGlyPheArgPheSerIleGluLys      | 540  |
| Db | 1561 | CAAAATCTGAACTGAGACACACATCAGAGAGAAAGCTTTCGCTCTCCATTAAGAG           | 1620 |
| QY | 541  | AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg      | 560  |
| Db | 1621 | AACCGATTGACATTTGMAAAGAGTACTCTCCCAACACAACTCTTTGTTGAGCACTCCGT       | 1680 |
| QY | 561  | GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg      | 580  |
| Db | 1681 | GGCTCCCTATTTTCCACCAAGGCCAAATACGACAGACAGGCTTTGACCTTTAGAGGGGGA      | 1740 |
| QY | 581  | AlaLysAspValGlySerGlnAsnAspPheAlaAspAspGlnHisSerThrPheGluAsp      | 600  |
| Db | 1741 | GCAAGAGATGGGATCTGAGAAACGACTTCGCGAGATGAGACACACGACCTTTAGAGAT        | 1800 |
| QY | 601  | AsnGlnSerArgArgAspSerLeuPheValProArgArgHisGlyLysArgArgAsnSer      | 620  |
| Db | 1801 | AACGAGAGCCGTAGAGATTCCTGTTGTTGTGCCCGACAGACAGAGAGAGAGCAACAGC        | 1860 |
| QY | 621  | AsnLeuSerGlnTrpSerArgSerSerArgMetLeuAlaValPheProAlaAsnGlyLys      | 640  |
| Db | 1861 | AACCTGATGACACCACTAGCTATCCCGGATGCTGGCAGTCTTTCCAGCGAATGGGAAG        | 1920 |
| QY | 641  | MetHisSerTrpValAspCysAsnGlyValValSerLeuValGlyProSerValPro         | 660  |
| Db | 1921 | ATGCACAGCACTGTGAGATTGCATATGGGTGTGTTCTCTTGTTGGTGGACCTTCAGTTCTCT    | 1980 |
| QY | 661  | ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp      | 680  |

|    |      |  |      |
|----|------|--|------|
| Db | 3028 | AAAGAGTAGACCTTATGTGTAAGAAAGAAATATATGTAATTATTATTCACAGTCCTTCATTAGC | 3087 |
| Qy | 1041 | LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnLysLysAspSer        | 1060 |
| Db | 3088 | AAACAAAGATTTTATGATGAATTTAAACACATTGATGATCTTAACACAAAGAAAGACAGT     | 3147 |
| Qy | 1061 | CysMetSerAsnHisThr**GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn      | 1080 |
| Db | 3148 | TGTATGTCCAAATCAACACACAAAGAAATTTGGAAAGATCTTGACATCTTAAAGATGTAAAT   | 3207 |
| Qy | 1081 | GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer     | 1100 |
| Db | 3208 | GGAATCTACAGGGTATAGAACTGCACAGCTGTGTAAGAAATATATGATGTAAGT           | 3267 |
| Qy | 1101 | AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly     | 1120 |
| Db | 3268 | GATTACATGTATCTATTAACAAACCCACCTTACTGTACGTACGTACCAATTCGTGTAGGA     | 3327 |
| Qy | 1121 | GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGlu        | 1140 |
| Db | 3328 | GAATCTGACTTTGAAATTTAAACAGGAAGACTTTAGTAGTAAGTAATCGGATCTGGAAGA     | 3387 |
| Qy | 1141 | SerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGly     | 1160 |
| Db | 3388 | AGCAAAAGAACTAAATGAATGAAGAGTACTCATCAGAAAGTAGACCTGTGGACATCGGC      | 3447 |
| Qy | 1161 | AlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCys     | 1180 |
| Db | 3448 | GCACCTGTAGAAAGAACGCCCTAGTGGACCTGAAAGAACTTTCACACAGAGCTTGT         | 3507 |
| Qy | 1181 | PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg     | 1200 |
| Db | 3508 | TTCACTGGAAGCTGTGTACAAAGATTCAGAGTGTGTCAATCATCATGTGGAAGAGCAGA      | 3567 |
| Qy | 1201 | GlyLysGlnIleTyrPheAsnLeuArgArgThrCysPheArgIleValGluHisAsnTyrPhe  | 1220 |
| Db | 3568 | GGAAAAACAATGTGTGAACCTGGAAGAGAGCTGTTCGGAATAGTTGAACATAACTGTTT      | 3627 |
| Qy | 1221 | GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle     | 1240 |
| Db | 3628 | GAGACCTTCATTTGTTTCTATGATTTCTCTTACTAGTGGTGGCTGTGGCATTTGAAGATTA    | 3687 |
| Qy | 1241 | TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr     | 1260 |
| Db | 3688 | TATATTGATCAACGAAGACGATTAAGACGATTTGGAATATGCTACAAAGTTTTCACG        | 3747 |
| Qy | 1261 | TyrIlePheIleLeuGluMetLeuLeuLysTyrValAlaTyrGlyTyrGlnThrTyrPhe     | 1280 |
| Db | 3748 | TACATTTTCATTTCTGGAATGCTTCGTAATGAGGTGGCATATGCTATCAACATATATTC      | 3807 |
| Qy | 1281 | ThrAsnAlaTyrCysTyrPheAsnPheLeuIleValAspValSerLeuValSerLeuThr     | 1300 |
| Db | 3808 | ACCAATGCTGGTGTGGTGGTGAACCTTTAAATGTTGATGTTTCATTTGGTCAGTTTAAAC     | 3867 |
| Qy | 1301 | AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla     | 1320 |
| Db | 3868 | GCAATGCTGTGGTGTACTCAGAACTGGAGCCATCAATCTCTCGACGACACGTAAAGCT       | 3927 |
| Qy | 1321 | LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValAlaAsnAlaLeu     | 1340 |
| Db | 3928 | CTGACACCTCTTAAGACCTTATCTGATTTGAAGGATGAGGTGGTGTGTAATGCCCTT        | 3987 |
| Qy | 1341 | LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheThrPheIle     | 1360 |
| Db | 3988 | TTAGAGACCAATCCACATCAATGAATGGCTTCGGTTTGTCTTATATTCGGCTAAAT         | 4047 |
| Qy | 1361 | PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThr     | 1380 |
| Db | 4048 | TTACACATCATGGGGCTAAATTTGTTTGGTGGCAATTTCTACACACGTATTAACACACACA    | 4107 |
| Qy | 1381 | ThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIle     | 1400 |
| Db | 4108 | ACTGTGTACAGTTTGTACACTGCAGACAGCTGAATATCATACATGATGATGCTTAAACCTAATA | 4167 |

QY 1761 ValGlyIlePhePheValSerTyrIleIleIleSerPheLeuValValAlaMet 1780  
 DB 5248 GTTGAATTTCTTTTGTGAGTTATCATCATTCCTTCTGTTGGTGAACATG 5307  
 QY 1781 TyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGluProLeu 1800  
 DB 5308 TACATGCGGTACTCTGGAGAACCTTCAGTGTGCTACTGACAAAGAGAGAGCTCTG 5367  
 QY 1801 SerGluAspAspPheGluMetPheTyrGluValTyrGluLysPheAspProAlaThr 1820  
 DB 5368 AGTGAGATGACCTTGTGATGTTCTATGAGGTTGGAGAGATTGATCCGATGCAACT 5427  
 QY 1821 GluPheMetGluPheGluLysLeuSerGluPheAlaAlaAlaLeuLupProPheLeuAsn 1840  
 DB 5428 CAGTTATGAGATTGATAAAATTAATTCAGATTGACGCTGCGCTTAACCGCTTCACAT 5487  
 QY 1841 LeuProGluProAsnLysLeuGluLeuIleAlaMetAspLeuProMetValSerGluAsp 1860  
 DB 5488 CTCGCCAACCAACCAACCTCCGACTCATTTGCCATGATTTGCCATGCTGAGTGTGAC 5547  
 QY 1861 ArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGluLysSerGly 1880  
 DB 5548 CGGATCCACTGCTGTGATATCTTAATTTGCTTTACAAAGCGGTTCTAGAGAGAGTGA 5607  
 QY 1881 GluMetAspAlaLeuArgIleGluMetGluGluArgPheMetAlaSerAspProSerLys 1900  
 DB 5608 GAGATGAGGCTCTACGAGATACGATGGAAGCGATTCATGCTTCAATCCTTCCAAAG 5667  
 QY 1901 ValSerTyrGluProIleThrThrLysArgLysGluGluLysSerAlaVal 1920  
 DB 5668 GCTCTCATACGCAATCATCTACTTAAACGAAACAAAGAGATATCTGCTGTC 5727  
 QY 1921 IleIleGluArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGluAlaSerPhe 1940  
 DB 5728 ATTAATCAGCGGCTTACAGAGCCGACCTTTTAAAGCGAAGCTTAAGACAGTTCCTT 5787  
 QY 1941 ThrTyrAsnLysAsnLysIleLysGlyAlaAsnLeuLeuLysGluLysPheTle 1960  
 DB 5788 AGCTAACAAATTAACAAATTAACAAAGGTGGGCTTAATCTTATTAACAGACATGATA 5847  
 QY 1961 IleAspArgIleAsnGluAsnSerIleThrGluLysThrAspLeuThrMetSerThrAla 1980  
 DB 5848 ATTGACAGAAATTAATTAATTAATTAATTAACGAAAGAACTGATGTCATGTCACCTGA 5907  
 QY 1981 AlaCysProProSerTyrAspArgValThrLysProIleValGluLysHisGluGlu 2000  
 DB 5908 GCTTGTCCACCTTCTATGACCGGAGCAAGCCAAATTTGTGAAAAACATGACAGAA 5967  
 QY 2001 GlyLysAspGluLysAlaLysGlyLys 2009  
 DB 5968 GGCNAAGATGAAGAAAGCCAAAGGAAA 5994  
 RESULT 6  
 ABL39689  
 ID ABL39689 standard: cDNA: 8131 BP.  
 AC ABL39689;  
 DT 10-MAY-2002 (first entry)  
 XX Human sodium channel SCN1A encoding cDNA SEQ ID NO:1.  
 DE Human; sodium channel; SCN1A; chromosome 2q24; gene; ss;  
 KW familial hypercalcaemic periodic paralysis; motor endplate disease.  
 XX Homo sapiens.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 15..6018  
 FT /tag= a  
 FT /product= "sodium channel SCN1A"  
 XX  
 PN W0200196552-A1.

XX 20-DEC-2001.  
 PD  
 XX  
 PF 12-JUN-2001; 2001WO-JP04956.  
 XX  
 PR 13-JUN-2000; 2000JP-0177540.  
 PR 13-JUN-2000; 2000JP-0177544.  
 XX  
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
 PI Kanazawa I, Goto J, Jeong S;  
 DR WPI: 2002-098066/13.  
 DR P-PSDB: ABB06026.  
 PT Human sodium channels SCN1A and SCN3A and encoded genes, useful in  
 PT studying physiological mechanism in which excitant cells participate  
 PT and causes of diseases and developing drugs for motor endplate disease  
 PS  
 XX Claim 5; Page 20-40; 88pp; Japanese.  
 CC  
 CC The present invention describes human sodium channels SCN1A and SCN3A.  
 CC The present sequence encodes the human sodium channel SCN1A. SCN1A and  
 CC SCN3A have been located to the human chromosome 2 long arm, positions  
 CC 2q24 and 2q24-31 respectively. The sodium channel proteins are useful  
 CC in studying the physiological mechanism in which excitant cells  
 CC participate and cause human diseases, and in developing remedies for  
 CC e.g. familial hypercalcaemic periodic paralysis of extremities and  
 CC motor endplate disease.  
 XX  
 SQ Sequence 8131 BP; 2453 A; 1530 C; 1719 G; 2422 T; 7 other:  
 Alignment Scores:  
 Pred. No.: 0 Length: 8131  
 Score: 10273.00 Matches: 1990  
 Percent Similarity: 99.00% Conservative: 0  
 Best Local Similarity: 99.00% Mismatches: 8  
 Query Match: 98.81% Indels: 12  
 DB: 24 Gaps: 2  
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 QY 1 MetGluGluThrValLeuValProProGlyProAspSerPheAsnPheThrArgLys 20  
 DB 19 ATGAGACAAACAGTGTGTACACAGAGACCTGACAGCTTCACTTCCACAGAGAA 78  
 QY 21 SerLeuAlaAlaIleGluArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40  
 DB 79 TCTCTTGGCGCTATTGAAAGAGCATTCGAGAAAGAAAGCAAAATCCCAAGCAGAC 138  
 QY 41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaLysAsn 60  
 DB 139 AAAAAGATGACGACAAATGAGCCCAAAAGATGAGCTTGAAGCTGAAAGAAAGC 198  
 QY 61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluLysLeu 80  
 DB 199 CTTCATTTATTTAAGAGACATTCCTCCAGAGATGTGTACAGCCCTCGAGAGACCTG 258  
 QY 81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100  
 DB 259 GACCCCTACTATATCAATTAAGAAACTTTATAGATTGAATTAAGGAAGGAGCCATCTTC 318  
 QY 101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAspProLeuArgLysIle 120  
 DB 319 CGGTTACGTGCCACTGCTGCTGATACATTTAACTCCCTTCAATCTCTTAAGAAATA 378  
 QY 121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140  
 DB 379 GCTATTAAGATTTTGTGATCATTTATTCACAGCATTAATTAATGTGACATTTTGTGAC 438  
 QY 141 AsnGlyValPheMetThrMetSerAsnProProAspTyrThrLysAsnValGluTyrThr 160

Db 439 AACGTGCTTTATGACAAATGAGTAACCTCCTGATGAGCAACAAAGATTCAGATCACC 498  
QY 161 PheThrGlyIleTyrThrPheGluSerLeuIleValIleAlaArgGlyPheCysLeu 180  
Db 499 TTCACAGCAATATATCTTTGATATCATTTAAATAATATGCAAGGAGATTCGTCTTA 558  
QY 181 GluAspPheThrPheLeuArgAspProTyrPheSerPheLeuAspPheThrValIleThrPhe 200  
Db 559 GAAGATTATCTTCTCTGGGATCCATGAACTGGCTGATTTCACTGCTCATTTACATTT 618  
QY 201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220  
Db 619 GCGTACGTACAGAGTTTGATGACCTGGGCAATGCTCCGCAATGAGAACATTCACAGATT 678  
QY 221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240  
Db 679 CTCGCGACATGAAAGCATTTTCAGATCATCCAGGCTGAAACCATTTGGGAGCCCTG 738  
QY 241 IleGlnSerValLysLysSerAspValMetIleLeuThrValPheCysLysSerVal 260  
Db 739 ATCCAGATCTGTAAAGAGCTCTCAGATGTAATGATCCTGATGTTCTGTGACCGTA 798  
QY 261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTyr 280  
Db 799 TTTCCTTAATGGCTGACGCTGTTTCATGGGCAACCTTACGAAATTAATGTATACAAATG 858  
QY 281 ProProThrAsnAlaSerLeuGlnLysSerIleGlyLysAsnIleThrValAsnTyr 300  
Db 859 CCGCCACCAATGCTTCCTTGGAGGAAATAGATAGAAAGAAATTAATCTGATTTAT 918  
QY 301 AsnGlyThrLeuIleAsnGlnThrValPheGluPheAspTyrLysSerTyrIleGlnAsp 320  
Db 919 AATGTGACACTATTAATGAACTGCTTGTGAGTTGACTGGAAGCATATATTCAGAT 978  
QY 321 SerArgTyrHisTyrPheLeuGlnLysPheLeuAspAlaLeuLysGlyAsnSerSer 340  
Db 979 TCAGATATCATATTTATTCGAGGGGTTTTTATGATGCACTCATATGTAAGTAATACCTCT 1038  
QY 341 AspAlaGlyLysCysProGlnGlyTyrMetCysValLysAlaGlyLysAsnProAsnTyr 360  
Db 1039 GATGCAAGGCAATGCTCAGAGGATATATGTGTGAAAGCTGTGAAATCCCATTTAT 1098  
QY 361 GlyTyrThrSerPheAspThrPheSerTyrPheLeuSerLeuPheArgLeuMetThr 380  
Db 1099 GGTATACAGACTTTGATACCTTCACTTGGCTTCTCTGTTGCTGACAAAGAGAT 1158  
QY 381 GlnAspPheTyrGlnLysLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400  
Db 1159 CAGGACTTCTGGGAAATCTTTATCACTGACATTCAGTGTGCTGGGAAACGTACATG 1218  
QY 401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420  
Db 1219 ATATTTTTTGTGTGATATTTCTTGGGCTCATTTCTACCTATTAATAATTTGATCCGTGGCT 1278  
QY 421 ValValAlaMetAlaTyrGlnGlnGlnAsnGlnAlaThrLeuGlnGlnAlaGlnLys 440  
Db 1279 GTGTGGCCATGCTCAGAGGAAAGAAATCAGGCCACCTTGGGAAACAGCAAGAA 1338  
QY 441 GluAlaGluPheGlnGlnMetIleGlnGlnLeuLysLysGlnGlnGlnAlaGlnGln 460  
Db 1339 GAGGCCGAATTTACAGATGATGTAACACTTAAAGAACAGAGAGGAGCTTCAGCCAG 1398  
QY 461 AlaAlaThrAlaThrAlaSerGlnLysSerArgGluProSerAlaAlaGlyLysLeuSer 480  
Db 1399 GCAAGCAAGGCAACTGCTCAGAAATTCAGAGAGCCAGCTCAGAGGAGCTCTCA 1458  
QY 481 AspSerSerSerGlnLysLysLysSerSerLysSerAlaLysGlnLysArgAsnArg 500  
Db 1459 GACAGCTCATCTGACACCTCTAGTTGAGTTCCAGAGAGCTTAAGAGAAAGAAATTCGG 1518  
QY 501 ArgLysLysArgLysGlnLysGlnLysSerGlyGlnGlnLysAspGlnLysPhe 520  
Db 1519 AGGAGAAAGAAAGAAAGCAAGAGAGAGCTGTGTGGGGAAGAGAAAGATGAGATTCATTC 1578

QY 521 GlnLysSerGlnSerGlnLysSerIleArgGlyGlyPheArgPheSerIleGlnGly 540  
Db 1579 CAAAATCTGAAATCTGAGAGACAGCATCAGAGAGAAAGTTTCGCTTCTCATTTGAAGG 1638  
QY 541 AsnArgLeuThrTyrGlnLysArgTyrSerSerProHisGlnSerLeuSerLeuArg 560  
Db 1639 AACCGATTAATGAAAGAGATCTCTCCACACAGCTGTTGTTGACATCCCT 1698  
QY 561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580  
Db 1699 GCGTCCCTATTTTACCAAGGCAAGTAATACAGAACAGGCTTTTACGTTTGAAGGCGCT 1758  
QY 581 AlaLysAspValGlySerGlnLysAspPheAlaAspAspGlnLysSerThrPheGluAsp 600  
Db 1759 GCAAGAGATGTGGATCTAGAACGCTTCGAGATGAGATGACACAGCACTTTGAGAGAT 1818  
QY 601 AsnGlnSerArgArgAspSerLeuPheValProArgArgHisGlyGlnLysArgAsnSer 620  
Db 1819 AACGAGCCGTAGAGATTTCTGTTGTGCCCCGACGACGAGAGAGAGCAACAGC 1878  
QY 621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValPheProAlaAsnGlyLys 640  
Db 1879 AACCTGACAGACCAAGTAGTATCCCGATCCGATCCGAGTGTTCACAGCAATGGAGAG 1938  
QY 641 MethSerSerThrValAspCysAsnGlyValSerLeuValGlyGlyProSerValPro 660  
Db 1939 ATGCACAGACATGTGATGATCAATGATGTTGTTCTGTGTTGGTGGACCTTCAGTTCT 1998  
QY 661 ThrSerProValGlyGlnLeuLeuProGlnValIleIleAspLysProAlaThrAspAsp 680  
Db 1999 ACATCCCGCTGTGAGACGTTCTGCA----- 2025  
QY 681 AsnGlyThrThrGlnThrGlnMetArgLysArgArgSerSerPheHisValSer 700  
Db 2026 GGGGCAACACCACTGAAATGAAATGAGAAAGAGAGCTCAAGTCTTTCCAGCTTCC 2085  
QY 701 MetAspPheLeuGlnLysProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720  
Db 2086 ATGCATTTCTAGAAAGATCTTCCCAAGGCAAGCAATGATGATAGCCAGCATTTCTA 2145  
QY 721 ThrAsnThrValGlnGlnLysGlnLysSerArgGlnLysCysProProCysTyrTyrLys 740  
Db 2146 ACAAAATACAGTAAAGAACTGAAAGATCCAGGCAAAATGCCACCGTGTGTAA 2205  
QY 741 PheSerAsnIlePheLeuIleTyrAspCysSerProTyrTyrLeuLysValIleVal 760  
Db 2206 TTTTCAACATATTTCTCATCTGAGCTGTCTCCATTTGCTTAAAGGAAACATGTT 2265  
QY 761 ValAsnLeuValAlaMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780  
Db 2266 GTTCAACCTGTGTGATGAGCCATTTGTTGACCTGGCATCCACTGTGTATTTGCTCTTA 2325  
QY 781 AsnThrLeuPheMetAlaMetGlnLysTyrProMetThrAspHisPheAsnValLeu 800  
Db 2326 AATACCTTTTCAATGAGGAGAGCACTATTCATATGAGGACCATTTCAATTAATGTCCT 2385  
QY 801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGlnMetPheLeuLysIleIle 820  
Db 2386 ACAGTAGAAACTGTGTTTCACTGAGATCTTTACAGCAAGAAATGTTTCGAAATATTT 2445  
QY 821 AlaMetAspProTyrTyrTyrPheGlnGlnGlnLysTyrPheAsnIlePheAspGlyPheIleVal 840  
Db 2446 GCCATGAGATCTTATATTTTCCAAAGAGGCTGGAATATCTTACAGGTTTATTTG 2505  
QY 841 ThrLeuSerLeuValGlnGlnGlyLeuAlaAsnValGlnGlnLysSerValLeuArgSer 860  
Db 2506 ACCCTTAGCGCTGTAGAACTTGACATCCGCAATGTGAAGATTAATCTTCCCTTCA 2565  
QY 861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTyrProThrLeuAsnMetLeuIle 880  
Db 2566 TTTTCATGCTGTGAGATTTTCAAGTTTGCAAAATCTTGCCACAGTTTAAATATCTAATA 2625

|    |      |  |      |
|----|------|--|------|
| OY | 881  | LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIlelle       | 900  |
| Db | 2626 | AAAGTCAATCGGCATTTCCGTGGGGGCTCTGGGAAATTAACCTCGTCTGGCCATTCATC        | 2685 |
| OY | 901  | ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal       | 920  |
| Db | 2686 | GTCCTTCAATTTTTGGCCGGTGGCCAGACAGCTCTTTGGTAAAGCTACAAAGATTGTCTC       | 2745 |
| OY | 921  | CysLysIleAlaSerAspCysGlnLeuPro--ArgTyrHisMetAsnAspPheHis           | 939  |
| Db | 2746 | TGCAGAGATCGCCAGATGTATGTGCACACTCCCAACAACGGTGGCATGAATGACTTCTCCAC     | 2805 |
| OY | 940  | SerPheLeuIleValPheAlaValLeuGlyGlyGlnIleTyrPheIleGlnThrMetTyrAspCys | 959  |
| Db | 2806 | TCTCTCCGATGTGTGTCGCGCGCTGTGTGGGAGATGATAGAACATGTGGGACGTG            | 2865 |
| OY | 960  | MetGluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGly       | 979  |
| Db | 2866 | ATGGAGGTGTGTGTCAAGCCATGTGCTTACTGTCTTATATATGTCTATGTGTGATTTGGA       | 2935 |
| OY | 980  | AsnLeuValValLeuAsnLeuPheLeuAlaLeuLeu**SerSerPheSerAlaAspAsn        | 999  |
| Db | 2926 | AACTAGAGGTGCTGAATCTCTTTCGGCCCTCTCTGAGCTCATTTTAGTGACAGACAC          | 2985 |
| OY | 1000 | LeuAlaAlaThrAspAspAspAsnGlnMetAsnAsnLeuGlnIleAlaValAspArgMet       | 1019 |
| Db | 2986 | CTTCCACACCCCTGTATGTATGTAAATGAAGAATAATCTCAATTCGTGTGATAGCATG         | 3045 |
| OY | 1020 | HisLysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIle       | 1039 |
| Db | 3046 | CACAAAGAGTAGCTTATGTGAAAAGAAAATATATGAATTTATTCACAGCTCTCATTT          | 3105 |
| OY | 1040 | ArgLysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAsp       | 1059 |
| Db | 3106 | AGGAAACAAAAGATTATAGATGAATAATTAACCACTGATGATCTAAACACAGAAAGAC         | 3165 |
| OY | 1060 | SerCysMetSerAsnHisThr**GluIleGlyLysAspLeuAspTyrLysLysAspVal        | 1079 |
| Db | 3166 | AGTTGTATGTCCAAATCTATACACAGAAATTTGGGAAAGACTTGATCTTAAAGATTA          | 3225 |
| OY | 1080 | AsnGlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleLeuAspGlu       | 1099 |
| Db | 3226 | AATGAACCTCAAGTGTATATAGGACTGGCAGCAGCTTTGAAAATATCACTTATTTGATGCA      | 3285 |
| OY | 1100 | SerAspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaVal       | 1119 |
| Db | 3286 | AGTATATACATGTCAATCATTAATAAACACCCAGCTTACTGTAGCTGTACCAATTCGTCTA      | 3345 |
| OY | 1120 | GlyLysLeuSerAspPheGlnAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGlu    | 1139 |
| Db | 3346 | GGAAATCTGACTTGTGAATAATTTAAACAGGAAAGACTTTAGTAGCAATCGGACTCGGAA       | 3405 |
| OY | 1140 | GluSerLysGluLysLeuAsnGlnLysSerSerSerSerSerGlnGlySerThrValAspIle    | 1159 |
| Db | 3406 | GAAAGCAAAGAACTGCAATGAAAGCACTAGCTCATCGAAGGATGACACTGTGGACAT          | 3465 |
| OY | 1160 | GlyAlaProValGluGlnGlnProValValGluProGluGluThrLeuGlnProGluAla       | 1179 |
| Db | 3466 | CGGGCCCTGTAGAAAGAACAGCCCGTAGTGAACCTGAAAGAACTCTGAACCAAGAAAGCT       | 3525 |
| OY | 1180 | CysPheThrGlnGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGlnGly       | 1199 |
| Db | 3526 | TGTTTCACTCAAGGCTGTGTACAAATTTCAAGTGTGTCCAATCAAAATGTGAACATPACGG      | 3585 |
| OY | 1200 | ArgGlyLysGlnTyrPheAsnLeuAlaGlyThrCysPheArgIleValGluHisAsnTyr       | 1219 |
| Db | 3586 | AGAGGAAACAAATGTGTGAACCTGTGACAGAGGACGTGTTTCCGATATGTTGAACATPACGG     | 3645 |
| OY | 1220 | PheGluThrPheIleValPheMetIleLeuLeuSerSerGlyValAlaLeuAlaPheGluAsp    | 1239 |
| Db | 3646 | TTTAGACCTTCATTTGTTTTCATGATTTCTCTTAGTAGTGGTGTCTGGCAATTTGAAGAT       | 3705 |
| OY | 1240 | IleTyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPhe       | 1259 |

[illegible]

Db 4786 TTATCAATGGAGTAATTTTGGATTGTTGGTGTGATTCCTCATTTGATGATG 4845  
 Qy 1620 PheLeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPheArgValIleArg 1639  
 Db 4846 TTCTTCCGAGCGATGATAGAAAGATATTTCTGTCCTCCATCCGTTCCGAGTGCCT 4905  
 Qy 1640 LeuAlaArgIleGlyArgGlyIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLeu 1659  
 Db 4906 CTTCGTGGATGTGGCCGAAATCTGATGTCAGTCAAGAGGAGAAAGGGGATCCGACGCTG 4965  
 Qy 1660 LeuPheAlaLeuMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPheLeu 1679  
 Db 4966 CTCTTCTGTTGATGATGATGCTCTGCTGCTGTTTAAACATCGGCTCTCTCTCTA 5025  
 Qy 1680 ValMetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgGluVal 1699  
 Db 5026 GTCATGTTCATCTACGCGATCTTTGGGATGTCAACATTTGCTATGTAAAGAGGAAATTT 5085  
 Qy 1700 GlyIleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPheGln 1719  
 Db 5086 GGGATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5145  
 Qy 1720 IleThrSerIleArgIleTyrAspGlyLeuLeuAlaProIleLeuAsnSerLysProPro 1739  
 Db 5146 ATTACAACTCTGCTGCTGGGATGATGATGATGATGATGATGATGATGATGATGATGAT 5205  
 Qy 1740 AspCysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsnPro 1759  
 Db 5206 GACGTGACCTGATTAAGATTAAACCTGGAAGCTGATTAAGGAGAGCTGAGGAAACCA 5265  
 Qy 1760 SerValIleLysPhePhePheValSerTyrIleIleIleSerPheLeuValValAsn 1779  
 Db 5266 TCTGTGTGAATTTCTTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 5325  
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 Db 5326 ATGTACATCGGCGTCACTGCTGAGACCTGAGTGTGCTGACGAAAGAGTCAAGACCT 5385  
 Qy 1800 LeuSerGluAspAspPheGluMetPheTyrGluValIleTyrGluLysPheAspProAspAla 1819  
 Db 5386 CTGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5445  
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 Qy 1860 AspArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyLysSer 1879  
 Db 5566 GACGGGATCCACTGCTGATATATTTATTTGCTTTACAAAGCGGGTCTTAGAGAGAGAT 5625  
 Qy 1880 GlyIleMetAspAlaLeuArgIleGlnMetGluLysArgPheMetAlaSerAsnProSer 1899  
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 Qy 1900 LysValSerTyrGlnProIleThrThrLeuLysArgLysGluGluValSerAla 1919  
 Db 5686 AAGGTCTCTATACAGCCATCACTACTTAAACGAAACAAAGAGAGAGATATCTGCT 5745  
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Qy 1980 AlaAlaCysProProSerTyrAspArgValThrLysProIleValGluLysHisGluGln 1999  
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 RESULT 7  
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 XX 01-JUL-2002 (first entry)  
 DE Human ion channel cDNA #7.  
 XX  
 XX Human; novel human protein; NHP; voltage-gated sodium channel;  
 KW gene therapy; bioreactor; mental disorder; biological disorder;  
 KW gene; medical disorder; ss.  
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 PN W0200214498-A2.  
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 PF 15-AUG-2001; 2001WO-US25650.  
 XX  
 PR 16-AUG-2000; 2000US-225989P.  
 XX  
 PA (LEXI-) LEXICON GENETICS INC.  
 XX  
 PI Turner CA, Mathur B, Mathur D;  
 DR WPI; 2002-280757/32.  
 DR P-PSDB; AAE20516.  
 XX  
 PT Novel polynucleotides encoding human sodium channel proteins,  
 PT particularly voltage-gated sodium channel proteins useful for drug  
 PT screening, diagnosis and in gene therapy of biological disorders -  
 XX  
 PS Claim 1; Page 62-64; 83pp; English.  
 XX  
 CC The present sequence is a cDNA encoding novel human protein (NHP), ion  
 CC channel protein. NHP share structural similarity with mammalian sodium  
 CC channel proteins particularly voltage-gated sodium channel proteins.  
 CC NHP oligonucleotides are useful as hybridisation probes for screening  
 CC libraries and assessing gene expression patterns. Sequences derived  
 CC from regions adjacent to the intron/exon boundaries of NHP gene can be  
 CC used to design primers for use in amplification assays to detect  
 CC mutations within the exons, splice sites, introns that can be used in  
 CC diagnostics and pharmacogenomics. NHP nucleotide sequences are useful  
 CC for drug screening effective in the treatment of symptomatic or  
 CC phenotypic manifestations of perturbing the normal function of NHP in  
 CC the body, and nucleotide constructs encoding NHP products are useful to  
 CC genetically engineer host cells to express NHP products in vivo. These  
 CC genetically engineered cells function as bioreactors in the body  
 CC delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion  
 CC protein to the body. Nucleotide construct encoding NHP products are  
 CC also useful in gene therapy for modulating NHP expression and to  
 CC produce genetically engineered host cells to express NHP products in  
 CC vivo. NHP nucleotide sequences may also be used as part of ribozyme





|    |      |   |      |
|----|------|---|------|
| Qy | 661  | MeHhSserThValAsPcyasnglyValValSerLeuValGlylyProSerValPro        | 660  |
| Db | 1921 | ATGCACACACACGTGGATTGCATAGGAGTGCGTTCCCTGGTGGTGGACCTTCAGTTCCT     | 1980 |
| Qy | 661  | ThSerProValGlyLeuLeuProGluValIleIleAspLySerProAlaThrAspAsp      | 680  |
| Db | 1981 | ACATGCCCTGTGGACAGCTTCTGCCAGAGGTGATATATAGTAAGCAGCTACTGATGAC      | 2040 |
| Qy | 681  | AsnglyThrThrGluThrGluMetArgLySarArgSerSerSerPheHisValSer        | 700  |
| Db | 2041 | AATGAGACACACACGTGAACCTGAAATGAGAAAGAGAGAGCTCAAGTCTTCCACGTTTCC    | 2100 |
| Qy | 701  | MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleIleAserIleLeu   | 720  |
| Db | 2101 | ATGGACTTTCVAGAAAGATCTTCCCAAGAGCAACGAGCATAGTGTATGGCCACCTATCVA    | 2160 |
| Qy | 721  | ThrAsnThrValGluGluLeuGluSerArgGlnLyAsCysArgProCysTrpTyrLyS      | 740  |
| Db | 2161 | ACAAATACAGTATGAAAGAACTTGAAAGATCCAGGCAGAAATGCCACCTCTGTGGTATAA    | 2220 |
| Qy | 741  | PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLySVal             | 760  |
| Db | 2221 | TTTTCACACATATTCCTATATCTGGAGCTGTTCATATGGTTAAAGTAAGTAACATGT       | 2280 |
| Qy | 761  | ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu    | 780  |
| Db | 2281 | GTCACACCTGGTGTGATGAGCACCATTTGTGTGACCTGGCCATCCACATCTGTATTTGCTTA  | 2340 |
| Qy | 781  | AsnThrIleuPheMetAlaMetGluHisTrpPrometThrAspIlePheAsnValLeu      | 800  |
| Db | 2341 | AATACTCTTTATGGCCATGAGGCATATCCATATACGAGCACTTCATTAATATGTCCT       | 2400 |
| Qy | 801  | ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLySleIle     | 820  |
| Db | 2401 | ACAGTAGGAAACTTGGTTTCACTGGGAGCTTTACAGCAGAAATGTTTCGAAATATATT      | 2460 |
| Qy | 821  | AlaMetAspProTyrTyrTyrPheGlnGluGlyTyrPheAsnIlePheAspGlyPheIleVal | 840  |
| Db | 2461 | GCCATGGATCCCTTACTATATTTTCCAAAGAGCGTCGAAATVCTTGTGACGGTGTATTTGTC  | 2520 |
| Qy | 841  | ThrIleSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValIleuArgSer   | 860  |
| Db | 2521 | ACGCTTAGCTGTAGAACTTGGACCTGGCCAAATGTGAAAGATTAATCTGTCTCCGTCA      | 2580 |
| Qy | 861  | PheArgLeuLeuArgValPheLySLeuAlaLySerTrpProThrIleuAsnMetLeuIle    | 880  |
| Db | 2581 | TTTCATTCTCTCGCACTTTTCAAGTTGGCAAAATCTTGGCAACGTTAAATATGCTATA      | 2640 |
| Qy | 881  | LySleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle     | 900  |
| Db | 2641 | AAGATCATGTGGCAATCCCTGGGGGCTGTGGGAAATTAACCTCGCTTGGCCATCATC       | 2700 |
| Qy | 901  | ValPheIlePheAlaValValGlyMetGluLeuPheGlyAsSerTyrLySAspCysVal     | 920  |
| Db | 2701 | GTCTTCATTTTGGCGGTGTGGCAATGCAAGCTTTTGGTAAAGCTACAAAGATGTGTC       | 2760 |
| Qy | 921  | CysLySleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPheHisSer        | 940  |
| Db | 2761 | TGCAGATGCCACGTATTTCTCACTGCCACCGCTGGCACATGATGACTTCTTCCACTCC      | 2820 |
| Qy | 941  | PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet    | 960  |
| Db | 2821 | TTTCGATTTGTGTGCGCGGTGTGTGGGGAATGATAGACACATGTGGAGCTGTATG         | 2880 |
| Qy | 961  | GluValAlaGlyGlnAlaMetCysLeuThrValPheMetCysValMetValIleGlyAsn    | 980  |
| Db | 2881 | GAGGTGTGCTCAACCCATGTGCTTACTACTCTTATCATGTGTGTCATAGGTGATTTGGAAC   | 2940 |
| Qy | 981  | LeuValValLeuAsnIlePheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu    | 1000 |
| Db | 2941 | CTAGTGCTCTGTGATCTCTTTCGGCTTGTGTGCTGATTAATATATGACAGCAACCTT       | 3000 |

|    |      |   |      |
|----|------|---|------|
| QY | 1001 | AlAlAlThrAspAspAspAsnGluMetCAsnAsnLeuGlnIleAlaValAspArgMetHis   | 1020 |
| Db | 3001 | GCACCCACTGATGTGATTAATGAATAAGAAATATCTCCAAATTCGTGTGGATAGGATGCAC   | 3060 |
| QY | 1021 | LysGlyValAlaArgValLysArgLysIleArgGluPheIleGlnGlnSerPheIleArg    | 1040 |
| Db | 3061 | AAAGAGTACGTTATGTGAAGAAAATATATGATTAATTATTCACAGCGCTCATTTAGG       | 3120 |
| QY | 1041 | LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysAspSer       | 1060 |
| Db | 3121 | AAACAAAGATTTTATGATGAAATTTAAACCACTTGATGATCTAAACACAGAAACACAGT     | 3180 |
| QY | 1061 | CysMetSerAsnHisThr***GluIleGlyAspLeuAspTyrLeuLysAspValAsn       | 1080 |
| Db | 3181 | TGTATGTCCATCTATACARAGAAATTTGGAAAGACTTGACTATCTTAAAGATTAAT        | 3240 |
| QY | 1081 | GlyThrThrSerGlyIleGlyThrGlySerSerValGlnLysTyrIleIleAspGlnSer    | 1100 |
| Db | 3241 | GGAACTACAACTGTTATAGGAAGCTGGCAGCAGGTGGAAAATATACATTATGATCAAGT     | 3300 |
| QY | 1101 | AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly    | 1120 |
| Db | 3301 | GATTACATGTCATCTAATAACCAACCCAGCTTACGTACGTACATGCTCAATTCCTAGGA     | 3360 |
| QY | 1121 | GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGlnGlu    | 1140 |
| Db | 3361 | GAATCTGCTTGAATTAATTTAAACGGGAAGACTTTAGTAGGAATCGGATCTGGAAAGAA     | 3420 |
| QY | 1141 | SerLysGluLysLeuAsnGlnUserSerSerSerSerGluGlySerThrValAspIleGly   | 1160 |
| Db | 3421 | AGCAAGAGAAACAGATGAATGAAGACAGTACGTCAATCGAAGGTAGCAGCTGTGGACATCGGC | 3480 |
| QY | 1161 | AlaProValGluGlnGlnProValGluGluProGluGluThrLeuGlnProGluAlaCys    | 1180 |
| Db | 3481 | GCACCTGTAGAGAACAGCCCGTAGTGGAACTCGAAGAAACTCTTGACCAACAGCACTTGT    | 3540 |
| QY | 1181 | PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGlnGlyArg    | 1200 |
| Db | 3541 | TTTCACTGAAAGCTGTGTACAAAGATTCACATGTTGTTCAAATCAATGTGGAAACAGCAGA   | 3600 |
| QY | 1201 | GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGlnHisAsnTrpPhe    | 1220 |
| Db | 3601 | GGAAACCAATGTGTGAACCTGAGAGAGAGCTGTTTCCGAATAGTTGAACATACACAGTGT    | 3660 |
| QY | 1221 | GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGlnAspIle    | 1240 |
| Db | 3661 | GAGACCTTCATGTTTTCATGATATCTCTTAGTAGTGGTCTGTGCACTTGAACAATATATA    | 3720 |
| QY | 1241 | TyrIleAspGlnArgLysThrIleLysThrMetLeuGlnTrpAlaAspLysValPheThr    | 1260 |
| Db | 3721 | TATATGTATCGACCAAGAGAGATTAACACATGTTGGAAATATGCTGACCAAGGTTTTCCT    | 3780 |
| QY | 1261 | TyrIlePheIleLeuGlnMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPhe    | 1280 |
| Db | 3781 | TACATTTTCATTCGGAATATGCTTCTTAAATGGGTGGCATATGGCATATAACATATATTC    | 3840 |
| QY | 1281 | ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr    | 1300 |
| Db | 3841 | ACCAATGCCGTGTGGTGGCTGGACACTTCTTAATGTTGATGATTTTCATTTGCTGACTTAACA | 3900 |
| QY | 1301 | AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla    | 1320 |
| Db | 3901 | GCAATATGCTTGGGTGTACTCGAGAACTTGAGCCATCAATATCTCTCGAGCACTTAAGACT   | 3960 |
| QY | 1321 | LeuArgProLeuArgAlaLeuSerArgPheGlnGluMetArgValValAsnAlaLeu       | 1340 |
| Db | 3961 | CTGAACTCTTAAGAGCTTATCTTCGATTTGAAAGGATGAGGGGTGTGTGATATCCCTT      | 4020 |
| QY | 1341 | LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIle    | 1360 |
| Db | 4021 | TTAGAGAGCAATTCATCATCATGATGAATATGCTCTGTGGTTTGCTTATATTCGTGGCTAAT  | 4080 |
| QY | 1361 | PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheThrIleCysIleAsnThrThr    | 1380 |

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|||||
Db 4081 TTGAGCATCATGAGCGGAAATTTGTTGCTGCGCAAAATTCCTCACTGATTAATCAACCCCA 4140
Oy 1381 ThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuIleuLeu 1400
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Oy 1401 GluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyPhe 1420
Db 4201 GAAGAAGATGAGACTGCTCGATGCAAAAATGTGAAGATTAACCTTGATTAATGATGATTT 4260
Oy 1421 GlyTrpLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetLysAla 1440
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Oy 1641 AlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgTrpLeuLeu 1660
Db 4921 GCTAGGATTTGGCCGAATCTCTACGTCGATCAAGAGCAAGAGGAGATCCGACGCTGCTC 4980
Oy 1661 PheAlaIleuMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPheLeuVal 1680
Db 4981 TTTCCTTTGATGATGCTCCCTTCTGCGCTGTTTAAACATCGGCTCTCTCTCTCTAGTGC 5040
Oy 1681 MetPheIleTrpAlaIlePheGlyMetSerAsnPheAlaTrpValLysArgGluValGly 1700
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Oy 1701 IleAspAspMetPheAsnPheGluThrPheGlyLysSerMetIleCysLeuPheGlnIle 1720
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Oy 1721 ThrThrSerAlaGlyTrpArgGlyLeuLeuAlaProIleLeuAsnSerLysProProAsp 1740
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Db 5161 ACAACCTCTGCTGGCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5220
Oy 1741 CysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsnProSer 1760
Db 5221 TGTGACCCCTAATAAAGTAAATACCTTGAACCTGAGTAAAGAGACGTGTGGAAACCATTT 5280
Oy 1761 ValGlyIlePhePhePheValSerTrpIleIleIleSerPheLeuValValAsnMet 1780
Db 5281 GTTGAATTTTCTTTTGTGCTAGTATACATCATCATATCTCTCTGTTGTGTGAACATG 5340
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Db 5581 CGGATTCACCTCTCTGATATCTTATTTGCTTTTACAAAGGGCTCTAGAGAGATGGA 5640
Oy 1881 GluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsnProSerLys 1900
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Oy 1901 ValSerTrpGlnProIleThrThrIleLysArgLysGlnGluGluValSerAlaVal 1920
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Oy 1921 IleIleGlnArgAlaTrpArgTrpHisLeuLysArgTrpValLysGlnAlaSerPhe 1940
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Oy 1941 ThrTrpAsnLysAsnLysIleLysGlyAlaAsnLeuLeuIleLysGluAspMetIle 1960
Db 5821 ACGTACAAATTAATAAACAATCAAGTGGGCTAATCTCTTATAAAGACATGATA 5880
Oy 1961 IleAspArgIleAsnGluAsnSerIleThrGluLys 1972
Db 5881 ATTGACAGAAATTAATGAAAACTTATTACAGAAAAA 5916

RESULT 8
AAD32840
ID AAD32840 standard; cDNA: 5889 BP.
XX
AC AAD32840;
XX
DE 01-JUL-2002 (first entry)
XX
XX Human ion channel cDNA #2.
XX
XX Human; novel human protein; NMP; voltage-gated sodium channel;
XX gene therapy; bioreactor; mental disorder; biological disorder;
XX gene; medical disorder; ss.
XX
OS Homo sapiens.
XX
FH Key
FH CDS 1..5889
FH FT /tag- a
FH FT /product- "Human ion channel protein #2"
FH FT /transl_except- (pos:2941..2943, aa:xaa)
FH FT /transl_except- (pos:3166..3168, aa:xaa)
FH FT /note- "Xaa - any amino acid"

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 QY 461 Ala1aThr1aThr1aSerG1uH1sSerArgG1uProSerAla1aG1uArgLeuSer 480  
 Db 1381 GCAGAGAGGAGAACTGCTCAGAACATTCACAGAGAGCCAGAGCCAGAGCGGCTCTCA 1440  
 QY 481 AspSerSerSerG1uAlaSerLysLeuSerLysSerLysSerAlaLysG1uArgArgAsnArg 500  
 Db 1441 GACACCTATCTGAGAGCCTCTAAGTTGAGCTTCCAGAGAGTGGCTTAAGAGAGAAATCGG 1500  
 QY 501 ArgLysLysArgLysG1uLysG1uG1uSerGlyG1uG1uLysAspG1uAspG1uPhe 520  
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 QY 521 G1uLysSerG1uSerG1uAspSerL1eArgArgLysG1uPheArgPheSerL1eG1uGly 540  
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 Db 1621 AACGATTCAGATATGAG 1680  
 QY 561 GlySerLeuPheSerProArgArgArgAsnSerArgTyrgSerLeuPheSerPheArgLysArg 580  
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 QY 581 AlaLysAspValGlySerG1uAsnAspPheAlaAspAspG1uH1sSerThrPheG1uAsp 600  
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 QY 601 AsnG1uSerArgArgArgAspSerLeuPheValProArgArgH1sG1uArgArgAsnSer 620  
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 Db 1861 AACCTGAGTACAGACAG 1920  
 QY 641 MetH1sSerThrValAspCysAsnG1uValValSerLeuValGlyGlyProSerValPro 660  
 Db 1921 ATGCACACAG 1980  
 QY 661 ThrSerProValGlyG1uLeuLeuProG1uValL1eL1eAspLysProAlaThrAspAsp 680  
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 Db 2128 ACAATATACAG 2187  
 QY 741 PheSerAsnL1ePheLeuL1eTrpAspCysSerProTyrgTrpLeuLysValLysH1sVal 760  
 Db 2188 TTTTCACACATATCTTATATCTGGAGAGCTGTCTCAATATGTTTAAAGTGAATGATGTT 2247  
 QY 761 ValAsnLeuValValMetAspProPheValAspLeuAlaL1eH1rL1eCysL1eValLeu 780  
 Db 2248 GTCAACCTGCTGTGATGAG 2307  
 QY 781 AsnThrLeuPheMetAlaMetG1uH1sTyrgPrometThrAspH1sPheAsnAsnValLeu 800  
 Db 2308 AATATCTTTTTCATGAG 2367

QY 801 ThrValG1uAsnLeuValPheThrGlyL1ePheThrAlaG1uMetPheLeuLysL1eL1e 820  
 Db 2368 ACAGTAGAGAACTTGATGTTTCACTGGAGATCTTACAGAGAGAAATGTTTCTGAAATATAT 2427  
 QY 821 AlaMetAspProTyrgTyrgTyrgPheG1uG1uGlyTyrgAsnL1ePheAspGlyPheL1eVal 840  
 Db 2428 GCCATGGAGATCTTATATATTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2487  
 QY 841 ThrLeuSerLeuValG1uLeuG1uLeuAlaAsnValG1uG1uLeuSerValLeuArgSer 860  
 Db 2488 AGCTTAGAGCCAGGATGAG 2547  
 QY 861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTyrgProThrLeuAsnMetLeuL1e 880  
 Db 2548 TTTTCATCTCTCGAGATTTTCAAGTTGGCAAAATCTGGCCACAGTAAATATGTAATA 2607  
 QY 881 LysL1eL1eGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaL1eL1e 900  
 Db 2608 AAGATCATCGGCAATTCCTGGGGGCTCGGAGAAATTTAACTCTGTTGGCCATCATC 2667  
 QY 901 ValPheL1ePheAlaValAlaGlyMetG1uLeuPheGlyLysSerTyrgLysAspCysVal 920  
 Db 2668 GTCTTCATTTTGGCGGTGGCATGCACTCTTGGTAAAGAGCTACAAAGATTTGTCT 2727  
 QY 921 CysLysL1eAlaSerAspCysG1uLeuProArgTyrgPheH1sMetAsnAspPhePheH1sSer 940  
 Db 2728 TCCAAAGATGCGCAGATGATGATCACTCCAGCCGTGGCAGATGAATGACTTCTCCACTCC 2787  
 QY 941 PheLeuL1eValPheArgValLeuCysGlyLysTyrgL1eGlyThrMetTrpAspCysMet 960  
 Db 2788 TTTCTGATGATGTTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2847  
 QY 961 G1uValAlaGlyAlaMetCysLeuThrValPheMetMetValMetAlaL1eGlyAsn 980  
 Db 2848 GAGGTGCTGGTCAAG 2907  
 QY 981 LeuValAlaLeuAsnLeuPheLeuAlaLeuLeu\*\*\*SerSerPheSerAlaAspAsnLeu 1000  
 Db 2908 CTAGTGCTCTAATCTCTTCTGCGCTGCTTGTAGAGCTCATTTAGTGCAGACACACTT 2967  
 QY 1001 Ala1aThrAspAspAspAsnG1uMetAsnAsnLeuG1uAlaValAspArgMetH1s 1020  
 Db 2968 GCAGCCACAGAGATGATGATGAATGAATGATGATGATGATGATGATGATGATGATGATGAT 3027  
 QY 1021 LysGlyValAlaLysValLysArgLysL1eTyrgLysPheL1eG1uG1uSerPheL1eArg 1040  
 Db 3028 AAGGAGATGCTTATGTAAG 3087  
 QY 1041 LysG1uLysL1eLeuAspG1uLysProLeuAspAspLeuAsnAsnLysLysAspSer 1060  
 Db 3088 AACAAGAGATTTTATGATGAATTAACCACTTGATGATGATGATGATGATGATGATGATGATGAT 3147  
 QY 1061 CysMetSerAsnH1sThr\*\*G1uL1eGlyLysAspLeuAspTyrgLeuLysAspValAsn 1080  
 Db 3148 TGTATGTCCAATCAACACACAG 3207  
 QY 1081 GlyThrThrSerGlyL1eGlyThrGlySerSerValG1uLysTyrgL1eL1eAspG1uSer 1100  
 Db 3208 GGAATCAAGAGTGTATGAG 3267  
 QY 1101 AspTyrgMetSerPheL1eAsnAsnProSerLeuThrValThrValProL1eAlaValGly 1120  
 Db 3268 GATTCATATGCTATCATATAACACCCAGCTTACTGTGACCTGATACCAATTTCTGTAGGA 3327  
 QY 1121 G1uSerAspPheG1uAsnLeuAsnThrG1uAspPheSerSerG1uSerAspLeuG1uG1u 1140  
 Db 3328 GATCTGACTTTGAAATTTTAAACACGAG 3387  
 QY 1141 SerLysG1uLysLeuAsnG1uSerSerSerSerSerG1uGlySerThrValAspL1eGly 1160  
 Db 3388 AGCAAGAGAGAACTGAATGAAG 3447



1161 AlaProValGluGluInpProValValGluProGluGluThrLeuGluInpProGluAlaCys 1180  
1181 PheThrGluGluCysValGlnArgPheLeuCysCysGlnIleAsnValGluGluArg 1200  
3508 ThrACGGAAGGCTGTGTACAAAGATTCACTGTGTCAATCAATGTGGAAGAAAGCAGA 3567  
1201 GlyLysGluInpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe 1220  
3568 GGAACCAATGCTGGAACCTGGAAGAGAGCTGTTCGAGATGTTGAACAATCACTGCTT 3627  
1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240  
3628 GAGACCTTCATTTCTTTCAGATTCCTTCAGTAGTGTCCTCGGATTTGGAAGATATA 3667  
1241 TyrIleAspGluArgLysThrIleLysThrMetLeuGluInpTrpAlaAspLysValPheThr 1260  
3668 TATATTGATCAGCGAAGAGAGATTAGACAGATTGGAATATGCTGACAAAGTTTTCACT 3747  
1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaArgGlyArgGluThrTrpPhe 1280  
3748 TACATTTTCATCTCGAAGATGCTTCAAAATGGGTGGCATATGCTATCAACATATTTC 3807  
1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300  
3808 ACCAATGCCCTGGCTTCGCTGCGACCTTCCTAATGTTGATGTTTCATGCTGACGTTTAA 3867  
1301 AlaAsnAlaLeuGluLysTrpSerGluLeuGlyAlaIleLysSerLeuArgTrpLeuArgAla 1320  
3868 GCAAAATGCTGGGTGTACTAGAACCTTGAGCCATCAAACTCTCAGAGACACTAAGAGCT 3927  
1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValAlaAsnAlaLeu 1340  
3928 CTGAGACCTTAAGAGCTTATCTCATTTGAAGGAGTAGAGGCTGTGGATGCCCTT 3987  
1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIle 1360  
3988 TTGAGGAGCAATTCATCCATCAATGAGATGATGCTGCTGTTGCTAATATCTGGCTAAT 4047  
1361 PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTrpHisCysIleAsnTrpThr 1380  
4048 TTGAGATCAATGAGCGTAATTTGTTGCTGGCAAAATCTACCACTGTATTAACACACA 4107  
1381 ThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIle 1400  
4108 ACGGTGACAGGTTTGACATCGAAGAGCTGAATATCATCTGATTCCTAAAACTATA 4167  
1401 GluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyPhe 1420  
4168 GAAGAGAAATGAGACTGCTCATGAAATAATGTAAGTAACCTTGATATGTAGAGATT 4227  
1421 GlyThrLeuSerLeuLeuGluGlnAlaIleThrPheLysGlyTrpMetAspIleMetTrpAla 1440  
4228 GGGTATCTCTCTTGTCTCAAGTTCACATTAAGAGATGAGTGAATAAAGTATAGCA 4287  
1441 AlaValAspSerArgAsnValGluLeuGluInpTrpLysTrpGluLeuSerLeuTrpMetTrp 1460  
4288 GCGATTGATTCGAAATATGGAATCGACCTCAGATATCAAGATTAAGAAAGTCTGTACATAT 4347  
1461 LeuTrpPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIleGly 1480  
4348 CTTTACTTGTATTTTCAATCAATCTTGGGTCTCTTCCTTCACCTGGAACCTGTTATATGT 4407  
1481 ValIleIleAspAsnPheAsnGluGlnLysLysLysPheGlyGlyGlnAspIlePheMet 1500  
4408 GTCATATATGATATTTTCAACGACGAGAAAAAAGTTTGGAGCTCAAGCAATCTTATG 4467  
1501 ThrGluGluGlnLysLysTrpTrpAsnAlaMetLysLysLeuLysSerLysLysProGln 1520  
4468 ACGAAGAACGAGAAATCTATATGCAATGAAAAAATTTAGAGTGCAGAAAAACCGCA 4527  
1521 LysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheValThrArg 1540  
4528 AAGCTATACCTGACCAAGAAACAAATTTCAAGAAAGGTCTTGTGCTGTACACAGA 4587  
1541 GlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMetVal 1560  
4588 CAGTTTGTACATACATCATATCTATCTATCTGTCTTAACATGATGATCATATGATG 4647  
1561 GluThrAspAspGlnSerGluTrpValThrThrIleLeuSerArgIleAsnLeuValPhe 1580  
4648 GAAACAGATACACAGATGATATGTGATACATCACTTTTGTTCACCCATCAATCTGTGTC 4707  
1581 IleValLeuPheThrGlyLysCysValLeuLysLeuIleSerLeuArgHisLysTrpPhe 1600  
4708 ATGTGCTATTTACTGAGAGGTGTGATCTGAATCAATCTCTACCCCATATATATTT 4767  
1601 ThrIleGlyTrpAsnIlePheAspPheValValIleLeuSerIleValGlyMetPhe 1620  
4768 ACCATTGATGAAATATTTTGTATTTGTGTGTCTCATTTCTTCATTTGATGATGTT 4827  
1621 LeuAlaGluLeuIleGluLysTrpPheValSerProThrLeuPheArgValIleArgLeu 1640  
4828 CTGCGAGCTGATAGAAAGTATTTCTGTGCCCCCTACCTGTTCCGAGTATCCGCTT 4887  
1641 AlaArgIleGlyArgGlyIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLeuLeu 1660  
4888 GCTAGGATTTGGCCAAATCTACGCTGATCAAAAGACCAAGGGGATCCGACCTGCTC 4947  
1661 PheAlaLeuMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuPheLeuVal 1680  
4948 TTGCTTGTAGATGCTCCCTTCCTGCTGTGTTAACTAGCCCTCACTCTTCTATGTC 5007  
1681 MetPheIleTrpAlaIlePheGlyMetSerAsnPheAlaTrpValLysArgValAlaGly 1700  
5008 ATGTTCAATACGCGCATCTTTGGGATGCCAATCTCCATGTGAAGAGGAAGTTGGG 5067  
1701 IleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPheGluIle 1720  
5068 ATGATGATACATGTTCAATTTGAGACCTTTGGCAACAGCATGATCTGCTTCCAAAT 5127  
1721 ThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIleLeuAsnSerLysProProAsp 1740  
5128 ACAACCTCTGCTGCTGGATGATGATCTGACACCCATCTCAACAGATACCCACCGAC 5187  
1741 CysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAspProSer 1760  
5188 TGTGACCTTAATAAGTTAAACCTCGAAGCGCATTAAGGAGAGCTGTGGGAACCATCT 5247  
1761 ValGlyIlePhePhePheValSerTrpIleIleIleSerPheLeuValValAsnMet 1780  
5248 GTTGGAAATTTTCTTTTGTGACATCATCATCATCTTCCCTGCTGTGTGTAACATG 5307  
1781 TyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGluProLeu 1800  
5308 TACATCGCGGATCTCGGAGAACTTCAAGTGTCTACTGAAGAAAGTGCAGACCTCTG 5367  
1801 SerGluAspAspPheGluMetPheTrpGlyValTrpGluLysPheAspProAspAlaThr 1820  
5368 AGTGAAGATACATTTGAGATGTTCTATGAGGTTGGAGAAAGTTGATCCGATGCAACT 5427  
1821 GlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaLeuGluInpProLeuAsn 1840  
5428 CAGTTCAATGAAATTTGAAATATATATCATTTTGCACCTGCTTGAACCGCCCTCAAT 5487  
1841 LeuProGluProAsnLysGluGlnLeuIleAlaMetAspLeuProMetValSerGlyAsp 1860  
5488 CTGCAACACCAACAAACCTCAGCTCATTGCAATGATTTGCCATGAGTGTAGTGATC 5547  
1861 ArgIleCysLeuAspIleLeuPheAlaPheThrLysArgValIleGlyLysGly 1880  
5548 CGGATCCACGCTGTGATATCTTATTTGCTTTTCAAAAGCGGCTTACGAGAGAGTGTGA 5607  
1881 GluMetAspAlaLeuArgIleGluMetGluGluArgPheMetAlaSerAsnProSerLys 1900



| Alignment Scores:                             |  |               |      |
|---|--|---------------|------|
| Pred. No.:                                    | 0  | Length:       | 8349 |
| Score:  | 9025.50  | Matches:      | 1759 |
| Percent Similarity:                           | 92.63%   | Conservative: | 113  |
| Best Local Similarity:                        | 87.04%   | Mismatches:   | 114  |
| Query Match:                                  | 86.81%   | Indels:       | 35   |
| Ds:   | 22   | Gaps:         | 13   |
| DS-09-930-871-12 (1-2009) x AAH55793 (1-8349) |  |               |      |
| QY  | 1 MetGluInThrValIleuValProProGlyProAspSerPheAsnPhetheThrArgGlu   | 20            |      |
| DB  | 106 ATGGCAGCGTGAAGTCGGTGGTCCGCCACGAGACTTCACAGCTTCGCTCTTTACACGGAA | 165           |      |
| QY  | 21 SerLeuAlaAlaIleGluArgArgIleAlaGluIuValAlaValAsnProLysProAsp   | 40            |      |
| DB  | 166 TCCCTGCTGCTATTGAAACAACGATTGCGAAGACGAAGCAAGCAACCCAAACAGAA     | 225           |      |
| QY  | 41 LysLysAsp---AspAspGluAsnGlyProLysProAsnSerAspLeuAlaGlyLys     | 59            |      |
| DB  | 226 CGCAAGATGAGAGATGATGAAAGAGGCCCAAGCCAAAGCTGACTGGAAGCAGAA       | 285           |      |
| QY  | 60 AsnLeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAsp  | 79            |      |
| DB  | 286 TCTCTTCATTTATTTATGAGAGACATTCCTCCAGATGAGTGCAGGCCCTGGAGAT      | 345           |      |
| QY  | 80 LeuAspProTyrTyrIleAsnLysLysThrPheIleValIleuAsnLysGlyLysAlaIle | 99            |      |
| DB  | 346 CTGGACCCCTCTATATCAATATAGAAACGTTTATGATATGATTAAGGAAGCAATC      | 405           |      |
| QY  | 100 PheArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLys | 119           |      |
| DB  | 406 TCTCATTCAGTGCACCCCTGCTTACATTTTAACTCCCTCAACCCCTATTAGAAA       | 465           |      |
| QY  | 120 IleAlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeu | 135           |      |
| DB  | 466 TTAGCTATTAAAGATTGGTGGTCAATCTTATCAATATGCAATATGTCACATTCCT      | 525           |      |
| QY  | 140 ThrAsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyr | 155           |      |
| DB  | 526 ACCAACCTGTATTTATATGACCATGATGACCTTCAGCTGGAAGAAAGATGTGACTAT    | 585           |      |
| QY  | 160 ThrPheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCys | 179           |      |
| DB  | 586 ACCTTTACAGCAATTATACCTTTGATTCATCTTTAAATATCTGCAGAGGGCTTTGT     | 645           |      |
| QY  | 180 LeuGluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThr | 199           |      |
| DB  | 646 TTAGAGATTTTCAATTTTTCAGGGATTCACAGGAATGGTGGATTTCACAGTCATTA     | 705           |      |
| QY  | 200 PheAlaTyrValThrGluPheValAspLeuLysAsnValSerAlaLeuArgThrPheArg | 219           |      |
| DB  | 706 TTTCGATATGTCAGACAGATTGTGTGACCTGGGCAATGTCTCAGCGTTGACAACTTGA   | 765           |      |
| QY  | 220 ValLeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAla | 239           |      |
| DB  | 766 GTTCTCCGAGCATGAAACAATTTCACTTCACAGGCTCGAAGACCATTTGGGGGCC      | 825           |      |
| QY  | 240 LeuIleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSer | 255           |      |
| DB  | 826 CTGAATCCAGTCAGAGAAACCTTTCTGATGTCTGATCTTGATCTTGCTGTCTAAGC     | 885           |      |
| QY  | 260 ValPheAlaLeuIleGlyLeuGluLeuPheMetCysLysAsnLysArgAsnLysIleGln | 279           |      |
| DB  | 886 GTGTTGGCGCTAATAGATTCAGATGTCTCACTGGGCAACCTCGAATAAATGTTTCCA    | 945           |      |
| QY  | 280 TrpProThrAsnAlaSerLeuGluGluIuHisSerIleGluLysAsnIleThr-----   | 297           |      |
| DB  | 946 TGGCCTCCAGATTAATTC-----TCCTTTAAATTAATATACACTCTCTTC           | 990           |      |
| QY  | 298 -----ValAsnTyrAsnGlyThrLeuIleAsnGluThrValPheGluPheAsp        | 313           |      |

Db 991 TTTAAACATTCATGGAGGGAATGCTACTTTCATAGACAGTGCATATTATAC 1050  
OY 314 TRPLYSERTYRILEGILNASPERARGYRHSITRYPHELEUGLUGIPHELEUSPALA 333  
OY 1051 TGGAGTGAATATATGAGATATAAAGCTCATTATTTTATAGAGGCGAATAATGCTG 1110  
OY 334 LEULEUCYSGLYASNSERSERASPALAGLYNCYSPROGLUGLYTYRNECCYSVALYS 353  
Db 1111 CTGCTTGGCCACACAGCTCAGATGCGCCAGTGTCTCGAAGAGATCATCTGTGTGAAG 1170  
OY 354 ALAGLYARGASPROASNTYRCLYTRHSPHEASFTHPHSETRPLAPHELEU 373  
Db 1171 GCTGTGAGAAACCCACATGCTGCTACAGAGCTTGACACCTTATGTTGGCCTTTTG 1230  
OY 374 SERLEUPHEARGLEUMETHRGLNASPHEPARGIUSASNULEUTYRGLNLEUTHREUARG 393  
Db 1231 TCCATTATTCGCTCATGCTCAGAGCTCTGGGAAAACCTTTATCAATGACACAGCT 1290  
OY 394 ALAALAGLYLSTHRTYRNETILEPHEVEALLEUVALILEPHELEUGLYSERPHELYR 413  
Db 1291 GCTGTGGGAAACGATCATGATATTTTGTGCTGCTCATTTTCTGGCTCATCTAT 1350  
OY 414 LEULIENASLEULILEUVALIAYALAMETALATYRGLUGLUGLNASGILNATHR 433  
Db 1351 CTAAATTAATTTATCTTGTGCTGTGCTGCTATGAGAGACAGATCAAGCCACA 1410  
OY 434 LEUGLUGLUALAGLUGLNASGILUALAGLUPHENGILNMETILEGILNLEULYS 453  
Db 1411 TTGGAGAGAGCTGACAGAGAGAGCTGAATTTACAGCAATGCTCAACAGTTGAAAAG 1470  
OY 454 GINGINGLUALAGLUGLNASGILUALATHRALATHRALASERGLNHSERARGLUPRO 473  
Db 1471 CAACAAGAGAAGACT---CAGCGGCGACGCGCCATGCTGTAATCAAGAGACTTC 1527  
OY 474 SERIALIAGLYARGLEU-----SERASPERSERSERGLNLSERILEUSER 490  
Db 1528 ACTGTGCTGCTGGATAGAGATTTTTCAGAGAGTCTTCACTACATCACTAAGTTGAG 1587  
OY 491 SERILYSERIALIAGLUGLARGASNARGARGLYLSARGLYSGILNYSGLUGLINSER 510  
Db 1588 TCCAAAAGTGAAGAGAGAGCTGAAAACAGAGAGAGAGAGAGAGAGAGAGAGAGCT 1647  
OY 511 GLYGLYGLUGLULASPSGLUPHENGILNYSERGLNLSERILEUSER 530  
Db 1648 GGAGAGAAG 1704  
OY 531 ARGGLYGLYSPHEARGPHESERTILEGILUGLYASNARGLEUTHRTYRGLNLSYASRTYR 550  
Db 1705 AGAAAAGGTTCCGTTTTCCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGATTTTCT 1764  
OY 551 SERPROHISGLINSERTILEUSERILEARGLYSERLEUPHESERPROARGASNSER 570  
Db 1765 TCTCCACACAGCTCTTACTAGACATCCGCTGCTCTCTCTCTCAAGACACAGAG 1824  
OY 571 ARGTRHSPHEUPHESERPHARGLYARGALILYSAPVALISERGLNLSANASPH 590  
Db 1825 AGGGCAGAGCTTTTCAAGCTTCAAGAGTGCAGAGAGAGAGAGAGAGAGAGAGAGAG 1884  
OY 591 ALASPSAPGLNHSERTRHSPHEGLUASPSAGLUSERTARGARGSPSERLEUPHEVAL 610  
Db 1885 GCTGATGATGAGCAGACAGCTTTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1944  
OY 611 PROARGHISGLIUGLARGARGASNSERASNULEUSERGLNHSERARGSERARG 630  
Db 1945 CCGCACAGACATGAG 2004  
OY 631 METLEUALIAYALPHEPROALASAGLYLSETHISERTHYVALSPCYASAGLYVAL 650  
Db 2005 GTGCTCCCATCTGCGCCATGAGATGGAGAGATGATAGCTGTGAGCTCATATGGTG 2064  
OY 651 VALISERLEUVALISGLYPROSERVALPROTHSERPROVALISGLNLEUTHREUARG 670  
Db 2065 GTCTCCCTGTGTGGGGGCTCTTACCTCATCATCT---GCTGGGAGCTGCTACAGAG 2121

OY 671 VALILEIILEASPLYSERPROALATHRASPSASAGLYTHTRHGLUTHRLIUMELARG 690  
Db 2122 -----GGCACACACTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2148  
OY 691 LYSARGARGSERSERPHEHISVALSERMETLASPHELEUGLUSPROSERGLNARG 710  
Db 2149 AAGAGAGCTGCTCAGTCTTATCATATGTTCCATGAGATTATTTGAGAGATCTTCAATCAAG 2208  
OY 711 GINARGALIMETSERILEASERILELEUTHRASNTHYVALISGLNUGLUGLUSER 730  
Db 2209 CAAGAGCATAGATATACAGATATTTGACCAACAGATGAGAGAGAGAGAGAGAGAGAG 2268  
OY 731 ARGGLNLSYSPROPCOSTYRTRYLSPHESERANILPHELEULIETRPASPCYS 750  
Db 2269 AGACAGAAATGCCACACAGCTGTGTAAATTTGCTAAATATGCTGTTGATTTGGCAGCTG 2328  
OY 751 SERPROTYRTRPLEULYSVALIYSHISVALIYASNULEUVALIMETASPPROPH 770  
Db 2329 TGTAAACATGCTTAAAGGTGAACACTGTGCACCTGCTGTATATGAGACCATTTGAT 2388  
OY 771 ASPLIUALIILETHRIECYSILEVALLEUASNTHRLEUPHEMETALIMETGLNHSIT 790  
Db 2389 GACCTGCGCATCAGCATCTGCATCTGTCTTAATNACCTCTTCATGCTATGAGAGACTAT 2448  
OY 791 PROMETHRASPHISPHESANASVALLEUTHRALVALISASNULEUVALPHETHRGLY 810  
Db 2449 CCCATGACGAGAGCTTCAAGAGTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2508  
OY 811 PHETHRILAGLIMETHEULYSILILEIILEAMETASPPROTYRTRYRPHENGILN 830  
Db 2509 TTCACAGCAGAAATGTTTTCAGAGATATTCATGATGATGATGATGATGATGATGATGAT 2568  
OY 831 GLYTRPASNILEPHEASPSGLYPHEILEVALTHRLEUSERLEUVALISGLUGLYLA 850  
Db 2569 GGCTGAAATATTTTATGATGCTTTATTTGAGAGCTTATGATGAGAGAGAGAGAGAGAG 2628  
OY 851 ASNVALISGLIYLEUSERVALLEUARGSERPHEARGLEUVALIPHELYSLEUAL 870  
Db 2629 AATGTGAAGAGATTTGACAGTCTCCGATCATCTCCGCTGCTGCTGCTGCTGCTGCTGCT 2688  
OY 871 LYSERTPRPROTHRIEUSNMETLEULIILEIILEGLYASNSERVALISGLIYAL 890  
Db 2689 AATCTTGGCCAACTGTAATATGCTAATTAATCATATGAGAGAGAGAGAGAGAGAGAG 2748  
OY 891 GLYASNULEUTHREUVALLEUALIILEIILEVALPHEILEPHEALVALISGLIYMETGL 910  
Db 2749 GGAACCTCAGCTTGTGATTTGGCATCATGCTTCTTATTTCTGTGTGTGTGTGTGTGT 2808  
OY 911 LEUPHEGLIYSERTYRTRYLSPASPCYSVALISGLYSLILEASERASPCYGLNLEUPRO 930  
Db 2809 CTCTTGTGAAGAGCTTCAAG 2868  
OY 931 ARGTRHISMETASNPHEPHEHISERPHLEULILEVALPHEARGVALILEUCYSGLY 950  
Db 2869 CGCTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2928  
OY 951 GLUTRPIILEGLUTHRETTTPASPCYMETGLIYVALISGLIYGLNIMETCYSLEUTH 970  
Db 2929 GAGTGATGAG 2988  
OY 971 VALPHEMETEVALMETVALILEGLYASNULEUVALIYLEUASNULEUPHELEUAL 990  
Db 2989 GCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3048  
OY 991 LEU\*\*\*SERSERPHESERALASPSANLEUALIATHRASPSASPSANGILUMETASN 1010  
Db 3049 CTTTGAGTCTCTTCAAGTCTTGAACATCTTGTGCGCACATGATATGATGATGATGATGAT 3108  
OY 1011 ASNLEUGLILILEALVALIYASPARGMETHSISGLIYVALIATYRVALIYASARGLYS 1030  
Db 3109 AATCTCAGATTTCTGTGGAGAGAGATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3168





Db 466 TTAGCTAATTAAGATTGGTGCATCTTCTTATTCATATATGCTCATTTATGTGCACGATTCTT 525  
 Oy 140 ThrAsnCyValIphemeThrMetSerAsnProProAspTrpThrIysAsnValGIuTyr 159  
 Db 526 ACCAACTGTGATTTATACACATGAGTAACCTCCAGCTGACAGCAAAATGTGGAGAT 585  
 Oy 160 ThrPheThrGIyleTyrThrPheGluSerLeuIleIleAlaArgGlyPheCys 179  
 Db 586 ACCTTACAGAAATTAATTAATCTTGAATCACTTATTAATAAATCTGCAAGGGGCTTTGT 645  
 Oy 180 LeuGluAspPheThrPheLeuArgAspProTrpAsnTrpIleAspPheThrValIleThr 199  
 Db 646 TTAGAAGATTTTCACATTTTACGGGATCCATGAAATGGTTGGATTTCACAGCTATTACT 705  
 Oy 200 PheAlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArg 219  
 Db 706 TTTCGATATGTGACAGAGTTTGTGGACCTGGCAATGTCTCAGCTTGAGAAATTCACA 765  
 Oy 220 ValLeuArgAlaLeuIysThrIleSerValIleProGlyLeuIysThrIleValGIuAla 239  
 Db 766 GTTCCGAGCATTTGAAACAATTCAGTCATTCAGGCTCGAAGACCATTTGTGGGGGCC 825  
 Oy 240 LeuIleGlnSerValIysIysLeuSerAspValMetIleLeuThrValIlePheCysLeuSer 259  
 Db 826 CTGATCCAGTACGTGAAGAGCTTCTGATGTCATGATCTTGACGTGTCTGTCTAAGC 885  
 Oy 260 ValPheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnIysCysIleGln 279  
 Db 886 GTGTTGGCGCTAATAGATTTGCAGTTGTTTCATGGGCAACCTACGAAATTAATGTTTGC 945  
 Oy 280 TrpProThrIleAsnAlaSerLeuGluIleHisSerIleGlyIysAsnIleThr----- 297  
 Db 946 TGGCCTCCAGATAATCTT-----TCTTTGAAATTAATTAATCACTTCTCTTC 990  
 Oy 298 -----ValAsnTyrAsnGlyThrIleLeuIleAsnGluThrValIlePheGluIleAsp 313  
 Db 991 TTTAACAATTCATTTGATGGAGGTGAGTACTACTTTCATATGACAGCATGATATTTAAC 1050  
 Oy 314 TrpIysSerTyrIleGlnIleAspSerArgTyrHisTyrPheLeuGluGluIlePheLeuAspAla 333  
 Db 1051 TGGGATGATATATATGATGATTAAGTACATCTTTATTTTATAGAGGGCAAAATGATGCT 1110  
 Oy 334 LeuLeuCyGlyAsnSerSerAspAlaGlyIleCysProGlyIleTyrMetCysValIys 353  
 Db 1111 CTGCTTTTGGCAACAGCTGATGATCCAGGCCAGCTCTCTGAAGATACATCTGTGTGAAG 1170  
 Oy 354 AlaGlyArgAsnProAsnTyrGlyTyrThrSerPheAspThrPheSerTrpAlaPheLeu 373  
 Db 1171 GCTGTGATAAACCCCACTATGTGCTACAGAGCTTTGACACCTTAAAGTTGGCCCTTTTGG 1230  
 Oy 374 SerLeuPheArgLeuMetThrGlnAspPheTrpGluAsnLeuTyrGluLeuThrLeuArg 393  
 Db 1231 TCCATATTTCCGTCTGATGATCTACACACTTCGTGGGAAAACCTTTATCAACTGACACTAGCT 1290  
 Oy 394 AlaAlaGlyIysThrTyrMetIlePhePheValLeuValIlePheLeuGlySerPheTyr 413  
 Db 1291 GCTGTGGGAAAACTACATGATATTTTGTGCTGATCTTCTGTGGGCTCAATTCAT 1350  
 Oy 414 LeuIleAsnLeuIleLeuAlaValIleAlaMetAlaTyrGluGluGlnAsnGlnAlaThr 433  
 Db 1351 CTAAATAATTTGATCTTGGCTGTGGTGGCCATGAGCCCTATGAGAAACAGATAGGCCACA 1410  
 Oy 434 LeuGluGluAlaGluGlnIysGluAlaGluPheGlnGlnMetIleGluGlnLeuIysIys 453  
 Db 1411 TTGGAGAAGGCTGACAGAGAACTGATTTTCAGAGATCTCTGACACAGTTGAAAAAG 1470  
 Oy 454 GlnGlnGlnAlaAlaGlnAlaAlaThrAlaThrAlaSerGluHisSerArgGluPro 473  
 Db 1471 CACACAGAGAAAGCT---CAGCGGCGAGCTGACCGGCATCTGTCATCAAGACACTTC 1527  
 Oy 474 SerAlaAlaGlyArgLeu-----SerAspSerSerSerGluAlaSerIysLeuSer 490  
 Db 1528 AGTGTGCTGTGGATGAGAGATTTTTCAGAGAGTCTTCTAGTACATCACTAAGTTGAGC 1587  
 Oy 491 SerIysSerAlaIysGluArgArgAsnArgArgIysArgIysGluGlnIleSer 510  
 Db 1588 TCCAAAAGTGAAGAAAGAGCTGAGAAAGAGAAAGAAAGAAAGAAAGAAAGAGCT 1647  
 Oy 511 GlyGlyGluGluIleAspGluAspGluPheGlnIysSerGlnSerGluAspSerIleArg 530  
 Db 1648 GGAGAGAGAGAGAGAAAT---GACAGAGTCTTAATTCGAATCTGACACAGCATMAA 1704  
 Oy 531 ArgIysGlyPheArgPheSerIleGluIleAsnArgLeuThrTyrGluIysArgTyrSer 550  
 Db 1705 AGAAAGAGTTCGTTTCTTCTGAGAGAGAGAGCTGACATATGAAAGAGATTTCT 1764  
 Oy 551 SerProHisGlnSerLeuLeuSerIleArgGlySerLeuPheSerProArgArgAsnSer 570  
 Db 1765 TCTCCACACACATCTCTATGAGCANTCGTGCTCCCTTTCTCTCCAGAGCAACAT 1824  
 Oy 571 ArgThrSerLeuPheSerPheArgGlyArgAlaIysAspValGlySerGluAsnAspPhe 590  
 Db 1825 AGGCGAGAGCTTTTTCAGCTTCAGAGCTCGAGCAAAAGACATTTGGCTGAGATGACTTT 1884  
 Oy 591 AlaAspAspGlnHisSerThrPheGluAspAsnGluSerArgArgAspSerLeuPheVal 610  
 Db 1885 GCTGATGATGACACACACCTTTGAGCAATGACAGCCGAGAGACTCTGTTCGTG 1944  
 Oy 611 ProArgArgHisGlyGluArgArgAsnSerAsnLeuSerGluThrSerArgSerArg 630  
 Db 1945 CGGCACAGACATGAGAAAGAGGGCCACACACATGTCAGCCAGGCCGCTGCTCCAG 2004  
 Oy 631 MetLeuAlaValIlePheProAlaAsnGlyIysMetHisSerThrValAspIysAsnGlyVal 650  
 Db 2005 GTGCTCCCATCTCCCTCGCATGATGGAGAAAGCATAGCGCTGTGAGCATAGCTGTG 2064  
 Oy 651 ValSerLeuValGlyGlyProSerValProThrSerProValGlyGlnLeuPheGlu 670  
 Db 2065 GTCTCCCTGTGGGGGCTTCTTACCTCCACATCT---GCTGGGAGCTCTCCACAGAG 2121  
 Oy 671 ValIleIleAspIysProAlaThrAspAsnGlyThrThrGluGluThrGluMetArg 690  
 Db 2122 -----GGCACAACTACTGAAACAGAAATMAA 2148  
 Oy 691 LysArgArgSerSerSerPheHisValSerMetAspPheLeuGluAspProSerGlnArg 710  
 Db 2149 AAGAGCGGTGCATCTTATCATGTTCCATGATTTATGGAAATCTCATCATCAAG 2208  
 Oy 711 GlnArgAlaMetSerIleAlaSerIleLeuThrAsnThrValGluGluLeuGluIleSer 730  
 Db 2209 CAAAGACATGATGATATGACATATTTGACCAACACCATGGAAGAACTTGAAGATCC 2268  
 Oy 731 ArgGlnIysCysProProCysTrpTyrIysPheSerAsnIlePheLeuIleTrpAspCys 750  
 Db 2269 AGCACAATAATGCCCAACATGCTGTGATTAATTTGCAATATATGTTGATTTGGAGCTGT 2328  
 Oy 751 SerProTyrTrpLeuIysValIysHisValIleAsnLeuValIleMetAspProPheVal 770  
 Db 2329 TGTAAACCATGTTAAAGTGAACACCTGTGCAACCTGTGTATGACCACTTTGTT 2388  
 Oy 771 AspLeuAlaIleThrIleCysIleValIleAsnThrLeuPheMetAlaMetGluHisTyr 790  
 Db 2389 GACCTGGCATCAACATGTCATGCTTTAAATACCTCTTCATGGCTATGGAGCACTAT 2448  
 Oy 791 PrometThrAspHisPheAsnAsnValIleThrValGIuAsnLeuValPheThrGlyIle 810  
 Db 2449 CCATGACGAGAGAGATTCAGAGTGAAGTGAAGTCTTTGGAACCTGTGCTTCACAGGAGCT 2508  
 Oy 811 PheThrAlaGluMetPheLeuIysIleIleAlaMetAspProTyrTyrThrPheGlnGlu 830  
 Db 2509 TTCACAGCAGAAATGTTTTCAGATTAATGCTCATGATCCATATTAATTAATTAATTA 2568  
 Oy 831 GlyTrpAsnIlePheAspGlyPheIleValIleLeuSerLeuValGIuLeuGlyLeuAla 850  
 Db 2569 GGCTGCAATATTTTATGATGTTTATTTATGAGCTTATGATGAACTGTGTTGGCA 2628

|    |      |   |      |
|----|------|---|------|
| QY | 851  | ASnValGluLeuSerValLeuAqSerPheAqGleuLeuAqValPheLysLeuA           | 870  |
| Db | 2629 | AAATGGAAAGGATGTCAGAGTTCGCATATATCCGGCTGCTCCGAGTTTCAAGTTGGCA      | 2688 |
| QY | 871  | LysSerTrpProThrLeuAsnMetLeuIleLysIleIleGlyAspSerValGlyAlaLeu    | 890  |
| Db | 2689 | AAATCTTGGCCAACTCTAAATATGCAATTAAGATGATTCGGCAATTCGTGTGGGGGCTCTA   | 2748 |
| QY | 891  | GlyAsnLeuThrLeuValLeuAlaIleIleValPheIlePheAlaValAlaGlyMetGln    | 910  |
| Db | 2749 | GGAACCTCACCTGGTATATGGCCATCATCGCTTCAATTTTGGCTGTGTGGCATCGAC       | 2808 |
| QY | 911  | LeuPheGlyLysSerTrpLysAspCysValLysLysIleAlaSerAspCysGlnLeuPro    | 930  |
| Db | 2809 | CTCTTTTGTTAAGAGCTACCAAGAAATGTGTCTCAAGATTTCCAATGATTTGAACTCCCA    | 2868 |
| QY | 931  | ArgTrpHisMetAsnAspPhePheHisSerPheLeuIleValPheArgValLeuCysGly    | 950  |
| Db | 2869 | CGCTGGACACATGCATGACTTTTCCACTCTCTTCGATCGTGTTCGGGTCTGTGGGA        | 2928 |
| QY | 951  | GluTrpIleGluThrMetTrpAspCysMetGluValAlaGlyGlnAlaMetCysLeuThr    | 970  |
| Db | 2929 | GAGTGATAGAGACCATGTGGAGCTGTATGGAGGTGCGGGCAAAACATGTGCCTTACT       | 2988 |
| QY | 971  | ValPheMetLeuValMetValIleGlyAsnLeuValValLeuAsnLeuPheLeuAlaLeu    | 990  |
| Db | 2989 | GCTCTTCATGATGTGCATGATGTGAATTCAGATGGTTCTGCAACTCTGTTGGCCCTGG      | 3048 |
| QY | 991  | Leu***SerSerPheSerAlaAspAsnLeuAlaIleAlaThrAspAspAspAsnGluMetAsn | 1010 |
| Db | 3049 | CTTTTGAGTTCTCTCACTTCTGTGCATATCTTGCTGCCACTGATGATGATACCAATGAT     | 3108 |
| QY | 1011 | AsnLeuGlnIleAlaValAspArgMetHisLysGlyAlaIleAlaTrpValLysArgLysIle | 1030 |
| Db | 3109 | AAATCCAGATGTGCTGTGGAGAGATGCAGAAAGAAATCGAATTTGTTAAAAAGAAAAATA    | 3168 |
| QY | 1031 | TyrGluPheIleGlnGlnSerPheIleArgLysGlnLysIleLeuAspGluIleLysPro    | 1050 |
| Db | 3169 | CGTAAATTTTATTCGAAAGAGCTTTGTTAGGAAGCAGAAAGCTTTTGATGAATTAATAACCG  | 3228 |
| QY | 1051 | LeuAspAspLeuAsnAsnLysLysAspSerCysMetSerAsnHisThr***GluIle       | 1069 |
| Db | 3229 | CTTAGAGTCTTAATATATATTAATAAAGACAGCTGATTTCCACACATACCACTACGATATA   | 3288 |
| QY | 1070 | GlyLysAspLeuAspTrpLeuLysAspValAsnGlyThrThrSerGlyIleGlyThrGly    | 1089 |
| Db | 3289 | GGCAAGACCGTCATATATCTCAAAAGACGGAATAGCACTAGTAGTGGCATA-----GGC     | 3342 |
| QY | 1090 | SerSerValGluLysTrpIleIleAspGluSerAspTrpMetSerPheIleAsnAsnPro    | 1109 |
| Db | 3343 | AGCAGTGTAGAAAAATATGTGCTGTGATGAAAGATTAACATCTCAATTAATAACAACCTT    | 3402 |
| QY | 1110 | SerLeuThrValThrValProIleAlaValGlyGlnSerAspPheGlnAsnLeuAsnThr    | 1129 |
| Db | 3403 | AGCCTCACTGTAGACAGTACCAATGTGTTGGAGATCTGACTTTGAAAAATTAATATACT     | 3462 |
| QY | 1130 | GluAspPheSerSerGluSerAspLeuGlnGluSerLysGlnLysLeuAsnGluSerSer    | 1149 |
| Db | 3463 | GAAAGATTACACACCGAGTCAGATATATGAGGAAGAAAGAAAGAAACACTAAAT---GCACCT | 3519 |
| QY | 1150 | SerSerSerGluLysSerThrValAspIleGlyAlaProValGlu---GluGlnProVal    | 1168 |
| Db | 3520 | AGTTCACTCTGAAAGCACACAGGTGTGATATGTGAGCTCCCGCGAGGAGAAACAGCTGAC    | 3579 |
| QY | 1169 | ValGluProGluGluThrLeuGluProGluAlaCysPheThrGluGlyCysValGlnArg    | 1188 |
| Db | 3580 | GTTGAACTGTAGGAATCCCTTGAACCTGGAAGCCTGTTTATACGAAGACTGTGTACGGAG    | 3639 |
| QY | 1189 | PheLysCysCysGlnIleAsnValGluGluGlyArgGlyLysGlnTrpTrpAsnLeuArg    | 1208 |
| Db | 3640 | TTCACAGCTTCTTCGATATACCATATGAAGAAGAAAGAAACCTGCTGCGGAATTTGGAG     | 3699 |
| QY | 1209 | ArgThrCysPheArgIleValGluHisAsnTrpPheGluThrPheIleValPheMetIle    | 1228 |

|    |      |  |      |
|----|------|--|------|
| Db | 3700 | AAACATGCTATAGAGTAAGTGGAGCACAATGGTTCGAAACCTTCATTGTCTCATGATT       | 3759 |
| QY | 1229 | LeuLeuSerSerGlyAlaLeuAlaPheGluAspIleTyrlleAspGlnArgLysThrIle     | 1248 |
| Db | 3760 | CTGCTGAGACAGTGGGCGCTCTGGCCCTTGGAAAGATATATACATTGAGCAGCGAAACCAATT  | 3819 |
| QY | 1249 | LysThrMetLeuGluTyrAlaAspLysValPheThrTyrIlePheHelleuGluMetLeu     | 1268 |
| Db | 3820 | AAGACCATGTAGAAATGTGTGACAGAGTTCACCTCAATATTCATCTCGAAATVGTG         | 3879 |
| QY | 1269 | LeuLysTrpValAlaTyrGlyTyrGlnThrTyrPheThrAsnAlaTrpCysTrpLeuAsp     | 1288 |
| Db | 3880 | CTAAAGTGGGTGCATATGGTTTTCAAAGTATATTATACCAATGCCGCGTGGCTATAC        | 3939 |
| QY | 1289 | PheLeuIleValAspValSerLeuValSerLeuThrAlaAsnAlaLeuGlyTyrSerGlu     | 1308 |
| Db | 3940 | TTCCGATTTGTGATGTCACGTGAGTGTAGCTTAACGTCAAAATGCTGGGTATCTACAA       | 3999 |
| QY | 1309 | LeuGlyAlaIleLysSerLeuAlaGlyThrLeuArgAlaLeuArgProLeuArgAlaLeuSer  | 1328 |
| Db | 4000 | CTTGCTGGCAATCAAAATCCCTCAGAACCTTAAGAGCTCTAGAGCCATGTAGACCTTTGGCC   | 4059 |
| QY | 1329 | ArgPheGluGlyMetArgValAlaValAsnAlaLeuLeuGlyValAlaIleProSerIleMet  | 1348 |
| Db | 4060 | CGGTTTGAGGAAGAAAGAGGCGCTTTGTAAATGCTCTTTTGGAGCCATTCCATCTATCATG    | 4119 |
| QY | 1349 | AsnValLeuLeuValCysLeuIlePheTrpLeuIlePheSerIleMetGlyValAsnLeu     | 1368 |
| Db | 4120 | AATGACTCTTGCTGTCTGCATCTTTGGCTAAATTCAGATACATGGAGATGAAATGC         | 4179 |
| QY | 1369 | PheAlaGlyLysPheTyrHisCysIleAsnThrThrThrGlyAspArgPheAspIleGlu     | 1388 |
| Db | 4180 | TTTCTCTGGCAAGTTTTCACATTTGATTAATTAATACACCACGTGAGAGATCTTTGATTAAGC  | 4239 |
| QY | 1389 | AspValAsnAsnHisThrAspCysLeuLysLeuIleGluArgAsnGluThrAlaTrpArg     | 1408 |
| Db | 4240 | GTGGTCACCAACTACAGTAGGTGAAAGCTCTCATTTAGAGCATATAAATCTCCAGGTGG      | 4299 |
| QY | 1409 | LysAsnValLysValAsnPheAspAsnValGlyPheGlyTyrLeuSerLeuLeuGlnVal     | 1428 |
| Db | 4300 | AAAAATGGAAGTAATTAATTTGATTAACGTAGAGCTTGGATATCTCTCTACTTCACAGA      | 4359 |
| QY | 1429 | AlaThrPheLysGlyTyrPheMetAspIleMetCtyrAlaAlaValAspSerArgAsnValGlu | 1448 |
| Db | 4360 | GCCAGCTTAAAGGATGATGATGATATATATATACGACGCTTGATTCACGAATGTAGAA       | 4419 |
| QY | 1449 | LeuGlnProLysTyrGluGlnSerLeuTyrMetTyrLeuTyrPheAlaIlePheIleIle     | 1468 |
| Db | 4420 | TTACACACCAAGTATGAAGACAAACCTTCATCATCTTATATTTATATTTTCATCTTTATAT    | 4479 |
| QY | 1469 | PheGlySerPhePheThrLeuAsnLeuPheIleGlyValIleLeuAspAsnPheAsnGln     | 1488 |
| Db | 4480 | TTTGGTTCATCTTACTTACCTTGAATCTTTTCATTTGGTGCATCATATATCAACTCAACCA    | 4539 |
| QY | 1489 | GlnLysLysLysPheGlyGlyGlnAspIlePheMetThrGluGlnLysLysTyrTyr        | 1508 |
| Db | 4540 | CAGAAAGAAAGATTGGAGCTGACAGATTTTATGTACAGAAAGAAAGAAATATATAC         | 4599 |
| QY | 1509 | AsnAlaMetLysLysLeuGlySerLysLysProGlnLysProIleProArgProGlyAsn     | 1528 |
| Db | 4600 | AATGCAATGAAGAAAACCTGGCTCAAAACCAACCAAAACCCATTCCTGACCTGCTAAC       | 4659 |
| QY | 1529 | LysPheGlnGlyMetValPheAspPheValThrArgGlnValPheAspIleSerIleMet     | 1548 |
| Db | 4660 | AAATTCCAAGAAATGCTCTTGAATTTTGTAAACCAAAACATCTTATATATGACATCATG      | 4719 |
| QY | 1549 | IleLeuIleCysLeuAsnMetValThrMetMetValGluThrAspAspGlnSerGlyTyr     | 1568 |
| Db | 4720 | ATCCCATCTCGCTTAACATGTCACCATGATGTGTGAAACCATGACACAGAGTCAAGA        | 4779 |
| QY | 1569 | ValThrThrIleLeuSerArgIleAsnLeuValPheIleValLeuPheThrGlyGlnGly     | 1588 |





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|------------------------|---------|---------------|------|
| Score:                 | 8664.00 | Matches:      | 1686 |
| Percent Similarity:    | 90.28%  | Conservative: | 134  |
| Best Local Similarity: | 83.63%  | Mismatches:   | 166  |
| Query Match:           | 83.33%  | Indels:       | 30   |
| DB:                    | 24      | Gaps:         | 12   |

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|    |      |   |      |
|----|------|---|------|
| QY | 1    | MeGlnGlnThrValLeuValProProGlyProAsnSerPheAsnPhePheThrArgGlu     | 20   |
| Db | 472  | ATGGACACGAGCAGCTGTGGTACCCCGAGAGCTGAAAGCTTCGCCCTTTTACTACGAGA     | 531  |
| QY | 21   | SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp    | 40   |
| Db | 532  | TCTGTCTGCTGCTATGCGAAAGAAAGCTGCTGAGAAAGAAAGCCAAAGACCCAAAAGAGA    | 591  |
| QY | 41   | LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuAlaGlyLysAsn       | 60   |
| Db | 592  | CAGATATATGATGATGAGAAACAAACCAAGCCAAATAGACGCTTGGAAGCGGAAGAAC      | 651  |
| QY | 61   | LeuProhelleIleArgIleAspIleProProGluMetValSerGluProLeuGluAspLeu  | 80   |
| Db | 652  | CTTCACATTATTTATGAGAGCATCTCTCCAGATAGTGTCTGAGACCCCTGTGAGAGACTG    | 711  |
| QY | 81   | AspProIleArgIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe    | 100  |
| Db | 712  | GATCCGCTACATATTCATAATAGAAACTTTTATATGTAATGAAATAAAGAAAGCAATTTTC   | 771  |
| QY | 101  | ArgPheSerAlaThrSerAlaLeuArgIleLeuThrProPheAsnProLeuArgLysIle    | 120  |
| Db | 772  | CGATTCAGTGCACACCTCGCTGCTGTATTTTAACTCCACTAAACCCGTGTAGAGAAATT     | 831  |
| QY | 121  | AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr    | 140  |
| Db | 832  | GCTATCAAGATTTTGGTACACTCTTATATTCAGACATGCTTATCATGTGACATATTTTGACC  | 891  |
| QY | 141  | AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluThrThr    | 160  |
| Db | 892  | AACGTGTATTTATTTAGACCTTGAGCAACCCCTCGACTGGACAAAGATGTGAGTACACA     | 951  |
| QY | 161  | PheThrGlyIleIleArgThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu | 180  |
| Db | 952  | TTTCACTGGAACTATACCTTTGAGTACCTTAAATAAATCTTGGAAGAGGGTTTGGCTTAA    | 1011 |
| QY | 181  | GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe    | 200  |
| Db | 1012 | GAAATTTTACGTTTCTTCTGCTGATCCATGGAACGTGCTGATTTGAGTGTCACTTGTATG    | 1071 |
| QY | 201  | AlaTrpValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal    | 220  |
| Db | 1072 | GCATATGTGACAGAGTTTGTGGACAGTGGGCAATGTCTCAGCTTGAGAAACATTCAGAGTT   | 1131 |
| QY | 221  | LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyValLeu    | 240  |
| Db | 1132 | CTCGGACACGAGAAACAAATTTAGTCATTCACAGGTTTAAACCACTGTGGGGCCCTG       | 1191 |
| QY | 241  | IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal    | 260  |
| Db | 1192 | ATCCAGTCGGTAAAGAAAGCTTTGTATGTATGATGATGATCTGACGTCTTGTCTGAGCGTG   | 1251 |
| QY | 261  | PheAlaLeuIleGlyLeuGluLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp    | 280  |
| Db | 1252 | TTTGTCTCTCATTTGGGCGCAGCTGTTCAATGGGCAATCTGGAGAAATAATGTTTGGACATGG | 1311 |
| QY | 281  | ProProThrAsnAlaSerLeuGluGluHisSerIleGluLys---AsnIleThrValAsn    | 299  |
| Db | 1312 | CCCCAAGCGATTTCTGCTTTTGAACCAACACACTTCTCTACTTTAAATGGCCAAATGGAT    | 1371 |
| QY | 300  | TyrAsnGlyIleLeuIleAsnGluThrValPheGluPheAspTrpLysSerTrpIleGln    | 319  |
| Db | 1372 | TCAATATGGACATTTGTTATATGTAACAATGAGACACTTTAACTGGAGAAGATTTACATTGGA | 1431 |
| QY | 320  | AspSerArgTrpHisIleArgPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSer | 339  |

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|----|------|---|------|
| Db | 1432 | GATGACGTCACCTTTATGTTTGGAATGGGCAAAAAGACCCCTTTACTGTGTGAAATGCC     | 1491 |
| Qy | 340  | SerAspAlaGlyIncysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsn     | 359  |
| Db | 1492 | TCAATGTCAGAGCCAGTGTCCAGAAAGATACATCTGTGTAAAGGTGTGCAACCCCAAC      | 1551 |
| Qy | 360  | TyrGlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMet    | 379  |
| Db | 1552 | TATGGCTACACAAACCTTTGACACCTTTAGCTGGGCTTCTCTCTATTTGTGACTCATG      | 1611 |
| Qy | 380  | ThrGlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaGlyLysThrTyr       | 399  |
| Db | 1612 | ACTCAAGACRATTTGGGAAAATCTTTACAGTTACATTTACGTGTCTGTGGAAAAACATAC    | 1671 |
| Qy | 400  | MetIlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeu    | 419  |
| Db | 1672 | ATGATATTTTGTTCGCGATTTCTTCTGGGCTCATTTTATTTGCTGAATTTGATTCCTG      | 1733 |
| Qy | 420  | AlaValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGln    | 439  |
| Db | 1732 | GCTGTGGTGGCCATGGCCCTTATGTAGAGACAAACAGCCACCTGTGAAGAACACAAACA     | 1791 |
| Qy | 440  | LysGluAlaGluIlePheGlnMetIleGluGlnLeuLysGlnGlnGluAlaGln          | 459  |
| Db | 1792 | AAAGAGGCCGATTTACGAGATGCTCGAAGACCTTAAAGAACAGAACAGAACACTCAG       | 1851 |
| Qy | 460  | GlnAlaAlaThrAlaThrAlaSerGlnLysSerArgGluProSerAlaAla             | 476  |
| Db | 1852 | -----GCAGTGGCGGACGATCAGCGCTGTCAAGAGATTTCACTGAGTACGTAGTGGGTTA    | 1905 |
| Qy | 477  | GlyArgLeuSerAspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGlu    | 496  |
| Db | 1906 | GGAAAGCTGTGGAAAGTCTTCTCAGAAAGCATCAAAAGTTAGTCCAAAGCTCTAAAGAA     | 1965 |
| Qy | 497  | ArgArgAsnArgArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAsp    | 516  |
| Db | 1966 | TGGAGGAACCGGAGGAAAGAAAGAACAGACAGAGACACCTTGAAAGGAAACAAAGGA       | 2025 |
| Qy | 517  | Glu---AspGluPheGlnLysSerGluLysSerGlnAspSerIleArgArgLysGlyPheArg | 535  |
| Db | 2026 | GAGAGAGACACCTTTCCCAATCCGATCTGGAAGACAGCGGTCAAAAGAACAGCTTCCT      | 2085 |
| Qy | 536  | PheSerIleGluGlnLysAsnArgLeuThrTyrGluLysArgTyrSerSerProHISGlnSer | 555  |
| Db | 2086 | TTCTCCATGAGTGAAGAAACACATGACACAGCAAGAAAAATTTCTGCTCCCTCATCAGTCT   | 2145 |
| Qy | 556  | LeuLeuSerIleArgGlySerLeuPheSerProArgArgSerSerTrpHisSerLeuPhe    | 575  |
| Db | 2146 | CTCTGACTATCCGTGGCTCCCTGTTTCCCAAGAGCGCAATGCAAAACAGCAATTTTC       | 2205 |
| Qy | 576  | SerPheArgGlyAlaGlnAlaLysAspValGlySerGlnAsnAspPheAlaAspAspGlnHis | 595  |
| Db | 2206 | AGTTCCACAGAGTCGGCCAAAGAGATCTGCATCTGAAAGATGACTTCTGATGTGACAC      | 2265 |
| Qy | 596  | SerThrPheGluAspAsnGluSerArgArgArgAspSerLeuPheValProArgArgHisGly | 615  |
| Db | 2266 | AGCACATTTGAAGACGGGGAAGAGAGAGAGATCTACTGTTGTGCTGCCGACAGACTGGA     | 2325 |
| Qy | 616  | GluArgArgAsnSerAsnLeuSerGlnThrSerArgSerSerTrpMetLeuAlaPhe       | 635  |
| Db | 2326 | GAGCAGCCCAACACTTAACGTTAGTCAGGCGCAATGTCATCCAGATGGGTGGCAGGGCTT    | 2385 |
| Qy | 636  | ProAlaAsnGlyLysMetHisSerThrValAspCysAsnGlyValAlaSerLeuValGly    | 655  |
| Db | 2386 | CCAGCAAAATGGGAAGATGCAACAGACAGCTGTGATTTGCAATGTGTGTGTTCTTCTGTGGGT | 2445 |
| Qy | 656  | GlyProSerValProThrSerProValGlyGlnLeuLeuProGluValIleIleAspLys    | 675  |
| Db | 2446 | GGACCTTACGCTTACAGTCAACCTACCTACGCAACACTTCCCCAGAG-----            | 2490 |
| Qy | 676  | ProAlaThrAspAspAsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSer    | 695  |



QY 1414 AsnPhespaSnValGlyPheGlyTyrLeuSerLeuLeuGlnValAlaThrPheGly 1433  
 |||||  
 DB 4666 AACCTTGATATATGTCGGCGCTGATCTTGCACCTTCACCTGCACATTTAAAGGC 4725  
 QY 1434 TrpMetAspIleMetTyrAlaAlaValAspSerArgAsnValGluLeuGlnProLysTyr 1453  
 |||||  
 DB 4726 TGGATGATATTTATGATGACGCTGTGATTCACGAGATTTAACTTCGCTGATAT 4785  
 QY 1454 GluGluSerLeuTyrMetTyrLeuTyrPheValIlePheIleIlePheGlySerPhe 1473  
 |||||  
 DB 4786 GAAGAATAATCTGATACATGATTTATACCTTTGATCATCTTTATCATCTTGGGTCATCTTC 4845  
 QY 1474 ThrLeuAsnLeuPheIleGlyValIleIleAspAsnPhespaSnGlnGlnLysLysPhe 1493  
 |||||  
 DB 4846 ACTCTGATCTATCTATCTGTCATCATGATACATGATACCTCAACAGAGAAAGAGATT 4905  
 QY 1494 GlyGluGlnAspIlePheMetThrGluGlnGlnLysLysTyrTyrAsnAlaMetLysLys 1513  
 |||||  
 DB 4906 GGGAGTCACACATCTTTATGACAGAGACAGAGAAATAATTTACATGCAATGAGAGAA 4965  
 QY 1514 LeuGlySerLysLysProGlnLysProIleProArgProGlyAsnLysPheGlnGlyMet 1533  
 |||||  
 DB 4966 CTGGATTCACAGAAACCTCAGAAACCATACCTGCGCCACAGAAACAAATTCAGAGATG 5025  
 QY 1534 ValPheAspPheValThrArgGlnValPheAspIleSerIleMetIleLeuIleCysLeu 1553  
 |||||  
 DB 5026 GCTTTGATTTTGTAAACACAGACAGCTTTGATATCAGATCATGATGATCCCATCTGCTCT 5085  
 QY 1554 AsnMetValThrMetMetValGluThrAspAspGlnSerIleLysTyrValThrThrIleLeu 1573  
 |||||  
 DB 5086 AACATGCTACACATGATGAGGAGAGATGACAGGAGCAATATACATGACCTGATTTTG 5145  
 QY 1574 SerArgIleAsnLeuValPheIleValIleLeuPheThrGlyGluCysValIleLysLeuIle 1593  
 |||||  
 DB 5146 TCCCGGATCAACCTAGTGTTCATTTGCTCTTCACCTGAGAAATTTGCGTGAAGCTGCT 5205  
 QY 1594 SerLeuArgIleTyrTyrPheThrIleGlyTyrAsnIlePheAspPheValValIle 1613  
 |||||  
 DB 5206 TCCCTCAGACACATCACTTCACTATGAGCTGAGAACATCTTGTGAGTGGTGCTGAT 5265  
 QY 1614 LeuSerIleValGlyMetPheLeuAlaGluLeuIleGluLysTyrPheValSerProThr 1633  
 |||||  
 DB 5266 CTCTCCATTTAGATGATTTTCTGCTGCTGACATGATGAGAAAGATTTGCTGCTCCCTACC 5325  
 QY 1634 LeuPheArgValIleArgLeuAlaArgIleGlyArgIleLeuArgLeuIleLysGlyAla 1653  
 |||||  
 DB 5326 TTGTTCGAGATGATCCGCTCTGCGAGATTTGGCGAATCTACGCTGATCAAGAGAGCA 5385  
 QY 1654 LysGlyIleArgThrLeuLeuPheAlaLeuMetLeuSerLeuProAlaLeuPheAsnIle 1673  
 |||||  
 DB 5386 AAGGGGATCCGACAGGCTGCTTGTGATGATGATGATGATGATGATGATGATGATGATGAT 5445  
 QY 1674 GlyLeuLeuLeuPheLeuValMetPheIleTyrAlaIlePheGlyMetSerAspPheAla 1693  
 |||||  
 DB 5446 GGCTCTCTGCTCTCTGCGGATGATTTATCATGACATCTTGGAGATCCACATTTGCC 5505  
 QY 1694 TyrValLysArgGluValGlyIleAspAspMetPheAsnPheGluThrPheGlyAsnSer 1713  
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 DB 5506 TATGTTAAAGAGAGCTGGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5565  
 QY 1714 MetIleCysLeuPheGlnIleThrThrSerAlaGlyTyrAspGlyLeuLeuAlaProIle 1733  
 |||||  
 DB 5566 ATGATCTGCTGTTGCCAAATACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5625  
 QY 1734 LeuAsnSerLysProProAspCysAspProAsnLysValAsnProGlySerSerValLys 1753  
 |||||  
 DB 5626 CTATATGATGACACACCGAGCTGACCTGACCAATTCACCTGCGAGCTGATGATG 5685  
 QY 1754 GlyAspCysGlyAsnProSerValGlyIlePhePhePheValSerTyrIleIleIleSer 1773  
 |||||  
 DB 5686 GGAGACCGTGGGAGCCATCTGTTGGGATTTCTTTTGTGCACTTACATCATCATATGCC 5745  
 QY 1774 PheLeuValValAlaAsnMetTyrIleAlaValIleLeuGluAsnPheSerValAlaThr 1793  
 |||||

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DB 5746 TTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5805  
 QY 1794 GluGluSerAlaGluProLeuSerGluAspAspPheGluMetPheTyrGluValTyrGlu 1813  
 |||||  
 DB 5806 GAAGAAGTGCAGAGCCCGGATGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 5865  
 QY 1814 LysPheAspProAspAlaThrGlnPheMetGluPheGluLysLeuSerGlnPheAlaAla 1833  
 |||||  
 DB 5866 AACCTTGATCCCATGCGAGCCAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 5925  
 QY 1834 AlaLeuGluProProLeuAsnLeuProGlnProAsnLysLeuIleLeuIleAlaMetAsp 1853  
 |||||  
 DB 5926 GGCTGATGATCTCTCTCTCATAGCAAAACCCAGCAAAAGTCCAGCTTATTTGCCATGAT 5985  
 QY 1854 LeuProMetValSerGlyAspArgGlnIleCysLeuAspIleLeuPheAlaPheThrLys 1873  
 |||||  
 DB 5986 CTGCGCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6045  
 QY 1874 ArgValLeuGluSerGlyLysLeuMetAspAlaLeuArgIleGlnMetGluGluValGly 1893  
 |||||  
 DB 6046 CGTGTGTTTGTGAGAGTGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 6105  
 QY 1894 MetAlaSerAsnProSerLysValSerTyrGlnProIleThrThrThrLeuLysArgLys 1913  
 |||||  
 DB 6106 ATGGCATCAAAACCCCTCCAAAGCTCTTATGACCTATTTACAAACCTTTGAAACGTAA 6165  
 QY 1914 GlnGluGluValSerAlaValIleIleGlnArgAlaTyrArgThrIleLeuLysArg 1933  
 |||||  
 DB 6166 CAGAGAGAGTGTCTGCGGCTATCATTCACGATATTCAGATGATGATGATGATGATGATGAT 6225  
 QY 1934 ThrValLysGlnAlaSerPheThrTyrAsnLysAsnLysIleLysGlyAlaAsnLeu 1953  
 |||||  
 DB 6226 AGGTTAAATAATATATCAATACTATATCAAAAGAGCAATTTAAAGGAGATGACTTA 6285  
 QY 1954 LeuIleLysGluMetIleIleAspArgIleAsnGluAsnSerIleThrGluLysThr 1973  
 |||||  
 DB 6286 CATTAAACAGACATGATGATTTATGACAACTAAATGGAATCTCCAGCTCCAGAAAGAA 6345  
 QY 1974 AspLeuThrMetSerThrAlaAlaCysProProSerTyrAspArgValThrLysProIle 1993  
 |||||  
 DB 6346 GATCGAGATGCTCTCTACACCCCT---CTCTCTCTCTATGATGATGATGATGATGATGAT 6402  
 QY 1994 ValGluLysHisGluGlnGluGlnGlyLysLysAspGluLysAlaLysGlyLys 2009  
 |||||  
 DB 6403 AAGCAAAAGTTTGAAGAAGCAAAACAGAAAGAAAGCAAAAGAGAGAA 6450  
 |||||

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RESULT 12  
 AAH5823  
 ID AAH5823 standard; cDNA; 9112 BP.  
 AC AAH5823;  
 XX  
 DE 04-SEP-2001 (first entry)  
 XX  
 DE Human adult form of SCN3A nucleotide sequence SEQ ID NO:65.  
 XX  
 DE Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;  
 KW diagnosis; mutation; chromosome 2q33-q31; neurological disorder;  
 KW anticonvulsant; neuroprotective; ss.  
 OS Homo sapiens.  
 PN MO200138564-A2.  
 PD 31-MAY-2001.  
 PD 24-NOV-2000; 2000MO-CA01404.  
 PF 26-NOV-1999; 99US-0167623.  
 PR  
 PA (UTMC-) UNIV MCGILL.  
 XX

PI Rouleau GA, Lafreniere RG, Rocheffort D, Cossette P, Ragsdale D;  
 XX WPI; 2001-355945/37.  
 DR P-PSDB; AAB99678.  
 XX  
 XX Determining a predisposition to epilepsy and/or development of epilepsy  
 PT comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a  
 PT DNA variant, equivalent, or mutation which shows a linkage  
 PT disequilibrium -  
 PS Disclosure: Page 150-154; 268pp; English.

XX The present invention describes a method (M1) of determining an  
 CC individual's predisposition to epilepsy and/or development of epilepsy,  
 CC as well as predicting the individual's response to medication. The  
 CC method comprises determining the genotype of at least one gene selected  
 CC from SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation  
 CC which shows a linkage disequilibrium. SCN1A, SCN2A and SCN3A are all  
 CC sodium channel genes located on chromosome 2. The idiopathic generalised  
 CC epilepsy (IGE) gene is more specifically localised on chromosome  
 CC 2q33-q31. Compounds identified as modulators of the biological activity  
 CC of SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating  
 CC epilepsy or other neurological disorders. They have anticonvulsant and  
 CC neuroprotective activities. AAH5763 to AAH56164 and AAH99674 to  
 CC AAH99679 represent SCN1A, SCN2A, and SCN3A CDNA's, gene fragments, PCR  
 CC primers, oligonucleotides and proteins given in the exemplification of  
 CC the present invention.

XX Sequence 9112 BP; 2769 A; 1695 C; 1861 G; 2785 T; 2 other;

Alignment Scores:  
 Pred. No.: 0 Length: 9112  
 Score: 8468.50 Matches: 1650  
 Percent Similarity: 88.44% Conservative: 133  
 Best Local Similarity: 81.85% Mismatches: 154  
 Query Match: 81.45% Indels: 79  
 DB: Gaps: 12

US-09-930-871-12 (1-2009) x AAH55823 (1-9112)

OY 1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhenethrArgGlu 20  
 DB 633 ATGGCAGGAGGACCTGTGGTACCCAGGACCTGAAAGCTGCGCTTTTCTGAGAGA 692  
 OY 21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluValAlaGlyAsnProGlyProAsp 40  
 DB 693 TCTCTGCTGCTATGAGAAAAGCTGCTGCGAGAGAGAAAAGCCAAAGGCCCAAAAAGAA 752  
 OY 41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60  
 DB 753 CAAGTAATGATGATGAGAACAAACCAAGCCAAATAGACTTGGAAGCTGGAAGAAC 812  
 OY 61 LeuProPheIleThrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80  
 DB 813 CTTCCATTTATTTATGAGACATCTCTCCAGAGATGCTGAGAGCCCTCGAGAGACTG 872  
 OY 81 AspProTyrTyrIleAsnLysLysThrPheIleValIleAsnLysGlyLysAlaIlePhe 100  
 DB 873 GATCCCTACTATATCAATTAAGAAAACCTTTATAGTAAGAAATTAAGAAAGCAATTTCC 932  
 OY 101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120  
 DB 933 CGATTCATGCGACCTGCGCTTGTATATTTAACTCCACCTAACCCGTGTAGAAAATTT 992  
 OY 121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140  
 DB 993 GCTAASAGATTTTGGTACATCTTTATTCACATGCTTATCATGTGACATAATTTTGACC 1052  
 OY 141 AsnCysValPheMetThrMetSerAsnProProAspTyrPheLysAsnValGluTyrThr 160  
 DB 1053 AACTGTGATTTATATGACCTTGAGCAACCTCTGACTGAGCAAAATATGTAGATACACA 1112  
 OY 161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180

DB 1113 TTCACCTGAAATCTATACCTTTGAGTCACTTATAAAACTTGGCAAGAGGCTTTGCTTA 1172  
 OY 181 GluAspPheThrPheLeuArgAspProThrPasnThrPheAspPheThrValIleThrPhe 200  
 DB 1173 GAGATTTTACCTTCTTCTGATCATGAGAACCTGCTGAGATTTCACTGATGATG 1232  
 OY 201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220  
 DB 1233 GCATATGTGACAGACTTTGTGAGACTGGGCAATGTCTCAGCTTGAGAAATTCAGAGTT 1292  
 OY 221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240  
 DB 1293 CTCCAGACACGTAAMAACTTTCATCTCCAGGCTTTAAAGACCATTTGCGGGCCCTTG 1352  
 OY 241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260  
 DB 1353 ATCCAGTGGTAAAGAACCTTTGATGTGATGATCTGACTGTGTCTGTGAGCGTG 1412  
 OY 261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTyrP 280  
 DB 1413 TTTCGTCATTTGGGCTGCTCAGCTGTTCATGGGCATCTGAGAAATTAATGTTGCACTGC 1472  
 OY 281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLys--AsnIleThrValAsn 299  
 DB 1473 CCCCAGACGATTCCTGCTTTGAAACCAACACACTCTCTACTTAAAGGCACAAATGAT 1532  
 OY 300 TyrAsnGlyThrIleLeuIleAsnGluThrValPheGluPheAspTyrPheSerTyrIleGln 319  
 DB 1533 TCAAATGGGACATTTTGTAATGAATGAACAGACATTTAATGAGAGATTAACATTGGA 1592  
 OY 320 AspSerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSer 339  
 DB 1593 GATGACACTCACTTTTATGTTTGGATGCGCAAAAGACCCCTTACTCTGTGGAATGGC 1652  
 OY 340 SerAspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsn 359  
 DB 1653 TCAGATGCAAGGCGCAGTGTCCAGAGAGATACATCTGTGTGAAGGCTGTGCGAAGCCCAAC 1712  
 OY 360 TyrGlyTyrThrSerPheAspThrPheSerThrPheLeuSerLeuPheArgLeuMet 379  
 DB 1713 TATGGCTACACAAAGCTTTGAGAACCTTGTAGCTGGCTTCCTCTCTATTTCTGACTCATG 1772  
 OY 380 ThrGlnAspPheThrPheAsnLeuTyrGlnLeuThrIleArgAlaAlaGlyLysThrTyr 399  
 DB 1773 ACTCAAGACTACTGGGAAAATCTTTACAGATTTACATGCTGCTGCTGCGGAAAACATAC 1832  
 OY 400 MetIlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeu 419  
 DB 1833 ATGATATTTTTCCTGCTGCTCATTTTCTTGGGCTCATTTTATTTGATGTAATTCCTG 1892  
 OY 420 AlaValAlaIleMetAlaTyrGluGluGlnLysGlnAlaThrLeuGluGluAlaGluGln 439  
 DB 1893 GCTGTGTGGCCATGCTTATGAGGGGCAAGATCAAGGCCACTTGGAAAGACAAACAA 1952  
 OY 440 LysGluAlaGluPheGlnGlnMetIleGluGlnLeuLysGlnGlnGluAlaGln 459  
 DB 1953 AAAGAGCCGAATTTCCACAGATGCTGCAACGCTTAATAAAGCAACAGAAAGACTCAG 2012  
 OY 460 GlnAlaAlaThrAlaThrAlaSerGluHisSerArgGluProSer-----AlaAla 476  
 DB 2013 -----GCAGTTGGCGGAGCATACACTCTCTCAAGAGATTCAGAGGAATAGTGGGTTA 2066  
 OY 477 GlyArgLeuSerAspSerSerSerGluAlaSerLysLysSerSerLysSerAlaLysGlu 496  
 DB 2067 GGAGAGCTGTGGAAGTCTTTCAGAACCAATCAAGTGAAGTTCGCAAAAGTCTTAAGAA 2126  
 OY 497 ArgArgAsnArgArgLysArgLysGlnLysGlnLysGlnLysGlnLysGlnLysGlnLys 516  
 DB 2127 TGGAGAACCCAGAGAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2186  
 OY 517 Glu---AspGluPheGlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArg 535

Db 2187 GAAGAGACAGCTTCCCAATCCGAATCTGAAGACAGCTCAAAAGACAGCTTCTT 2246  
OY PheSerIleGluIleValAsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSer 555  
OY 536 PheSerIleGluIleValAsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSer 555  
Db 2247 TTCATCATGATGAGAAACAGACATGACATGACAAAAATTCCTCCCTCATCATGCT 2306  
OY 556 LeuLeuSerIleArgGlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPhe 575  
Db 2307 CTCCTAGATATCCGTGCTCCCTGTTTCCCAAGACGCAATATACAAAAACAGATTTTC 2366  
OY 576 SerPheArgGlyValArgAlaLysAspValGlySerGluAsnAspPheAlaAspGluHis 595  
Db 2367 AGTTTCAGAGGTGGGCAAGAGATGTTGGATCTGAAAAATGACTTGGTGTGATGAACAC 2426  
OY 596 SerThrPheGluAspAsnGlnSerArgArgAspSerLeuPheValProArgGlnHisGly 615  
Db 2427 AGACATTTGAAGACAGCAAGAGAGAGACATGACTGTTTGGCCGACAGACATGGA 2486  
OY 616 GluArgArgAsnSerAsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValPhe 635  
Db 2487 GACGACGCGCAACAGT----- 2501  
OY 636 ProAlaAsnGlyLysMetHisSerThrValAspCysAsnGlyValValSerLeuValGly 655  
Db 2501 ----- 2501  
OY 656 GlyProSerValProThrSerProValGlyGlnLeuLeuProGluValIleIleAspLys 675  
Db 2501 ----- 2501  
OY 676 ProAlaThrAspAspAsnGlyThrThrGluThrGluMetArgLysArgArgSerSer 695  
Db 2502 ----- 2502  
OY 696 SerPheHisValSerMetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSer 715  
Db 2547 TCTTACCAAGATTCATCAAGAGATGCTGAGAGATTCCTCTGAGACGCAAGAGCCGTGAC 2606  
OY 716 IleAlaSerIleLeuThrAsnThrValGluGluLeuGluSerArgGlnLysCysPro 735  
Db 2607 ATAGCCAGCATTCGACCAACACAAATGAGAACTTGAAGATCTAGACAAATATGTCGC 2666  
OY 736 ProCysTrpTyrLysPheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeu 755  
Db 2667 CCATGCTGATATGATGTCGCAATGCTGCTGATCTGGGACTGCTGATGATGATGCTTA 2726  
OY 756 LysValLysHisValValAsnLeuValValMetAspProPheValAspLeuAlaIlePhe 775  
Db 2727 AAGGTAAACATCTGTGAATTAATGATTAATGATCCATTTGTTGATCTGGCATCTACT 2786  
OY 776 IleCysIleValLeuAsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHis 795  
Db 2787 ATTTCGATGTGCTTAATTAACCTCTTTATGCGCATGAGACACACCATGATGAGAGAA 2846  
OY 796 PheAsnAsnValLeuThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMet 815  
Db 2847 TTCAGTAGTGTTGACTGTGAGAAACCTGCTTACTGAGATTTTACAGCAAAATG 2906  
OY 816 PheLeuLysIleIleAlaMetAspProTyrTyrTrpPheGlnGluGlyTrpAsnIlePhe 835  
Db 2907 GTTCTCAAGATCATTTGCAATGAGATCTTATTAATTTCCAAAGAGCGTGAATAATCTT 2966  
OY 836 AspGlyPheIleValThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeu 855  
Db 2967 GATGGAATTTATGTCACCTCAGCTTAATGAGACCTTGTCTGCTCAAAATGTCGAGAGATG 3026  
OY 856 SerValLeuArgSerPheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThr 875  
Db 3027 TCTGTACTGGGATCATTCAGACCTGCTTAAGATTTCAAGTTGGCAAAATCTGCGCCCA 3086  
OY 876 LeuAsnMetLeuIleLysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeu 895  
Db 3087 CTAAATATGCTAAATTAATGATCATTTGCAATTCGTGGGGGCTTGAAGAAACCTGACCTG 3146

OY 896 ValLeuAlaIleIleValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSer 915  
Db 3147 GTGTGGCCATCATATGCTTCAATTTTGGCTGTGGTCGATGAGCTCTTGTGTAAAGC 3206  
OY 916 TyrLysAspCysValCysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsn 935  
Db 3207 TACAAAGATGTGTCTGCAGATCATGATGACTGTACGTCCACGCTGACATATAC 3266  
OY 936 AspPheHisSerPheLeuIleValPheArgValLeuGlyGlnTrpIleGluThr 955  
Db 3267 GACTTTCGACTCCTTCATGATTTGTTCCGGGTGTGTGGAGAGTGAAGAGAAC 3326  
OY 956 MetTrpAspCysMetGluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetVal 975  
Db 3327 ATGTGGGACTGTATGAGGCTGCGTGCACCAACATGAGCCCTTATGTTTCATGCTTGC 3386  
OY 976 MetValIleGlyAsnLeuValIleLeuAsnLeuPheLeuAlaLeuLeu\*\*\*SerSerPhe 995  
Db 3387 ATGCTCATGGAACCTTGTTGTTCTGACCTCTTCTGCTTATGTTGAGTTCAAT 3446  
OY 996 SerAlaAspAsnLeuAlaIleThrAspAspAsnGluMetAsnAsnLeuGlnIleAla 1015  
Db 3447 AGCTCAGACAACTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3506  
OY 1016 ValAspArgMetHisLysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGln 1035  
Db 3507 GTAGAGAGATATGCAAAAGGAATGATTGTAATAATGATGATGATGATGATGATGATGAT 3566  
OY 1036 GluSerPheIleArgGlyGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsn 1055  
Db 3567 AAGGCTTTTGTGAAAGCCCAAAAGTATAT---GAAATCCATGAA-----GGC 3611  
OY 1056 AsnLysLysAspSerCysMetSerSerAsnHisThr---\*\*GluIleGlyLysAspLeuAsp 1074  
Db 3612 AATTAAGATATGACAGCTGATCATATATATATGATGATGATGATGATGATGATGATGAT 3671  
OY 1075 TyrLeuLysAspValAsnGlyThrThrSerGlyIleGlyThrGlySerSerValGluLys 1094  
Db 3672 TATCTTGAAGATGGAATGGAACACACAGGTGTAGTACTGTGAGACAGTGTGAATAA 3731  
OY 1095 TyrIleIleAspGluSerAspTyrMetSerPheIleAsnAsnProSerLeuThrValThr 1114  
Db 3732 TACGTAAATCATGAAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 3791  
OY 1115 ValProIleAlaValGlyGluSerAspPheGluAsnLeuAsnThrGluAspPheSerSer 1134  
Db 3792 GTGCCATTTGCTGTGAGAGCTGACTTTGAAACTTAATTAATTAATTAATTAATTAAT 3851  
OY 1135 GluSerAspLeuGluGluSerLysGluLysLeuAsnGluSerSerSerSerSerGluGly 1154  
Db 3852 GAGTCAGACATGAGAAAGCAAGAGCAAAATTAAT---GCAACACACTCATCTGAAGAA 3908  
OY 1155 SerThrValAspIleGlyAlaProValGlu---GluGlnProValValGluProGluGln 1173  
Db 3909 AGCAGCTGTATGTTGTTTCAACCCGAGAGGTAAACCTGAACCTGAACCCGAGAGAA 3968  
OY 1174 ThrLeuGluProGluAlaCysPheThrGluGlyCysValGlnArgPheLysCysGlyGln 1193  
Db 3969 GACCTTAACCGGAGAGCTGTTTACGAAAGATGATTAATAAAGTTTCCATTTGTGCAA 4028  
OY 1194 IleAsnValGluGluGlyArgLysGlnTrpTrpAsnLeuArgArgTrpCysPheArg 1213  
Db 4029 GTAGTACAGAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 4088  
OY 1214 IleValGluHisAsnTrpPheGluThrPheIleValPheMetIleLeuLeuSerSerGly 1233  
Db 4089 ATTGTTGAGACAACTGTTGAGACCTTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 4148  
OY 1234 AlaLeuAlaPheGluAspIleTyrIleAspGlnArgTrpThrIleLysThrMetLeuGln 1253  
Db 4149 GCATTTGCTTGAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4208







Dh 1713 TATGGTACACAGCTTGAACACTTACGCGGCTTCTGTCATATTGCACTATG 1772  
Qy 380 ThGlnAspHeTrpGluAsnLeuTyGlnLeuThrLeuArgAlaGlyLysThrTy 399  
Dh 1773 ACTCAACACTACTGGGAAATCTTACCAGTTGACATTAAGCTGCGGGAACATAC 1832  
Qy 400 MetLeuPheValLeuValIlePheLeuGlySerPheTyLeuIleAsnLeuIleLeu 419  
Dh 1833 ATGATATATTTTGGTCGGTCATTTCTTGGCTCATTTATTTATTTGCAATTTGATCTG 1892  
Qy 420 AlaValAlaIleMetAlaTyGlnGluGlnAsnGlnAlaThrLeuGlnAlaGluGln 439  
Dh 1893 GCTGTGTGGCCATGGCTTATGAGGGCAGATAGGCCACTTGGAGAAAGCAGACAA 1952  
Qy 440 LysGlnAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnAlaGln 459  
Dh 1953 AAAGAGCCCAATTTACAGAGATCTGCAACAGCTTAAAGCAACAGAGAAAGCTCAG 2012  
Qy 460 GlnAlaIleAlaThrAlaThrAlaSerGluHisSerArgGluProSer-----AlaAla 476  
Dh 2013 -----GCAGTTGGCGCAGATCAGCTCTTCAAGAGATTTCACTGGAAATGCTGGGTTA 2066  
Qy 477 GlyArgLeuSerAspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGlu 496  
Dh 2067 GGAAGAGCTGTGGAAATCTTCTGAAAGCATCAAAAGTTGAGTTCCAAAGTCTCAAGAA 2126  
Qy 497 ArgArgAsnArgArgLysLysArgLysGlnLysGlnLeuSerGlyGlnGluGluAsp 516  
Dh 2127 TGGAGCAACCGAAGAGAAAGAAAGAGAGAGAGACCTTGAAGAAACAAACAAAGGA 2186  
Qy 517 Glu---AspGluPheGlnLysSerGlnLysSerGlnLysSerIleArgArgLysGlyPheArg 535  
Dh 2187 GAGAGAGACAGCTTCCCAATCCGAATCTGAAACAGCGCAAAAGACAGCTTCTCTT 2246  
Qy 536 PheSerIleGluGlnAsnArgLeuThrTyGlnLysArgTySerSerProHisGlnSer 555  
Dh 2247 TTCTCCATGGATGGAACACAGACTACAGAGACAAAAATTTCTCTCCCTCATCAGCT 2306  
Qy 556 LeuLeuSerIleArgLysLeuPheSerProArgArgAsnSerArgTyThrSerLeuPhe 575  
Dh 2307 CTTCTGGATTCGCTGCTGCTCTCTTCCCAAGACGACATATACAAACAGCATTTTTC 2366  
Qy 576 SerPheArgGlyArgAlaLysAspValGlySerGlnAsnSerPheAlaAspAspGluHis 595  
Dh 2367 AGTTTCAGAGCTCGGGAAGAGATGGATCTGAAATGATCTTGGATGATGAACAC 2426  
Qy 596 SerThrPheGluAspAsnGlnLysSerArgArgAspSerLeuPheValProArgArgHisGly 615  
Dh 2427 AGCACATTTAAACACGGAAGCAGAGAGACTCAGCTTTTGTCCGACAGACATGGA 2486  
Qy 616 GluArgArgAsnSerAsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValPhe 635  
Dh 2487 GACGAGCAGCAACAGT----- 2501  
Qy 636 ProAlaAsnGlyLysMetHisSerThrValAspCysAsnGlyValValSerLeuValGly 655  
Dh 2501 ----- 2501  
Qy 656 GlyProSerValProThrSerProValGlyGlnLeuLeuProGluValIleIleAspLys 675  
Dh 2501 ----- 2501  
Qy 676 ProAlaThrAspAspAsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSer 695  
Dh 2502 -----AACGCAACCCACACACGAAACGCAAGCTCAGAAAGAGAGGTTAAGC 2546  
Qy 696 SerPheHisValSerMetAspPheLeuGlnAspProSerGlnArgGlnAlaMetSer 715  
Dh 2547 TCTTACACAGATTCATGAGAGAGAGCTGGAGATTCCTCTGAAAGGCAAAAGACGCTAGC 2606  
Qy 716 IleAlaSerIleLeuThrAsnThrValGlnGluLeuGlnGlnLysSerArgGlnLysCysPro 735  
Dh 2607 ATAGCCAGCATTTCTGACCAACACATGGAAGAACTTGAAGAACTCTAGACGAAATGTCCG 2666

Qy 736 ProCysTrpTyLysPheSerAsnIlePheLeuIleTrpAspCysSerProTyTrpLeu 755  
Dh 2667 CCATCTGCTGATAGATTTGGCCAAATGTTCTGATCTGGAGACTGCTGATGATCAATGTTA 2726  
Qy 756 LysValLysHisValAlaAsnLeuValValMetAspProPheValAspLeuAlaIleThr 775  
Dh 2727 AAAGTAAACATCTGTGAATTAATTTATTTATGATTCATTTGTTGATCTGCCATCACT 2786  
Qy 776 IleCysIleValLeuAsnThrLeuPheMetAlaMetGluHisTyProMetThrAspHis 795  
Dh 2787 ATTGCATTTGTTTAAATACCTCTTTATGCGCATGAGCACTACCCATGACAGCA 2846  
Qy 796 PheAsnAsnValLeuThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMet 815  
Dh 2847 TTCAGTACTGTTGTGACGTAGGAACbCTGGCTTACTGGGATTTTACACAGAAATG 2906  
Qy 816 PheLeuLysIleIleAlaMetAspProTyTyTyTyPheGlnGlnGlyTyTrpAsnIlePhe 835  
Dh 2907 GTTCCAAAGATCATCTGCATGATCCATCTTATTAATTTCAAAAGAGCTGGAAATCTTT 2966  
Qy 836 AspGlyPheIleValThrLeuSerLeuValGlnLeuGlyLeuAlaAsnValGlnGlyLeu 855  
Dh 2967 GATGGAATTAATTTGAGCTCAGTTAAATGAGAGCTTGGCTGTCTCAAAATGAGGAGATG 3026  
Qy 856 SerValLeuArgSerPheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThr 875  
Dh 3027 TCTGTAGCGCATCATTCAGCTGCTTATGATTTTCAAGTTGGCAAAATCTGCGCCACA 3086  
Qy 876 LeuAsnMetLeuIleLysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeu 895  
Dh 3087 CTAATATAGCTAAATTAATATATGATGGCAATCTGGGGGCTCTAGAAACCTCACTTG 3146  
Qy 896 ValLeuAlaIleIleValPheIlePheAlaValAlaGlyMetGlnLeuPheGlyLysSer 915  
Dh 3147 GTTTGGCATCATGCTTATATTTTCTGTGTGGCAGACAGCTTGTGGTAAAGAGC 3206  
Qy 916 TyrLysAspCysValCysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsn 935  
Dh 3207 TACAAGAAATGTGCTGGAATCATCATGATGACGTACGCTCCACGGTGGCACATGAAAC 3266  
Qy 936 AspPhePheHisSerPheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThr 955  
Dh 3267 GACTTCTTCCACTCTTCTCTATTTGTTCCGCGCTGTGGAGATGATGAGAGAC 3326  
Qy 956 MetTrpAspCysMetGluValAlaGlyGlnAlaMetCysLeuThrValPheMetLeuVal 975  
Dh 3327 ATGTGGAGCTATAGAGGTGCTGGCCAAACATGTGCTTATTTGTTTCATGTGTGTC 3386  
Qy 976 MetValIleGlyAsnLeuValValLeuAsnLeuPheLeuAlaLeuLeu\*\*SerSerPhe 995  
Dh 3387 ATGTCATTTGAAACCTTGTGCTGCTGACCTCTTTCGGCTTATTTGATGATCAATTT 3446  
Qy 996 SerAlaAspAsnLeuAlaIleThrAspAspAsnGlnLysLeuAsnLeuGlnIleAla 1015  
Dh 3447 AGCTCAGACCAACTTGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 3506  
Qy 1016 ValAspArgMetHisLysGlyValAlaIleTyThrValLysArgLysIleTyGluPheIleGln 1035  
Dh 3507 GTAGGAAGATGCAAAAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 3566  
Qy 1036 GlnSerPheIleArgLysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsn 1055  
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Qy 1056 AsnLysLysAspSerCysMetSerAsnHisThr---GluIleGlyLysAspLeuAsp 1074  
Dh 3612 AATTAAGATAGACACTCAGCTCCAAATTAATACGAAATTTGAAATTAACAAAGACTTAAT 3671  
Qy 1075 TyrLeuLysAspValAsnGlyThrThrSerGlyIleGlyThrGlySerSerValGlnLys 1094  
Dh 3672 TATCTTAGAGTTGGAATGATGACCAACAGAGTGTAGTACTGGAACAGTGTGAAGAA 3731

1095 TyrIleIleAspGluSerAspTyrMetSerPheIleAsnAsnProSerLeuThrValThr 1114  
1115 ValProIleAlaValAlaGlyGluSerAspPheGluAsnLeuAsnThrGluAspPheSer 1134  
3792 GTTCCAAATGCTGCTTGGAGAGCTGACTTGAAGAACTTAATATCTGAGAGCTTCCAGCAGT 3851  
1135 GluSerAspLeuGluGluSerLysGluLysLeuAsnGluSerSerSerSerGluGly 1154  
3852 GAGTCAGAACTAGAGAAAGCAAGCAAGAAATTAAT---GCAACCACTCATCTGGAAGA 3908  
1155 SerThrValAspIleGlyAlaProValGlu---GluGlnProValValGluProGluGlu 1173  
3909 AGCAGCTGATGCTGCTTCTTACCCCGAAGAGGTGAACACCTGAACCTGAACCCGGAAGAA 3968  
1174 ThrLeuGluProGluLysPheThrGluGlyCysValAlaIleArgPheLysCysCysGlu 1193  
3969 GACCTTAACCCGAGACCTGCTTCTTACTGAAAGATGATTAATAAGTTTCCATCTGTCGAA 4028  
1194 IleAsnValGluGluGlyArgGlyLysGlnTrpIlePheAsnLeuArgTrpCysPheArg 1213  
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1214 IleValGluHisAsnTrpPheGluThrPheIleValIlePheMetIleLeuSerSerGly 1233  
4089 ATGTGTGAGCACAACAGTGTGAGACTTCAATGCTGATGATCCCTTCCAGTAGAGT 4148  
1234 AlaLeuAlaPheGluAspIleThrIleAspGluArgLysThrIleLysThrMetLeuGlu 1253  
4149 GCATGAGCTTGAAGATATATACATATGAACAGCAAGCAACTATCAAAACCAAGCTAGAA 4208  
1254 TyrAlaAspLysValPheThrTrpIlePheIleLeuGluMetLeuLeuLysTrpValAla 1273  
4209 TATGCTGACAAACTCTTACTATATATCATCTGGAATGCTTCCAAATGGTGTGCT 4268  
1274 TyrGlyTyrGlnThrTyrPheThrAsnAlaIleTrpCysTrpLeuAspPheLeuIleValAsp 1293  
4269 TATGATTTTCAACATATTTCACTAATGCTGTGCTGCTAGATTTCTTGATCGTTGAT 4328  
1294 ValSerLeuValSerLeuThrIleAsnAlaIleGluIleTyrSerGluLeuGlyAlaIleLys 1313  
4329 GTTCTCTTGGTGAAGCTGAGTGAAGCAATGCTCTTGGCTACAGACCTGGTCCATGAAA 4388  
1314 SerLeuArgThrLeuArgAlaLeuArgProLeuArgAlaLeuSerArgPheGluGlyMet 1333  
4389 TCATTTAGGACATTAAAGCTTTAAAGCCTTAAGACCTTAATCCCGTTTGAAGGATG 4448  
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1354 CysLeuIlePheTrpLeuIlePheSerIleMetGlyValAsnLeuPheAlaGlyLysPhe 1373  
4509 TGCTCATCTTCTGCTGATCTTTAGCATATGGGTGATTTGTTGCTGGCAATGTC 4568  
1374 TyrHisCysIleAsnThrThrThrGlyAspArgPheAspIleGluAspValAsnAsnHis 1393  
4569 TACCACGCTGTAACATGACAAAGGATTAATGTTTACATGATGATGATTAACAATTTG 4628  
1394 ThrAspCysLeuLysLeuIleGluArgAsnGluThrAlaArgTrpLysAsnValLysVal 1413  
4629 AGGACGCTGACGCTCTT-----GCCAAGCAAGCTCGGTGAGAAACGTCGAAGTA 4679  
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4680 AACTGTGATATATGTGGCGCTGCTATCTTGCACCTGCTTAAGTGGCCAAATTTAAAGGC 4739  
1434 TrpMetAspIleMetTyrAlaAlaValAspSerArgAsnValGluLeuGlnProLysTyr 1453  
4740 TGGATGATATATATGATGACGCTGTTGATTCAGAGATGTTAAACTTCAAGCCGTATAT 4799  
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4800 GAAAGAAATCTGTCATGATATTTATCTTTGCTCAATCTTTATCATCTTTGGCTCAATCTTC 4859  
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1554 AsnMetValThrMetCysValGluThrAspAspGlnSerGluTyrValThrIleLeu 1573  
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1574 SerArgIleAsnLeuValPheIleValLeuPheThrGlyLysValLeuLysLeuIle 1593  
5160 TCCCGATTCACACCTAGAGTTCATTTGCTGCTCACTGAGAAATTTGGTGAACCTGCTC 5219  
1594 SerLeuArgHisTyrTyrPheThrIleGlyTrpAsnIlePheAspPheValValIle 1613  
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1614 LeuSerIleValGlyMetPheLeuAlaGluLeuIleGluLysTyrPheValSerProThr 1633  
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1654 LysGlyIleArgThrLeuLeuPheAlaLeuMetSerLeuProAlaLeuPheAsnIle 1673  
5400 AAGGGATCCGACAGCTGCTGCTTGTGATGATGATGATGATGATGATGATGATGATGAT 5459  
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5580 ATGATGCTGCTTGTCCAAATTAACAACCTGCTGATGATGATGATGATGATGATGATGAT 5639  
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5640 CTTAATATGTCACACACCGACTGACCTGACCAACAATTAACCTGACGACTCACTAAG 5699  
1754 GlyAspCysGlyAsnProSerValGlyIlePhePhePheValSerTyrIleIleIleSer 1773  
5700 GGAAGCTGTGGAAACCATCTGTTGGGATTTCTTTTTCAGATATCATATCATATCAATCC 5759  
1774 PheLeuValValAlaAsnMetTyrIleAlaValIleLeuGluAsnPheSerValAlaThr 1793  
5760 TTCTGCTGCTGCTGACAGATTAATCCGCTATCTGAGAGACTTGAAGTGTGCTACT 5819  
1794 GluGluSerAlaGluProLeuSerGluAspAspPheGluMetPheTyrGluValTrpGlu 1813  
5820 GAAGAAAGTGAAGAGCCCTGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 5879  
1814 LysPheAspProAspAlaThrGlnPheMetCysLeuGluLysLeuSerGlnPheAlaAla 1833

Db 5880 AAGTTGATCCGATGCCAGCCAGTTTATAGATCTCTAATCTCTGATTTTGACGCT 5939  
 Oy 1834 AAlaEuglupProleuansleuProgluProAsnlyleuEugluleuAlaMetasp 1853  
 Db 5940 GCCGTGATGCTCCTCTCTCATAGCAAAACCAAGTCCGATTTATGCGATGAT 5999  
 Oy 1854 LeuPrometAlaSerGlyAspArgIleHisCysLeuAspIleuAlaPheThrLys 1873  
 Db 6000 CTGCCATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 6059  
 Oy 1874 ArgValleuGlySerGlyMetAlaLeuArgIleGlnMetGluGluArgPhe 1893  
 Db 6060 CCGTGTTCGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 6119  
 Oy 1894 MetAlaSerAspProSerLysValSerLysArgIleProIleThrThrLeuLysArgLys 1913  
 Db 6120 ATGGCATCAAAACCCCTCCAAAGCTCTTATGAGCCATTACAAACCACTTGAAGCTAA 6179  
 Oy 1914 GlnGluGluValSerAlaValIleIleGlnArgAlaThrArgArgHisLeuLeuLysArg 1933  
 Db 6180 CAAGAGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6239  
 Oy 1934 ThrValleuGlnAlaSerPheThrThrAsnLysAsnLysIleLeuGlyAlaAlaLeu 1953  
 Db 6240 AGCTTAAATAATATATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 6299  
 Oy 1954 LeuIleLysGluAspMetIleIleAspArgIleAsnGluAsnSerIleThrGluLysThr 1973  
 Db 6300 CCTATTAACCAAGACATGATTTATGCAAAAGTGAATGGAGACCCCACTCCAGAAAAACA 6359  
 Oy 1974 AspLeuThrMetSerThrAlaAlaCysProProSerLysArgValThrLysProIle 1993  
 Db 6360 GATGGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6416  
 Oy 1994 ValGluLysHisGlnGluGlnLysAspGluLysAlaLysGlyLys 2009  
 Db 6417 AAGGAAAGTTTGTGAGAAAGCAAAACCAAGAAAAAGAAAGAAAA 6464  
 RESULT 14  
 ID ABR63697 standard; cDNA; 6822 BP.  
 AC ABR63697;  
 DT 18-JUN-2002 (first entry)  
 XX  
 DE Rat sequence differentially expressed in response to a hepatotoxin #1604.  
 XX  
 KW Rat; ss; hepatotoxin; expressed sequence tag; EST; drug screening;  
 XX differential expression; centrilobular necrosis; steatosis.  
 OS Rattus norvegicus.  
 XX  
 PN W0200210453-A2.  
 PD 07-FEB-2002.  
 XX  
 PF 30-JUL-2001; 2001WO-US23872.  
 XX  
 PR 31-JUN-2000; 2000US-222040P.  
 PR 02-NOV-2000; 2000US-244880P.  
 PR 11-MAY-2001; 2001US-290029P.  
 PR 15-MAY-2001; 2001US-290645P.  
 PR 22-MAY-2001; 2001US-292336P.  
 PR 06-JUN-2001; 2001US-295798P.  
 PR 13-JUN-2001; 2001US-297457P.  
 PR 19-JUN-2001; 2001US-298844P.  
 PR 09-JUL-2001; 2001US-303459P.  
 XX  
 PA (GENE-) GENE LOGIC INC.  
 XX  
 PI Mendrick D, Porter MM, Johnson KR, Castle AL, Elashoff MR;  
 XX

DR WPI: 2002-241625/29.  
 XX  
 PR Predicting toxic effects of compounds or the progression of these toxic  
 PR effects by determining the changes in gene expression in tissues or  
 PR cells exposed to the toxin and comparing these to gene expression in  
 PR unexposed tissues or cells -  
 PS Claim 1: Seq ID NO 1604; 239pp; English.  
 XX  
 CC The invention relates to methods for predicting toxic effects of  
 CC compounds or the progression of these toxic effects by determining the  
 CC global changes in gene expression in tissues or cells exposed to the  
 CC toxin and comparing these to gene expression in unexposed tissues or  
 CC cells. Also included are methods of predicting at least one toxic  
 CC effect of a compound or progression of a toxic effect, preferably the  
 CC hepatotoxicity of a compound, comprising detecting the level of  
 CC expression in a tissue or cell sample exposed to the compound of two or  
 CC more genes listed in the specification, where differential expression of  
 CC the genes is indicative of at least one toxic effect or progression.  
 CC The method can also be used to identify an agent which modulates the  
 CC toxic response and predict cellular pathways that a compound modulates  
 CC in a cell. The methods utilize a set of at least two probes (on a solid  
 CC support in kit form), where each of the probes comprises a sequence that  
 CC specifically hybridises to a gene listed in the specification, a computer  
 CC system comprising a database containing information identifying the  
 CC expression level in a tissue or cell sample exposed to a hepatotoxin of a  
 CC set of genes comprising at least two genes listed in the specification,  
 CC and a user interface to view the information used to present information  
 CC identifying the expression level in a tissue or cell of at least one gene  
 CC listed in the specification. The method is useful for elucidating global  
 CC changes in gene expression and for identifying toxicity markers in  
 CC tissues or cell exposed to a known toxin. The genes may be used as  
 CC toxicity markers in drug screening and toxicity assays. The genes and  
 CC gene expression information may be used as diagnostic markers for the  
 CC prediction or identification of the physiological state of tissue or cell  
 CC sample that has been exposed to a compound or agent. Hepatotoxicity  
 CC is characterised by centrilobular necrosis and steatosis. The present  
 CC sequence is an expressed sequence tag (EST) or cDNA derived from a gene  
 CC which is differentially expressed in response to a hepatotoxic agent.  
 XX  
 SO Sequence 6822 BP; 1861 A; 1525 C; 1650 G; 1786 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 0 Length: 6822  
 Score: 8448.50 Matches: 1648  
 Percent Similarity: 88.49% Conservative: 136  
 Best Local Similarity: 81.75% Mismatches: 153  
 Query Match: 81.26% Indels: 79  
 DB: 24 Gaps: 12  
 US-09-930-871-12 (1-2009) x ABR63697 (1-6822)  
 Oy 1 MetGluGlnThrValleuValProProGlyProAspSerPheAsnDpPheThrArgGlu 20  
 Db 414 ATGGCCAGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 473  
 Oy 21 SerLeuAlaAlaIleGluArgArgIleAlaGluLysAlaLysAsnProLysProAsp 40  
 Db 474 TCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 533  
 Oy 41 LysLysAspAspAspGluAsnGlyProLysProAspSerAspLeuGluAlaGlyLysAsn 60  
 Db 534 CAAGACATGACGATGAGAAACCAAGCAAGAGGAGCTGGAACCTGGAGAAAGC 593  
 Oy 61 LeuProPheIleLysGlyAspIleProProGluMetValSerGluProLeuGluLysAsn 80  
 Db 594 CTTCCTATATCTATGAGACATCTCTCCAGAGATGCTGCTGAGAGCCCTGAGAGACCTG 653  
 Oy 81 AspProTyThrLysAsnLysLysThrPheIleValIleAsnLysGlyLysAlaIlePhe 100  
 Db 654 GACCCCTACTATGCTGATGAGAAACCTTTGTAGTGTATTAATTAAGGAGGCGATTTT 713  
 Oy 101 ArgPheSerAlaThrSerAlaLeuThrIleLeuThrProPheAsnProLeuArgLysIle 120





|    |      |  |      |
|----|------|--|------|
| OY | 836  | AspGlyPheIleValThrIleSerIleValGlnIleGlyIleuAlaAsnValGlnIleu          | 855  |
| Db | 2748 | GATGGAAATTATTGTTACCGTCCGAGTTTAAAGCACTAGGCTG6CAAATGTGGAGGGCTG         | 2807 |
| OY | 856  | SerValIleuArgSerPheArgIleuLeuArgValPheIleuAlaIleuAlaSerTrpProThr     | 875  |
| Db | 2808 | TCTGTGCTGGGTCTTCACAGACTGCTCCGAGTCTTCAAGTTG6CAAAAGTCTGGCCACA          | 2867 |
| OY | 876  | LeuAsnMetIleuIleIysIleIleGlyAsnSerValGlyAlaIleuGlyAsnIleuThrIleu     | 895  |
| Db | 2868 | CTGAACATGCTCATTAAGATCAATGCAATCGCACTCGTGGGCACTGGCAACTGACCTG           | 2927 |
| OY | 896  | ValIleuAlaIleIleValPheIlePheAlaValAlaGlyIleuGlnIleuPheGlyIysSer      | 915  |
| Db | 2928 | GTGCTGGCCATCAATCGCTTCATTATTTTCCGCTGCTGGCATGACACTGTTTGGAAAGAC         | 2987 |
| OY | 916  | TyrIlyAspCysValCysIlyIleAlaSerAspCysGlnIleuProArgTrpHisMetAsn        | 935  |
| Db | 2988 | TACAAAGGAGTGTGTCTGCAGATCAATGTGGAGCTGCACATCTCCGCTGGCATCATGAC          | 3047 |
| OY | 936  | AspPhePheHisSerPheIleuIleValPheArgValIleuCysGlyGlnTrpIleIleuThr      | 955  |
| Db | 3048 | GACTCTTCACATCTCTTCGATCGATGCTTCGAGTCTCTGTGGGAGAGTGATTAAGAC            | 3107 |
| OY | 956  | MetTrpAspCysMetGlnValAlaGlyGlnAlaMetCysIleuThrValPheMetIleVal        | 975  |
| Db | 3108 | ATGTGGGACTGCATGAGAGGTGCGGGGCGACACATGTGCTTATGTGTTCATATTTGGTC          | 3167 |
| OY | 976  | MetValIleGlyAsnIleuValIleuAsnIleuPheIleuAlaIleuLeu**SerSerPhe        | 995  |
| Db | 3168 | ATGGTGTATGGGAACCTTGTGTGTTCTGAACCTCTTCTGCGCTTATGTGTGAGTCTCTT          | 3227 |
| OY | 996  | SerIlaAspAsnIleuAlaIleThrAspAspAsnGlnMetAsnIleuGlnIleAla             | 1015 |
| Db | 3228 | AGTTCAGATTACCTTGTGCTGCTACTGACGATGATTAACGAATGACACACTCCAGATGCGG        | 3287 |
| OY | 1016 | ValAspArgMetHisIlysgIlyValAlaIleValIlyValIlyValIlyIleTyrGlnPheIleGln | 1035 |
| Db | 3288 | GTGGGAAGAGCATGCAAAAGGGAATGTATTTGTCAAAAATTAATGATACGGAGGCTTCCGA        | 3347 |
| OY | 1036 | GlnSerPheIleArgIlysgIlyIleuAlaPqluIleIlyProIleuAspAspIleuAsn         | 1055 |
| Db | 3348 | AAAGCGTTTTCACAAAAGCCGAAAGTGAT*--GAAATCCAAAGA-----GGC                 | 3392 |
| OY | 1056 | AsnIlyIlyAspSerCysMetSerAsnHisThr---**GlnIleGlyIlyAspIleuAsp         | 1074 |
| Db | 3393 | AACAAAATAGACACTGCTCATGTCCAATTAACACGGGATCGAATTAAGCAAAAGACTTAC         | 3452 |
| OY | 1075 | TyrIleuIlyAspValaIleGlyThrTrhSerGlyIleGlyTrhGlySerSerValGluIys       | 1094 |
| Db | 3453 | TACCTTAAAGCGGTAAATGGAACCCAGCGGGGTGGGAACCGGAACGTCGTGGAAAA             | 3512 |
| OY | 1095 | TyrIleIleAspGlnSerAspTyrIlyMetSerPheIleAsnAspProSerIleuThrValThr     | 1114 |
| Db | 3513 | TAGTAAATCGATGAATAATGACTCAATGATCATTAATCAAAATCCACGCTACCGTACT           | 3572 |
| OY | 1115 | ValProIleAlaValGlyIleuSerAspPheGlnAsnIleuAsnTrhGluAspPheSerSer       | 1134 |
| Db | 3573 | GTGGCAATTTGCTGTGGGAGAGTCTGACTTGTGAATAATTAAATACGGAAGAGTTCAGCAGT       | 3632 |
| OY | 1135 | GlnSerAspIleuGlnIlyuSerIlysgIlyIlyIleuAsnGlnIlySerSerSerSerGlnIly    | 1154 |
| Db | 3633 | GAGTCACAAATTGGACAAAGTAAGGCAAAATTAAAT---GCAACAAGCTCTTCTGAAGCA         | 3689 |
| OY | 1155 | SerThrValAspIleGlyAlaProValGlu---GlnIleProValIleValGlnProGlnIly      | 1173 |
| Db | 3690 | AGCACACTGATGTGTGCTCCACCCGAGGAAGGTGAACAAGCAGAAATTAAGCACTGAGGAG        | 3749 |
| OY | 1174 | ThrIleuTrpGlnIlaIysPheThrGlnIlyCysValGlnArgPheIysCysGlySerGln        | 1193 |
| Db | 3750 | GACCTTAAGCCAAAGCTTATTTACTGAAGGCTGATTAATAAAATTCCTCCCTTGTGTA           | 3809 |

|    |      |  |      |
|----|------|--|------|
| QY | 1194 | ILeasnaValIGluIngluValagGlyLysGInTTPTrpAsnLeuArbArfThrCysPheArg  | 1213 |
| Db | 3810 | GTAAAGTACAGAAAGAGTAAAGGAAAAAATATGGTGGAAATCTTATAGGAAGACATGCTACAGC | 3869 |
| QY | 1214 | ILeValGIuHtAsaNTpPheGIuThrPheILeValPheMetILeueuSerSercly         | 1233 |
| Db | 3870 | ATTGGGAGCAACAATCGTTTGAAGACATTCATGTGTCTCATGTATCTCTCCATGATGTGG     | 3929 |
| QY | 1234 | AlaLeuAlaPheGIuAspILeYrILeAspGlnArgLysThrILeYsThrMetLeuGln       | 1253 |
| Db | 3930 | GCTTGGCGCTTGGAGTATATATACATTGAGCAACGAAAGACATCAAGACCATGCTGGAG      | 3989 |
| QY | 1254 | TyrILaAspLysValPheThrYrILePheILeLeuGlnMetLeuLeuYsTrpAla          | 1273 |
| Db | 3990 | TATGACAGCAAGGCTTCACGTACATCTTCATCTCGAATCTCTCCAAAGGGGTGCC          | 4049 |
| QY | 1274 | TyrGlyTyrGlnThrYrPheThrAsnAlaTrpCysTrpLeuAspPheLeuILeValAsp      | 1293 |
| Db | 4050 | TATGATTTCAAAACCTATTTCACCAATGCGTGGTGGTGGACTTCTGTATCTTAT           | 4109 |
| QY | 1294 | ValSerLeuValSerLeuThrAlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaILeLys     | 1313 |
| Db | 4110 | GTTCTTGTGGTTACCTGGTAGGCAATGCTTGTTACTCAGAAACTGGTGCATCAAA          | 4169 |
| QY | 1314 | SerLeuArghTrLeuArgAlaLeuArghProLeuArgAlaLeuSerArghLeuGlyMet      | 1333 |
| Db | 4170 | TCCCTACGAGACACTGAGAGCGCTGAGCGCGCTCCGACCTTATCCGCTTGAAGGCATG       | 4229 |
| QY | 1334 | ArgValValAlaAsnAlaLeuLeuGlyAlaILeProSerILeMetAsnValLeuLeuVal     | 1353 |
| Db | 4230 | AGGGGGGTGTAAATVGGCTCTGTGGTGGCAATTCCTCCATCATGAATGTTATTTGGTG       | 4289 |
| QY | 1354 | CysLeuILePheTrpLeuILePheSerILeMetGlyValAsnLeuPheAlaGlyLysPhe     | 1373 |
| Db | 4290 | TGTCTCAATCTTCGCGCATTTTTCACATCATGGGTGATCACTGTTCTCGAAAATGTC        | 4349 |
| QY | 1374 | TyrILeCysILeAsnThrThrArgAspArgPheAspILeGluAspValAsnAsnILs        | 1393 |
| Db | 4350 | TATACACTGTGTTAAACGACACAGCAACGACATGTTGAATTAAGAAAGTGCACAAATTC      | 4409 |
| QY | 1394 | ThrsProCysLeuLysLeuILeGluArgAsnGluThrAlaArgTrpLysAsnValLysVal    | 1413 |
| Db | 4410 | AGTGACTGTACAGGCTCTT-----GGCAACCAAGCCCGGTGGAAAGATGTGAAATGC        | 4460 |
| QY | 1414 | AsnPheAspAsnValIGlyPheGlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGly    | 1433 |
| Db | 4461 | AACTTTGACAAACGTGGGGGTGGCTACGTGGCATTCCTGCATAGTGGCCACATTCAAAGGC    | 4520 |
| QY | 1434 | TrpMetAspILeMetYrAlaAlaValAspSerArgAsnValGluLeuGlnProLysTr       | 1453 |
| Db | 4521 | TGGATGGCATCATCATGTATGACAGCTGTGTGATCCGGGAGCTGCACACGCCCATATAT      | 4580 |
| QY | 1454 | GluGlnSerLeuYrMetYrLeuYrPheValILePheILeILePheGlySerPhePhe        | 1473 |
| Db | 4581 | GAAAGAAACCTGATACATGACCTGTACTGACTTGTATTCATATCTTGCGCTGCTTTC        | 4640 |
| QY | 1474 | ThrLeuAsnLeuPheILeGlyValILeILeAspAsnPheAsnGlnGlnLysLysPhe        | 1493 |
| Db | 4641 | ACTGTAATCATTCATCAGCGGTGCATCATRAGCAACTTCAACACAGAGAAAGATTT         | 4700 |
| QY | 1494 | GlyGlyGlnAspILePheMetThrGluGlnGlnLysLysTyrTrpAsnAlaMetLysLys     | 1513 |
| Db | 4701 | GGAGGCTCAAGCATCTTTATAGACAGAAAGAAACAGAAATATCTCAAGATGCAAGAG        | 4760 |
| QY | 1514 | LeuGlySerLysLysProGlnLysProILeProArgProGlyAsnLysPheGlnGlyMet     | 1533 |
| Db | 4761 | CTCGGCTCAAAAGAACTCGAAGGCCATCCCTCGGCGCTGCACAAATAATTCAGGGATG       | 4820 |
| QY | 1534 | ValPheAspPheValThrArgGlnValPheAspILeSerILeMetILeLeuILeCysLeu     | 1553 |
| Db | 4821 | GTCCTTGATTTTGTAAACCAACAAAGGTTTGACATCAGCATATATCTCATCTGCTTC        | 4880 |
| QY | 1554 | AsnMetValThrMetLeuValGluThrAspAspGlnSerGluTrpValThrThrLeu        | 1573 |

|   |      |   |      |
|---|------|---|------|
| D | 4881 | AAATGATGTGACCATGATGTGGAAACGGATGACAGACAAATACATGACCCCTGTTTGG        | 4940 |
| Q | 1574 | SeTaTgTlLeaSnLeuValPheLleValLeuPheThrGlyGlyValLeuLysLeuIle        | 1593 |
| D | 4941 | TCCCGAATCAACCTACTGTTCTTCTTCCTTCCTGAGGGGTTTCTGGAAAGCTCATC          | 5000 |
| Q | 1594 | SeTLeuAaRHisTyrTyrPheThrLleGlyTrpAsnLlePheAspPheValValIle         | 1613 |
| D | 5001 | TCCCTAGAGTACTACTACTTCACGATAGGGTGGAAACATCTTGGACTTTGGTGGTATT        | 5060 |
| Q | 1614 | LeuSerLleValGlyMetPheLeuAlaGluLeuLleGlyLysTyrPheValSerProthr      | 1633 |
| D | 5061 | CTCTGCATGTGTAGAGATGTTCTTCACAGACGGATAGAGAGATATTCTGCTCCCTAC         | 5120 |
| Q | 1634 | LeuPheAaTgValLleAaTgLeuAlaAaTgIleGlyAaTgIleLeuAaTgLeuLleLysGlyAla | 1653 |
| D | 5121 | CTGTCCGAGATCACTCCGCTGGCCAGATTTGGACAAATCTTACCCCTGATCAAAAGGCC       | 5180 |
| Q | 1654 | LysGlyLleAaTgThrLeuPheLeuPheAlaLeuMetSerLeuProAlaLeuPheAsnIle     | 1673 |
| D | 5181 | AAAGGGATCCGCACTGCTGCTTGTGGTATGATGATGCCCTTCTGGCGCTTTCACATC         | 5240 |
| Q | 1674 | GlyLeuLeuLeuPheLeuValMetPheLleTyrAlaLlePheGlyMetSerAsnPheAla      | 1693 |
| D | 5241 | GGCCTCTGCTTTTCTCGGTGATGATTCATCTACGCCATCTTGGAGTGCACATTTGCC         | 5300 |
| Q | 1694 | TyrValLysAaTgValGlyLleLysAspMetPheAsnPheGluThrPheGlyAsnSer        | 1713 |
| D | 5301 | TATGTTAAAAAAGCGCTGGAAATGTATGTGATCATGTTCAACTTGTGAGACTTTGGCAACGC    | 5360 |
| Q | 1714 | MetLleCysLeuPheGlnLleThrTrpSerAlaGlyTrpAspGlyLeuValAlaProIle      | 1733 |
| D | 5361 | ATGATCTGCTGTGTCCAAATCACCACTTGGCCGCTGGAGCGAGCTGTGCCCCATC           | 5420 |
| Q | 1734 | LeuAsnSerLysProPheAspCysAspProAsnLysValAsnProGlySerSerValLys      | 1753 |
| D | 5421 | CTCAAGAGCGCACTCCGACCTGACCCCGATGCAATTCACACCTGGAAAGCTCGGTAG         | 5480 |
| Q | 1754 | GlyAspCysGlyAsnProSerValGlyLlePhePheValSerTyrLleIleIleSer         | 1773 |
| D | 5481 | GGGAGACTGTGGAAACCATCCGGGGATTTCTTTTGTGCAGTACATCATATATATCC          | 5540 |
| Q | 1774 | PheLeuValValAlaAsnMetTyrLleAlaValIleLeuGluAsnPheSerValAlaThr      | 1793 |
| D | 5541 | TTTTTCTGTGTGTGGTGAACATGTACATGCTGTGATCTGGAAACCTTGAGGTGCCAC         | 5600 |
| Q | 1794 | GluGluSerAlaGluProLeuSerGluAspAspPheGluMetPheTyrGluValTrpGlu      | 1813 |
| D | 5601 | GAATAAAGTCAGACGCCCTCGACTGAGAGACACTTGTAGATTTGTACAGAGCTGGGAG        | 5660 |
| Q | 1814 | LysPheAspProAspAlaThrGlnPheMetGluPheGluLysLeuSerGlnPheAlaIle      | 1833 |
| D | 5661 | AAAGTTCACCTGACGCCACTGATTCATTAAGATTTCTGAAAGCTTCTGACTTTGGACGT       | 5720 |
| Q | 1834 | AlaLeuGluProProLeuAsnLeuProGlnProAsnLysLeuGlnLleIleAlaMetAsp      | 1853 |
| D | 5721 | GGCCTGATCTCCCTCTCTCATGCGCAAGGCCAAAGAGTCCAGCTATTGGCATGGAC          | 5780 |
| Q | 1854 | LeuProMetValSerGlyAspAaTgIleAsnLysLeuAspIleLeuPheAlaPheThrLys     | 1873 |
| D | 5781 | CTGGCCATGGTGAAGTGAAGACCCATCACTGCTGGACATCTGTTGCTTTAACAAAG          | 5840 |
| Q | 1874 | ArgValLeuGlyGluSerGlyGlyMetAspAlaLeuAaTgIleGlnMetGluGluAaPhe      | 1893 |
| D | 5841 | CGGGTCTCGGGCGAGATGTGAAGATGTGACGCTTTCGATTCCAATGAAATGCGCTTC         | 5900 |
| Q | 1894 | MetAlaSerAsnProSerLysValSerTyrGlnProLleThrThrLeuLysAaTgLys        | 1913 |
| D | 5901 | ATGGCTTCAACCCCTCAAGGTCTCTTAAGACCCATTAACCAACCACTGAACGGGAA          | 5960 |
| Q | 1914 | GlnGluGluValSerAlaValIleLleGlnAaTgAlaTyrArgArgHisLeuLysArg        | 1933 |

|   |   |  |      |
|---|---|--|------|
| Dd  | 5961  | CAGAGGAGGTGCTGCTGCATCATTCACGGCAATTAAATGATGTTACTTAAAACGA      | 6020 |
| Oy  | 1934  | ThrValIysSglnAlaSerPheThrTYrAsnLysAsnLysIleLysGlyAlaAsnLeu   | 1953 |
| Dd  | 6021  | CGGTAATAAACAATATGACAGTAATACGACAAAAGACACATCAAGGAGGATTGACTTG   | 6080 |
| Oy  | 1954  | LeuIleLysGluAspMetIleIleAspArgIleAsnGluAsnSerIlethrGluYsthr  | 197  |
| Dd  | 6081  | CCCTATTAAGAAGAGATATGCGTTATGTGACAAATGGAATTCACACCAGAAAAAGACG   | 6144 |
| Oy  | 1974  | AspleuthrMetSerThrAlaAlaCysProProSerTyrAspArgValThrLysProIle | 199  |
| Dd  | 6141  | GATGGAGACTTCCTCCACAACCTCT--CTCCCTTCCTATGACAGTGTAAACAAAACGAT  | 619  |
| Oy  | 1994  | ValGluLysHisGluGlnGluGlyLysAspGluLysAlaLysGlyLys             | 2009 |
| Dd  | 6198  | AAGGAAAGCTTGAGAAAGAACAAACAGAAAGAAATCAAAGGAGA                 | 6245 |
| <b>RESULT 15</b>  |   |  |      |
| ID  | AAT30195  |  |      |
| XX  | AAT30195 standard; cDNA; 6404 BP.                                     |  |      |
| XX  | AAT30195;   |  |      |
| Df  | 25-OCT-1996 (first entry)   |  |      |
| De  | Peripheral nervous system sodium channel peptide-1 alpha-subunit gene |  |      |
| XX  | Human; peripheral nervous system; sodium channel; PNIB;               |  |      |
| KM  | dorsal root ganglion; sodium-agonist; sodium-antagonist;              |  |      |
| KW  | drug screening; analgesic; hypotensive; antiinflammatory; trauma;     |  |      |
| RN  | pain; neurological disorder; antisense; gene therapy; ss.             |  |      |
| OS  | Homo sapiens.   |  |      |
| FH  | Key   | Location/Qualifiers  |      |
| FT  | CDS   | 49..6015   |      |
| FT  |   | /tag= a  |      |
| FT  |   | /product= PNIB protein                                       |      |
| FT  | misc_difference   | 334..336   |      |
| FT  |   | /tag= b  |      |
| FT  |   | /codon-seq:ACA, aa:Ala                                       |      |
| FT  | misc_difference   | 1738..1740   |      |
| FT  |   | /tag= c  |      |
| FT  |   | /codon-seq:ATA, aa:Leu                                       |      |
| PX  | WO9614077-A1.   |  |      |
| PD  | 17-MAY-1996.  |  |      |
| PF  | 02-NOV-1995;  | 95WO-US14251.  |      |
| PR  | 07-JUN-1995;  | 95US-0482401.  |      |
| PA  | (TROF-) TROPHIX PHARM INC.  |  |      |
| PI  | (UTNY ) UNIV NEW YORK STATE RES FOUND.                                |  |      |
| PT  | Borden LA, Halegoua S, Mandel G;                                      |  |      |
| DR  | WI, 1996-251547/25.   |  |      |
| PS  | P-PSDB; AAR99641.   |  |      |
| PT  | Nucleic acid encoding peripheral nervous system specific sodium       |  |      |
| PT  | channel peptide - useful for sodium channel-associated disease or     |  |      |
| PT  | tRNA.   |  |      |
| Example 4; Fig 14; 80pp: English.                                     |   |  |      |
| The sequence encodes a human peripheral nervous system sodium channel |   |  |      |
| peptide-1 alpha-subunit (PNIB), with sodium channel activity. A       |   |  |      |
| probe has been isolated by PCR from a human peripheral nervous        |   |  |      |
| system cDNA library, using probes derived from the rat PNI protein    |   |  |      |

CC sequence (AAR9638-39), and has been used to screen a human dorsal root ganglion cDNA library, to give the full-length sequence, using PCR primers AAR30198-99 and AAR18167. A related sequence (AAR30194) has also been isolated. The sodium channel peptide may be used to isolate sodium-agonists and sodium-antagonists for use as analgesics, hypotensives, antiinflammatories, and in therapy of sodium channel-associated pathology or trauma, e.g. neurological disorders. The DNA (in sense or antisense orientation) may be used in gene therapy.

XX Sequence 6404 BP; 1961 A; 1236 C; 1381 G; 1826 T; 0 other:

Alignment Scores:

| Pred. No.:             | 0       | Length:       | 6404 |
|------------------------|---------|---------------|------|
| Score:                 | 7903.00 | Matches:      | 1538 |
| Percent Similarity:    | 86.00%  | Conservative: | 194  |
| Best Local Similarity: | 76.37%  | Mismatches:   | 244  |
| Query Match:           | 76.01%  | Indels:       | 38   |
| DB:                    | 17      | Gaps:         | 13   |

US-09-930-871-12 (1-2009) x AAR30195 (1-6404)

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OY 2 GlnGlnThrValLeuValProProGlyProAspSerPheAsnPhenThrArgGlnSer 21
DB   ::::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 46 AAGATGGCAATGTCGTCCTCCAGAGACCTGACCTTGTCCATTTCACAAACAGTCT 105
OY 22 LeuAlaAlaIleGluArgArgIleAglGluGlySalAlaLysAsnProLysProAspLys 41
DB   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 106 CTGGCCCATTCATGAAACAGCATGCTCTGAAAGAAATCAAGAAAGAACCCAAAGAAAG 165
OY 42 LysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsnLeu 61
DB   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 166 AAGATGATGATGAAAGAACCCCAAGCCAGCATGATGATGGAAGCGGCAAAACATCTG 225
OY 62 ProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAsnAsp 81
DB   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 226 CCTTCATCATATGGGAGACATTCCTCCGCGCATGGGTAGAGACCCCTGAGGACTGAGAC 285
OY 82 ProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePheArg 101
DB   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 286 CCCATCATATGACAGACAAAGAAAGCTTTCATGATTAATGAAAGAAAGAAAGAAAGCTTC 345
OY 102 PheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIleAla 121
DB   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 346 TTCAATGCGACACCTGCTTATATATGCTTCTCTTCACCTCCATGAGAAATATCT 405
OY 122 IleLysIleLeuValIleSerLeuPheSerMetLeuIleMetCysThrIleLeuThrAsn 141
DB   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 406 ATTAAGATTTTATGACACTCTTATTCAGCATGCTCATGTCATGTCATATTCGACAAAC 465
OY 142 CysValAlaPheMetThrMetSerAsnProProAspThrThrLysAsnValGluTyrThrPhe 161
DB   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 466 TGCATATTTATGACATGAAATACCCCGGACGACGACAAAGATGCGATCACTTT 525
OY 162 ThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeuGlu 181
DB   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 526 ACTGGATATATATCTTTGATATCACTGTGTAAATTCCTCAAGAGCTTGTGTGAGA 585
OY 182 AspPheThrPheLeuArgAspProTyrAsnThrLeuAspPheThrValIleThrPheAla 201
DB   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 586 GAATTCACCTTCTCTGTCGACCGGTGACACTGCTGATTTTGTGCGCATGTTTGTGGC 645
OY 202 TyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgValLeu 221
DB   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 646 TATTTAAACAAATTTGAAACCTAGGCAATGTTCACTCTTCACTTCAATATATG 705
OY 222 ArgAlaLeuTyrThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeuIle 241
DB   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 706 AGAGCTTTGAAACATATTTCTGTATATCCAGGCTGAAAGCAATGTGAGGCGCTTGATGC 765
OY 242 GluSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerValPhe 261
DB   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 766 CAGTCAGTGAAGAGCTTCTGATGTCATGATCTGATCTGTCTGTCTGAGTGTGTTT 825

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OY 262 AlaLeuIleGlyLeuGluLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTyrPro 281
DB   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 826 GCACATATGAGCTACAGCTGTTCATGAGGAACCTGAAACATAAAGTTTCA----- 879
OY 282 ProThrAsnAlaSerLeuGluLeuIleSerIleGluLysAsnIleThrValAsnTyrAsn 301
DB   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 880 -----AATTCATCTGAAATAATCAACATTTAGAA----- 909
OY 302 GlyThrIleLeuIleAsnGluThrValPheGluPheAspTyrPheSerTyrIleGlnAspSer 321
DB   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 910 ---ACCATTAATGAATACCTTACAGAGTGAAGAGACTTTAGAA----- 948
OY 322 ArgTyrHisTyrPheLeuGluGluPheLeuAspAlaLeuLeuCysGlyLysSerSerAsp 341
DB   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 949 AATATTTTATATCTTTGAAAGATTCACAAAGATGCTCTCTTGTGTGTCAGCACAGAT 1008
OY 342 AlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyrGly 361
DB   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1009 TCAGGTCAGTGCCAGAGGGGTACACCTGTGGAATAATGGCAGAAACCTCATTAATGCG 1068
OY 362 TyrThrSerPheAspThrPheSerThrAlaPheLeuSerLeuPheArgLeuMetThrGln 381
DB   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1069 TACAGACCTTGTACACTTTCAGCTGAGCGCTTCTTAAGCTTGTTAAGCTATATGACCAA 1128
OY 382 AspPheThrGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMetIle 401
DB   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1129 GATTAAGTGGAAACCTTACCAACAGACGCTGCTGCTGCGGCAAAACATCATGATC 1188
OY 402 PhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAlaVal 421
DB   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1189 TTTCTTGTGCGTAGATTTTCTCTGCGCTCTTATATCTTAATTAATCTTATCTCTGCTGTG 1248
OY 422 ValAlaMetAlaTyrGluGluGluAsnGlnAlaThrLeuGluGluAlaGluGlnGlu 441
DB   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1249 GTTCCATATGGCATATGAAGAACACAGACCAACANTGAAGAACATTAACAGAAAGAA 1308
OY 442 AlaGluPheGlnIleMetIleGluGlnLeuLysLysGlnGlnGluAlaIleGlnIleAla 461
DB   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1309 TTGAATTTTCAACAGATGTAGACCGTCTTAAGAAAGCAAGAAAGAAAGCTGAGCAAT 1368
OY 462 AlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSerAsp 481
DB   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1369 GCAGCGCAGCGCGCTGAATATACAAAGTATTAAGGAAGACACAAATTAAGCGCTTCAGAG 1428
OY 482 SerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArgArg 501
DB   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1429 AGTTCTTCTGAACATCCAAAGCTGAGCTTAAAGTCTTAAAGAAAGAAAGAAAGAA 1488
OY 502 LysLysArgLysGlnLysGlnSerGlyGlnSerGlyGlnLysLysLysLysLysLysLys 520
DB   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1489 AAGAAAAGAAATCAAAAGAAAGCTCTCCAGTGGAGAGGAAAGGAGATGCTGAGAAATTTG 1548
OY 521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGlnGly 540
DB   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1549 TCGAAATCAAGAAATCAAGAGACACATCAAGAAAGAAAGTCTCACCTTGTGTGAAAGG 1608
OY 541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
DB   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1609 CATAGCGCAGACATCAAGAAAGTGTGTACCCCAATGATGATCACACATTCATTCGT 1668
OY 561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580
DB   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1669 GGTCTCTGTGTCTCAAGGCGCAAGCAGCAAGCAAGCTTTTGTGTTCAAGAGCAGA 1728
OY 581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspLeuHisSerThrPheGluAsp 600
DB   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1729 GGAAGAGATATGAGATCTGAGATGATATTTGCCAGATGATGACAGCATTTTGTGAGAC 1788
OY 601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyLysLysArgAsnSer 620
DB   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1789 AATGAGAGCAGAAAGGCGTCACTGTTGTGCCCCACAGACCCAGAGAGGAGCAGACACT 1848

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621 AsnLeuSerGlnThrSerArgSerArgMetLeuAlaValPheProAlaAsnGlyLys 640  
1849 AACATCACCAAGCCAGTAGGTGCCACCAATCTG-----CCGGTGAACGGGAAA 1899  
641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyIleProSerValPro 660  
1900 ATGCACATGCTGCTGACTGACAGAGGTGTGCTCCCTGGTGTGATGAGCAGCAGCCCTC 1959  
661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680  
1960 ATGCCCAATGACAGACCTCTGCCAGAGTGATATAGATAAAGCAACTCTGTATGAC 2019  
681 AsnGlyThrThrGlnThrGlnMetLeuArgLysArgArgSerSerSerPheHisValSer 700  
2020 AGCCGACAGACCAATCAATACAC---AAGAAAAGCGTTGATGCTCATCTCTTCA 2076  
701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleLeuSerIleLeu 720  
2077 GAGGATATGCTAATGATGCCAACCACAGACAGAGCAGATGATGAGCAGACCATATTA 2136  
721 ThrAsnThrValGluGlnLeuGlnLeuSerArgGlnLysCysProProCysTrpTrpLys 740  
2137 ACAAAACAGCTGGAGAACTGTGAAGAGTCCAGACAAATAATGCCCTTGCTGTACAG 2196  
741 PheSerAsnIlePheLeuIleTrpAspCysSerProTrpTrpLeuLysValLysHisVal 760  
2197 TTTCGACACAAATCTGTGATCTGGAATCTCTCCATATGGAATTAATAAATCAAAAGTGT 2256  
761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780  
2257 ACCTATTTATTTGATATGATGATCTTTGTGATGATCTTGCAATTCACATTTGCATAGTTTA 2316  
781 AsnThrLeuPheMetAlaMetGlnHisIleTrpPromethrAspHisAsnAsnValLeu 800  
2317 AACACATTTATTTATGCTATGGAACACACCAACCAATGATGAGAAATTAATAATGACTT 2376  
801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGlnMetPheLeuLysIleIle 820  
2377 GCTATGAGAAATTTGCTCTTACTGATCTTTCAGACCTGCAATGATGATTAATAATGAT 2436  
821 AlaMetAspProTrpTrpTrpPheGlnGlnGlyTrpAsnIlePheAspGlyPheIleVal 840  
2437 GCCATGATTCATATGATGATTTTCCAGATGAGGCTGCAATTTTTCACACCTATTTGTC 2496  
841 ThrLeuSerLeuValGlnLeuGlyLeuAlaAsnValGlnLysLeuSerValLeuArgSer 860  
2497 ACTTAACTTTAGTGAAGCTCTTTCTAGACAGATGGAAGATGTCAGTATGTCGATCA 2556  
861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880  
2557 TTCAGACTCTCCGAGCTCTTCAAGTTGGCAAAATCCGCGCAACATTTGAACATGCTGAT 2616  
881 LysIleIleGlnSerSerValGlyAlaLeuGlyAsnLeuThrLeuValIleAlaIleIle 900  
2617 AGATATTTGGTACTGACTAGTAGGAGGCTCTAGGACTCTACCTTAACTGTTGGCCATATC 2676  
901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTrpLysAspCysVal 920  
2677 GTCCTCATTTTCTGCTGCTGCGCATGCTCTTGTGTAAGACCTCAAAAGATGTCGTC 2736  
921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940  
2737 TGCAAATCAATGATGATGCTGCTGCTGCGCATGCTGCGCATGATGCACTTCTCCACTCC 2796  
941 PheLeuIleValPheArgValLeuCysGlyIleTrpIleGlnTrpMetCysPaspCysMet 960  
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961 GluValAlaGlyAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980  
2857 GAGGTGCTGCTGATGATGCTTATTTTACATGATGATGATGATGATGATGATGATGATG 2916  
981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu\*\*\*SerSerPheSerAlaAspAsnLeu 1000

2917 CTGTGTCCTTAACCTATTCTGCTTATTTAGAGCTATTAGTTAGTCAACATCTT 2976  
1001 AlaIleThrAspAspAsnGlnMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020  
2977 ACAGCAATTAATTAATGTAACAAACCTTACGTGAATTTATTTAAACATTTTCCAAA 3036  
1021 LysGlyValAlaThrValLysArgLysIleTrpGluPheIleGlnIleSerPheLeuArg 1040  
3037 AAGGGAATTAATTAATGTAACAAACCTTACGTGAATTTATTTAAACATTTTCCAAA 3096  
1041 LysGlnLysIleLeuAspIleLysProLeuAspAspLeuAsnLysLysAspSer 1060  
3097 AAGCAAAATTTTCCAGGAGATTAAGACAGAGATGATCTGAATCTTAAGAGAAAC 3156  
1061 CysMetSerAsnHisThr---\*GluIleGlyLysAspLeuAspTrpLeuLysAspVal 1079  
3157 TATATTTCTAATCAATCACTTCTGTAATGACAAAGTCAATATTTCTCAAGGAAAA 3216  
1080 AsnGlyThrThrSerGlyIleGlyThrGlySerSerValGlnLysTrpIleIleAspGlu 1099  
3217 GATTAATAATCAGT-----GGTTTGGAGCAGCTGACAAACATTTGATGAGAAC 3267  
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1120 GlyGluSerAspPheGlnAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGlu 1139  
3328 GGGCAATCCGATTTGGAAATATGATGCTGGAATCTTCAAGTATGCTGATGATGAT 1159  
1140 GluSerGlyGluLysLeuAsnGlnLysSerSerSerSerGlnGlySerThrValAspIle 1159  
3388 TACAGAAAGTGAATTAACCGG---TCAAGCTCTCTGAGAGCGACAGAGTGAATAC 3444  
1160 GlyAlaProValGlu---GluGlnProValValGluProGluLeuGlnLeuGluProGlu 1178  
3445 CCTTGCTGCGAGACAG 3504  
1179 AlaCysPheThrGlnGlyCysValGlnArgPheLysCysCysGlnIleAsnValGlnGlu 1198  
3505 GCCTGTTTCAAGATGATGTTGTGACGAGGTTCTCATGCTGCGCAAGTTAACAATGAGTCA 3564  
1199 GlyArgGlyLysGlnTrpTrpPheAsnLeuArgArgThrCysPheArgIleValGlnHisAsn 1218  
3565 GGGAAAGGAAATAATCTGCTGGAACATCAGGAAACCTGCTACAGATGTTGAACACAGT 3624  
1219 TrpPheGlnThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGlu 1238  
3625 TGCTTGAAGCTTCATTTGCTCATGATCTCTGCTGACAGTGTGCTGCTGCTTGA 3684  
1239 AspIleTrpIleAspGlnArgLysTrpIleLysThrMetLeuGlnTrpAlaAspLysVal 1258  
3685 GATATTTAATTTGAAGGAAAGAAAGACCATTAATATCTCGGAGTATGACAGACAGATC 3744  
1259 PheThrTrpIlePheIleLeuGlnMetLeuLysTrpValAlaArgLysTrpGlnThr 1278  
3745 TTCACCTTACATCTTCATCTGGAATGCTTAAAGATGATGATGATGATGATGATGATG 3804  
1279 TyrPheThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSer 1298  
3805 TATTTACCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3864  
1299 LeuThrAlaAsnAlaLeuGlyTrpSerGlnLeuGlyAlaIleLysSerLeuArgTrpLeu 1318  
3865 TTAGTGAACAAACCTTCTGCTACTCAGATGATGCTGCTGCTGCTGCTGCTGCTGCTG 3924  
1319 ArgAlaLeuArgProLeuArgAlaLeuSerArgPheGlnGlyMetArgValValAsn 1338  
3925 AGAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAA 3984  
1339 AlaLeuGlnAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrp 1358

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Db 3985 GCACATAGAGGACCAATTCCTCCATCATGAAATGCTACTTGTGTCTTAAATTCGG 4044
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Db 4045 CTGATATTCACATCATGATGAGTAATTTGTTGCGCAAGTCTCATGAGCTATTAAC 4104
Oy 1379 ThrThrThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLys 1398
Db 4105 ACCACAGATGGGTCAAGGTTTCTCTCAAGTCACAGTCACAAATCCCTCCGAAGTTTTC 4164
Oy 1399 LeuIleGluArgAsnGluThrAlaArgTyrPlysAsnValLysValAsnPheAspAsnVal 1418
Db 4165 CTATGAAATGTTAGTCAAAATGTGGATGGAAAACTGAAAGTAACTTGAATATGTC 4224
Oy 1419 GlyPheGlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTyrMetAspIleMet 1438
Db 4225 GGACTGGTACCTATCTCTGCTTCAAGTGCACACTTTTAAAGGATGACGATTAATAG 4284
Oy 1439 TyrAlaAlaValAspSerArgAsnValGluLeuGlnProLysTyrGluGluSerLeuTyr 1458
Db 4285 TATGACAGAGTGGATTCGTTAAATGTAGACACAGCCCAATATGAAATATAGCTTAC 4344
Oy 1459 MetTyrLeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPhe 1478
Db 4345 ATGTATATTTATTTTGTGTCTTAAATCTTGGGTCAATCTTCACTTGAATCTGTC 4404
Oy 1479 IleGlyValIleIleAspAsnPheAsnGlnGlnLysLysPheGlyGlyGlnAspIle 1498
Db 4405 ATGTGTATCATCATGATGATTAATTTCAACACAGAAAAAGAACTTGGAGGTCAACATTC 4464
Oy 1499 PheMetThrGluGluGlnLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLys 1518
Db 4465 TTTAAGACAGAGAAACACAAAGAAATACATATGCAATGAAAGAAAGCTGGGTCCAAAG 4524
Oy 1519 ProGlnLysProIleProArgProGlyLysAsnLysPheGlnGlyMetValIleAspPheVal 1538
Db 4525 CCACAAAAGCCAAATTCCTCGACAGGAAACAAATCCAGAGATGATATTTGACCTAGTG 4584
Oy 1539 ThrArgGlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMet 1558
Db 4585 ACAATATCAAGCCTTGAATATAGTATCATGCTTCTTATCTGTCACATGATGTAACATG 4644
Oy 1559 MetValGluThrAspAspGlnSerGluTyrValThrThrIleLeuSerArgIleAsnLeu 1578
Db 4645 ATGGTAGAAAGAGGCGTCAAGACATCATATGCTGAAGTTTATATGGAATTAATGTC 4704
Oy 1579 ValPheIleValLeuPheThrGlyGlyLysValLeuLysIleuIleSerLeuArgHisTyr 1598
Db 4705 GTTTTATTAATCCCTTTCACAGGAGATGTGCTTAAACAGATCTCCCTCAGACACTAC 4764
Oy 1599 TyrPheThrIleGlyTyrPAsnIlePheAspPheValValIleLeuSerIleValGly 1618
Db 4765 TACTTCACTAGATGAGATGAATATTTGATTTGTTGTTGATTAATCTCATGTAAGT 4824
Oy 1619 MetPheLeuAlaGluLeuIleGlyLysTyrPheValSerProThrLeuPheArgValIle 1638
Db 4825 ATGTTTCTAGCTAGTATGATGAACGATATTTGTCCTCCCTACCTGTCCTCCGAGTATC 4884
Oy 1639 ArgLeuAlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThr 1658
Db 4885 CGTCTTCCAGATTTGGCCCAATCTTACGCTTACTCAAGAGAGCAAAAGGGGATCCGACG 4944
Oy 1659 LeuLeuPheAlaLeuMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPhe 1678
Db 4945 CTGCTCTTGTGCTTGAATGATGCTCCCTTCGCGTGTGTTAAACATCGGCTCCGCTCTTC 5004
Oy 1679 LeuValMetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgGlu 1698
Db 5005 CTGGTCAATGTTCAATCATCGCATCTTGTGAATGCCAACTTGTCTATGTTAAAAAGGAA 5064
Oy 1699 ValGlyIleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPhe 1718
Db 5065 GATGGAATTAATGACATGTTCAATTTTGAACCTTTGGCAACAGATATGATTTGCTGTTTC 5124

Oy 1719 GlnIleThrSerAlaGlyTyrPAspGlyLeuAlaProIleLeuAsnSerLysPro 1738
Db 5125 CAATTAACAACCTCTCTGCTGGGATGAGATTCGACACATTTCTTAACTAAGCA 5184
Oy 1739 ProAspCysAspProAsnLysValAsnProGlySerSerValLysGlyLysAspCysGlyAsn 1758
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Oy 1759 ProSerValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValVal 1778
Db 5245 CCATCTGTTGAATATTCATCTTGTAGTATATCATCATATTCCTTCTGTTGGTG 5304
Oy 1779 AsnMetTyrIleAlaValIleLeuGlnAsnPheSerValAlaThrGluLeuSerAlaGlu 1798
Db 5305 AACATGTATCTGACGTCTACTGAGAAATTTAGTGTCCACATGAAAGAACTGTGAA 5364
Oy 1799 ProLeuSerGluAspAspPheGluMetPheTyrGluValTyrGlyLysPheAspProAsp 1818
Db 5365 CCTGTAGTAGAGGATGACTTGAATGTTCTATGAGGTTGGGAGAAAGTTTATCCGAT 5424
Oy 1819 AlaThrGlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaLeuGluProPro 1838
Db 5425 GCGACCGATTTATAGATTCCTTAACCTCTGATTTTGCAGCTGCCCTGATCCTCT 5484
Oy 1839 LeuAsnLeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSer 1858
Db 5485 CTTCATCATGCAAAACCCACAAACATCCAGCTATGTCATGTCATGCTGCCATGGTGTAGT 5544
Oy 1859 GlyAspArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGlu 1878
Db 5545 GGTGACCGGATCATGCTGTCTTACATCTTATTTGCTTTTACAAACGCTGTTTGGGTAG 5604
Oy 1879 SerGlyGluMetAspAlaLeuArgIleGluMetGluGluArgPheMetAlaSerAsnPro 1898
Db 5605 AGTGGGAGATGATCTCTTCTGTCACAGATGAGAAAGATCATGCTCAATATCT 5664
Oy 1899 SerLysValSerTyrGlnProIleThrThrThrLeuLysArgGlyGlnGluValSer 1918
Db 5665 TCCAAGGTCTCTATGAAACCCATGCACACACACACACACACACACACACACACACAC 5724
Oy 1919 AlaValIleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGlnAla 1938
Db 5725 GCTACTGTCATTCACGCGCTTATAGACGTTAACCGCTTAAGCAAAAGTCAAAATATTA 5784
Oy 1939 SerPheThrTyrAsnLysAsnLysIleLysGlyLys-----AlaAsnLeuLeuIle 1955
Db 5785 TCAAGTATATAC-----ATAAAGATGGAGACAGATGATGATTAATCTCAAT 5832
Oy 1956 LysGluAspMetIleIleAspArgIleAsnGlnLysAsnSerIleThrGluLysThrAspLeu 1975
Db 5833 AAAAAGATATGCGCTTGTGATATGATGAACTCAAGTCCAGAAAAACAGATCC 5892
Oy 1976 ThrMetSerThrAlaAlaCysProProSerTyrAspArgValThrLysProIleValGlu 1995
Db 5893 ACTTCATCCACACACCTCT---CAACCTCATATGATAGTGTAAACCAAGCAGCAAGAG 5949
Oy 1996 LysHisGluGlnGluGlyLysAspGluLysAlaLysGlyLys 2009
Db 5950 AAATATGAAACAGACAGAACAGAAAAAGAGAACAGAAAGGAAA 5991

Search completed: April 22, 2003, 23:37:48
Job time : 1071 secs
```

GenCore version 5.1.4-p5.4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

# OM protein - nucleic search, using frame\_plus.p2n model

Run on: April 22, 2003, 20:52:35 ; Search time 3697 Seconds

(without alignments)  
8800.847 Million cell updates/sec

Title: US-09-930-871-12

Perfect score: 10397

Sequence: 1 MEOYLVLPKPGSPDSFNFETRE.....TKRIVEKHEQKDEKAKK 2009

Scoring table:

|             |             |             |
|-------------|-------------|-------------|
| BLOSUM62    | Xgapop 10.0 | Xgapext 0.5 |
| Ygapop 10.0 | Ygapext 0.5 |             |
| Delop 6.0   | Delext 7.0  |             |
| Delop 6.0   | Delext 7.0  |             |

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-MODEL=frame.p2n.model -DEV=xlh
-O/cg2_1/USPTO.spool/US09930871/runat_16042003_114838_8471/app.query.fasta_1.2183
-DB=EST -QFMT=fastcap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45
-LOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09930871.ecgn.1.1.2946.ernat.16042003.114838_8471 -NCPU=6 -ICPU=3
-NO_XLPHY -NO_MMAP -LARGOQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Database :

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EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: gb_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score  | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------|
| 1          | 2231   | 21.5        | 1777   | 11    | BC029489    |
| 2          | 1368   | 13.2        | 928    | 14    | BC015936    |
| 3          | 1167.5 | 11.2        | 816    | 14    | BC044145    |
| 4          | 1148   | 11.0        | 735    | 13    | BC048967    |
| 5          | 1107   | 10.6        | 908    | 14    | BC046179    |
| 6          | 1100   | 10.6        | 674    | 12    | BC343331    |
| 7          | 1093   | 10.5        | 951    | 9     | AL333359    |
| 8          | 1076   | 10.3        | 902    | 12    | BC676119    |
| 9          | 1062   | 10.2        | 778    | 9     | AU035605    |
| 10         | 1046   | 10.1        | 665    | 10    | BB653350    |
| 11         | 1019   | 9.8         | 618    | 10    | BB622500    |
| 12         | 1007.5 | 9.7         | 809    | 12    | BC541438    |
| 13         | 987.5  | 9.5         | 706    | 9     | AA984063    |
| 14         | 976.5  | 9.4         | 689    | 12    | BC347024    |
| 15         | 974    | 9.4         | 602    | 9     | AL706368    |
| 16         | 965    | 9.3         | 774    | 13    | BI488799    |
| 17         | 952    | 9.2         | 579    | 14    | BM718214    |
| 18         | 940    | 9.0         | 731    | 9     | AI796228    |
| 19         | 927    | 8.9         | 562    | 14    | BM682680    |
| 20         | 903.5  | 8.7         | 1043   | 17    | CMS02Y68    |
| 21         | 894    | 8.6         | 671    | 13    | BA488035    |
| 22         | 888    | 8.5         | 831    | 12    | BC403969    |
| 23         | 880    | 8.5         | 547    | 12    | BF470392    |
| 24         | 876    | 8.4         | 934    | 9     | AL517958    |
| 25         | 853.5  | 8.2         | 952    | 13    | BI458325    |
| 26         | 851    | 8.2         | 662    | 12    | BC253038    |
| 27         | 846.5  | 8.1         | 608    | 10    | AM140953    |
| 28         | 845.5  | 8.1         | 700    | 10    | BB631922    |
| 29         | 844    | 8.1         | 561    | 12    | BF076296    |
| 30         | 843.5  | 8.1         | 939    | 13    | BI600029    |
| 31         | 830    | 8.0         | 610    | 9     | AL588672    |
| 32         | 823    | 7.9         | 873    | 12    | BF527027    |
| 33         | 819.5  | 7.9         | 694    | 9     | AL705279    |
| 34         | 817    | 7.9         | 598    | 14    | BM726341    |
| 35         | 806.5  | 7.8         | 656    | 10    | AV721039    |
| 36         | 801.5  | 7.7         | 944    | 14    | BO731018    |
| 37         | 800.5  | 7.7         | 615    | 10    | AM133907    |
| 38         | 800    | 7.7         | 665    | 10    | AV956239    |
| 39         | 794.5  | 7.6         | 544    | 12    | BF323267    |
| 40         | 791    | 7.6         | 509    | 11    | BC034643    |
| 41         | 791    | 7.6         | 510    | 11    | BC023034    |
| 42         | 789    | 7.6         | 547    | 12    | BE724185    |
| 43         | 788    | 7.3         | 877    | 12    | BF682878    |
| 44         | 754    | 7.3         | 1066   | 17    | CMS056AK    |
| 45         | 751.5  | 7.2         | 812    | 12    | BC666779    |

## ALIGNMENTS

RESULT 1  
LOCUS BC029489 1777 bp mRNA  
DEFINITION Homo sapiens, clone IMAGE:578436, mRNA.  
ACCESSION BC029489  
VERSION BC029489.1 GI:20809571  
KEYWORDS HTC.  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 1777)  
AUTHORS Strausberg, R.  
TITLE Direct Submission  
JOURNAL Submitted (01-MAY-2002) National Institutes of Health, Mammalian



REMARK  
COMMENT

Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
 NIH-MGC Project URL: <http://mgc.ncl.nih.gov>  
 Contact: MGC help desk  
 Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
 cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shliraki Toshiyuki and Piero Carninci (RIKEN)  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)  
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305  
 Web site: <http://www-shgc.stanford.edu>  
 Contact: (Dickson, Mark) [mdickpaxil.stanford.edu](mailto:mdickpaxil.stanford.edu)  
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.lnl.gov>  
 Series: IRAX Plate: 48 Row: h Column: 9  
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 10337596  
 This clone has the following problem: frame shifted.

## FEATURES

## source

1. 1777  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5278436"  
 /tissue\_type="brain, hypothalamus"  
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 /lab\_host="DH10B"  
 /note="Vector: pBluescript"

BASE COUNT 526 a 333 c 395 g 523 t  
 ORIGIN

## Alignment Scores:

Pred. No.: 3.48e-208 Length: 1777  
 Score: 2231.00 Matches: 441  
 Percent Similarity: 90.31% Conservative: 25  
 Best Local Similarity: 85.47% Mismatches: 34  
 Query Match: 21.46% Indels: 16  
 DB: 11 Gaps: 5

US-09-930-871-12 (1-2009) x BC029489 (1-1777)

QY 1 MetGluGlnThrValIleuValProGlyProAspSerPheasnphethrargGlu 20  
 DB 248 ATGGCAGAGTGGTGGTACCGCAGACCGTCCGCTCTTTTACCGAGGAA 307  
 QY 21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProasp 40  
 DB 308 TCCCTTGGCGATTCGAACAACGCAATTCGAGAAGAAGAAAGCTTAAGACCCAAACAGGAA 367  
 QY 41 LysLysAsp---AspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLys 59  
 DB 368 CCCAAGAGATGAGATGATGATAAATGCCCAAGCCAAACAGTCACTGGAAACAGGAAAA 427  
 QY 60 AsnLeuProPheIleGlyArgIleProGluMetValSerGluProLeuGluAsp 79  
 DB 428 TCTCTTCAATTAATTAATGAGACATTCCTCCAGAGATGGTGTCACTGGAGAGAT 487  
 QY 80 LeuAspProGlyTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIle 99  
 DB 488 CTGGACCCCTACTATCTCAATAAAGAAAGCTTAATGATTAATAAGGAAAGCAATC 547  
 QY 100 PheArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLys 119  
 DB 548 TCTCGATTAGTCCACCCCTGCTTACATTTTAATCTCCCTCAACCTATTAGAAA 607  
 QY 120 IleAlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeu 139  
 DB 608 TTAGCTATTAAAGATTTGGTACATCTTATTCATAATGCTCATTAATGTCACGATTTCT 667

QY 140 ThrAsnGlnValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyr 159  
 DB 668 ACCAAGCTGTATTTATGACCATGAGTAACCTCCAGACATGACAAAGAAATGTGAGAT 727  
 QY 160 ThrPheThrLysIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCys 179  
 DB 728 ACCCTTAACAGAAATTAATATCTTTTGAATCACTATTAATAATATCTGCAACGGCTTTTGT 787  
 QY 180 LeuGluAspPheThrPheLeuArgAspProTyrAsnTrpLeuAspPheThrValIleThr 199  
 DB 788 TTGGAAGATTTGCATTTTACGGGATCCATGCAATTTGGTGTGATTTTCACAGTCATTA 847  
 QY 200 PheAlaIleValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArg 219  
 DB 848 TTTCGATATGTCAGAGATTTGTGAGCTGGAGCTGGCAATGTCAGAGTTGAGAACATTCAGA 907  
 QY 220 ValLeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAla 239  
 DB 908 GTTCTCCGACCATTTGAACAAATTCAGTCACTTCACAGCCCTGAGACCATTTGGGGGCC 967  
 QY 240 LeuIleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSer 259  
 DB 968 CTGATCCAGTCAGTGAAGAAAGCTTTTCAATGTATGATCTTGAAGTGTCTGTCTTAAC 1027  
 QY 260 ValPheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGln 279  
 DB 1028 GTGTCCGCGCTAATAGATTCAGATTTGTCATGGGCACTACGAATTAATGTTTCCAA 1087  
 QY 280 TrpProThrAsnAlaSerLeuGluGlnHisSerIleGluLysAsnIleThr----- 297  
 DB 1088 TGGCTCCACAGATATATCT-----TCCCTTGAATTAATTAATCACTCTCTTC 1132  
 QY 298 -----ValAsnTyrAsnGlyThrLeuIleAsnGluThrValPheGluPheAsp 313  
 DB 1133 TTTAACATTCATTTGGATGGGAATGATGATGATCTTCAATGAGACAGTACATTAATTAAC 1192  
 QY 314 TrpLysSerTyrIleGlnAspSerArgTyrHisTyrPheLeuGluGluPheLeuAspAla 333  
 DB 1193 TGGGATGAATATATATGAGTAATAAAGTCACTTTATTTTAAAGGGGCAAAATGATGCT 1252  
 QY 334 LeuLeuGlnLysAsnSerSerAspAlaGlyGlnCysProGluGlyTyrMetCysValLys 353  
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 QY 354 AlaGlyArgAsnProAsnTyrGlyTyrThrSerPheAspThrPheSerTrpAlaPheLeu 373  
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 QY 374 SerLeuPheArgLeuMetThrGlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArg 393  
 DB 1373 TCTTATTTTGTCTCAGATCAAGACTTCTGGGAAACCTTTATCAACGACATGCT 1432  
 QY 394 AlaAlaGlyLysThrTyrMetIlePhePheValLeuValIlePheLeuGlySerPheTyr 413  
 DB 1433 GCTGCTGGGAAACGTAATGATATTTTGTGTGTCTATTTTCTTGGGCTCAATCTAT 1492  
 QY 414 LeuIleAsnLeuIleLeuAlaValAlaMetAlaTyrGluGluGlnAsnGlnAlaThr 433  
 DB 1493 CTATTAATTTGATCTTGGCTGTGGTGGCCATGATGAGGACGAATTCAGGCGACA 1552  
 QY 434 LeuGluGluAlaGluGlnLysGluAlaGluPheGlnGlnMetIleGluGlnLeuLysLys 453  
 DB 1553 TTGGAAGAGGCTGACAGGAAGAAAGCAATTCACAGATGCTGCAAGAGTTGAAAGAG 1612  
 QY 454 GlnGlnGluAlaAlaGlnGlnAlaAlaThrAlaThrAlaSerGluHisSerArgLysPro 473  
 DB 1613 CAACAGAAAGAAAGCT---CAGGGGCGAGCTGACCGCCATCTGTGATTAAGAGACTTC 1669  
 QY 474 SerAlaAlaGlyArgLys-----SerAspSerSerGluLysSerLysSer 490  
 DB 1670 AGTGGTCTGTGGAGATGAGAGTTTTCAGAGAGTCTTCAAGATCTTAAGTTGAGC 1729  
 QY 491 SerLysSerAlaLysGluArgArgAsnArgArgLysLysArgLysGln 506

|  |  |  |      |
|--|--|--|------|
| Db   | 1730   | TCGAAAGTGAAGAGCTGAAAAACAGAGAAAAA                               | 1777 |
| RESULT 2                                     |  |  |      |
| LOCUS  | BQ715936   |  |      |
| DEFINITION                                   | BQ715936   |  |      |
| ACCESSION                                    | BQ715936   |  |      |
| VERSION                                      | BQ715936   |  |      |
| KEYWORDS                                     | BQ715936.1   |  |      |
| SOURCE                                       | GI:21854835  |  |      |
| ORGANISM                                     | house mouse.   |  |      |
| REFERENCE                                    | Mus musculus   |  |      |
| AUTHORS                                      | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  |  |      |
| TITLE  | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. |  |      |
| JOURNAL                                      | NIH-MGC http://mgc.ncl.nih.gov/.                                   |  |      |
| COMMENT                                      | 1 (bases 1 to 928)   |  |      |
|  | National Institutes of Health, Mammalian Gene Collection (MGC)     |  |      |
|  | Unpublished (1999)   |  |      |
|  | Contact: Robert Strausberg, Ph.D.                                  |  |      |
|  | Email: cgapbs@mail.nih.gov   |  |      |
|  | Tissue Procurement: Susan L. Sullivan, PhD.                        |  |      |
|  | cDNA Library Preparation: Reggen, Invitrogen Corp                  |  |      |
|  | cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)          |  |      |
|  | -DNA Sequencing by: Agencourt Bioscience Corporation               |  |      |
|  | Clone distribution: MGC clone distribution information can be      |  |      |
|  | found through the I.M.A.G.E. Consortium/LLNL at:                   |  |      |
|  | http://image.llnl.gov  |  |      |
|  | Plate: LLAM13730 row: g column: 08                                 |  |      |
|  | High quality sequence stop: 715.                                   |  |      |
| FEATURES                                     |  |  |      |
| Source                                       | Location/Qualifiers  |  |      |
|  | 1..928   |  |      |
|  | /organism="Mus musculus"   |  |      |
|  | /db_xref="taxon:10090"   |  |      |
|  | /clone="IMAGE:6309535"   |  |      |
|  | /clone_lib="NIH-MGC_129"   |  |      |
|  | /lab_host="DH10B (phage-resistant)"                                |  |      |
|  | /note="Organ: olfactory epithelium; Vector:                        |  |      |
|  | pcwv-SPOrte.1.cdcd; Site_1: EcoRV; Site_2: NotI; Cloned            |  |      |
|  | unidirectionally. Primer: Oligo dT. Average insert size            |  |      |
|  | 2.2 kb. Constructed by: Reggen, Invitrogen Corp. Note: This        |  |      |
|  | is a NIH-MGC Library."   |  |      |
| BASE COUNT                                   | 204 a 247 c 227 g 249 t  | 1 others   |      |
| ORIGIN                                       |  |  |      |
| Alignment Scores:                            |  |  |      |
| Pred. NO.:                                   | 1,11e-123  | Length:  | 928  |
| Score:                                       | 1368.00  | Matches:   | 279  |
| Percent Similarity:                          | 94.52%   | Conservative:  | 14   |
| Best Local Similarity:                       | 90.00%   | Mismatches:  | 13   |
| Query Match:                                 | 13.16%   | Indels:  | 4    |
| DB:  | 14   | Gaps:  | 0    |
| MS-09-930-871-12 (1-2009) x BQ715936 (1-928) |  |  |      |
| OY   | 1610   | ValValValIleLeuSerTlleValGlyMetPheLeuAlaGluLeuIleGlyLysTyrrPhe | 1629 |
| Dd   | 1  | GGGGTGCGATTCCTCCTCAATTCTAGCAATGTCTTCCGTGACCTGATGAGAATATTT      | 60   |
| OY   | 1630   | ValSerProThrLeuPheArgValIleArgLeuAlaArgIleGlyArgIleLeuArgLeu   | 1649 |
| Dd   | 61   | GTGTCTCTACCCCTTCCTCCGACTCATCCGCCCGCAGAGATTGAGCAATCCTACGCCG     | 120  |
| OY   | 1650   | IleuysGlyAlaIleGlyIleArgThrLeuLeuPheAlaLeuMetSerLeuProala      | 1659 |
| Dd   | 121  | ATCAAAGGCCCAAGGGAGATCCGACGCTGCTTTCCTCTATATATGCTCTTCTGCG        | 180  |
| OY   | 1670   | LeuPheAsnIleGlyLeuLeuLeuPheLeuValMetPheIleTyrAlaIlePheGlyMet   | 1689 |
| Dd   | 181  | CTGTTCAACATCGGCTCCTGCTTTCCTCCGTCATGTCATCTACGCCATCTTGGGAG       | 240  |
| OY   | 1690   | SerAnpHeaIatryValIlyArGluValGlyIleApPhMePheAsnPheGluTr         | 1709 |

|            |   |  |      |
|------------|---|--|------|
| Db         | 241   | TCCAACTTGGCTTAAGTTAAAAAAGAAGCGCTGGAATTTGACATTGTCACTTCACCTTGAGACT | 300  |
| Oy         | 1710  | PhegIyaanSerMerIIcylSenphelInIlethrPrSerAlaGIYTPraSglyLeu        | 1729 |
| Db         | 301   | TTTTGGCAACAGCATGATGTGCCTGTTCCAAATCACACCACCTCTGCCGGCTGGAGTAGCATG  | 360  |
| Oy         | 1730  | LeuaIAProIleLeuaNsSerLySProPoaSpCYasAPProAsnLysValaSnProGly      | 1749 |
| Db         | 361   | TTGGCCCCCATTCTCAACAGTCACCTCTGACTGTGACCCTGATGCATTACCTACCTTGA      | 420  |
| Oy         | 1750  | SerSerValIysglYaspCySglYasnProSerValGIylePhapheVaslSerTyR        | 1769 |
| Db         | 421   | AGCTGAGTGAAGGAGAGACTGTGGGAACCAACATCTGTGGGAGATTTCTTTTGTACAGTAC    | 480  |
| Oy         | 1770  | IlelleIieserPheluvalValValaSmectrYrIlelaValIlleluansphe          | 1789 |
| Db         | 481   | ATCAACAATATCCCTCTGTGTGTGTGAACAATGATCAATTCGTATCTCCGAGAACCTTC      | 540  |
| Oy         | 1790  | SerValAlaThGluglUserAlaglUpProleuSerGluaSPASPpHeGlumepHetYr      | 1809 |
| Db         | 541   | AGCGTTGCCACAGAAAGATGACAGACCCCTGAGTGAAGACGACTTGGATGTCTTAC         | 600  |
| Oy         | 1810  | GluaValITripGlulYspPheaSPProaSPalArhGlnPheMetGlupHeglulYlsEusEr  | 1829 |
| Db         | 601   | GAGGTCTGGAGAAATTTGCACCTCTACGCCACCCAGTTTCATGATTTTGCAGAGTCTCT      | 660  |
| Oy         | 1830  | GlnPheAlaIalaIleuGlupRobProleuSnleUProgInProaSnLysLeuGlnLeu      | 1849 |
| Db         | 661   | GACTTGGAGCTGCCTGTGATCTCTCCCTCCCTCAATCCAGAAAGCCAAAGTCCAGCTGC      | 720  |
| Oy         | 1850  | IleAlaMetAspLeuProMetValSerGIyAsparGIleHisCylEuaSprIleLeupe      | 1869 |
| Db         | 721   | ATTGCCATGAGACTCTCCCATGGTGAAGAGACCCATCCACTGTGCGACATCTTATTT        | 780  |
| Oy         | 1870  | AlaPheThrLysArgVal-IeuGIY-GluSerGIYGlumetAsPalaleu-ArgIleGln     | 1888 |
| Db         | 781   | GCTTTTACAAACGGGGTCCCTGGGTGANNAGTGAAGAAATGATGCCCTTCAATCAGA        | 840  |
| Oy         | 1899  | MecGlugluary-PhemetAlaSerAsnProSerLysValSerTYrGlnProIlethrTh     | 1908 |
| Db         | 841   | ATGGAAGATAGGGGTTCATGCGTTCCAATCCCACGAGGGCTCTPTATWGAGCCATTAAAC     | 900  |
| Oy         | 1908  | rThreutysArGLysGlnGlu 1915                                       |      |
| Db         | 901   | CACCTGTGAAGCGCCAACACGAA 922                                      |      |
| RESULT 3   | BQ444145  | 816 bp mRNA linear EST 29-MAY-2002                               |      |
| LOCUS      | BQ444145  |  |      |
| DEFINITION | UT-M-EXO-bxj-d-14-0-UI.r1 NIH_BMAP_EXO Mus musculus cDNA clone IMAGE:5708893 5', mRNA sequence. |  |      |
| ACCESSION  | BQ444145  |  |      |
| VERSION    | BQ444145.1 GI:21247257  |  |      |
| KEYWORDS   | EST.  |  |      |
| SOURCE     | house mouse.  |  |      |
| ORGANISM   | Mus musculus  |  |      |
| REFERENCE  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;                               |  |      |
| AUTHORS    | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.                              |  |      |
| TITLE      | 1 (bases 1 to 816)  |  |      |
| JOURNAL    | NIH-MGC http://mgc.ncl.nih.gov/.  |  |      |
| COMMENT    | National Institutes of Health, Mammalian Gene Collection (MGC) unpublished (1999)               |  |      |
|            | Contact: Robert Strausberg, Ph.D.   |  |      |
|            | Email: rgs@bhs-riemail.nih.gov  |  |      |
|            | Tissue Procurement: Dr. James Lin, University of Iowa   |  |      |
|            | cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa                               |  |      |
|            | cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa                                |  |      |
|            | DNA Sequencing by: Dr. M. Bento Soares, University of Iowa                                      |  |      |
|            | Clone Distribution: MCC clone distribution information can be                                   |  |      |
|            | found through the I.M.A.G.E. Consortium/LIML at:  |  |      |
|            | http://image.liml.gov   |  |      |
|            | This clone was contributed by the Brain Molecular Anatomy Project (BMAP)                        |  |      |





|                        |  |  |                             |
|------------------------|--|--|-----------------------------|
| OY                     | 1573   | IeuSerArgIleasnLeuValPheIleValIleuPheThrGlyIuCysValIleuLysLeu    | 1592                        |
| Dd                     | 546  | CCTACATGGATTAACTGGCTTCGTGCATCTTCCACCCTCGCACTGTGTGCTCAAATAG       | 605                         |
| OY                     | 1593   | IleSerLeuArgHisTyrTyrrPheThrIleGlyTTPAsnIlePheAspPheValValAl     | 1612                        |
| Dd                     | 606  | TTCGCTTGAGACACTACTAATTTCACCAATTTGGCTGGAAACATCTTGACTTTGTGTGGC     | 665                         |
| OY                     | 1613   | IleLeuSerIleValGlyMetPheLeuNlaGluLeuIleGlu-LysTyrPheValSerPro    | 1632                        |
| Dd                     | 666  | ATTCTCTCATTTGTGGGAATGTTCCTGGCTGATATCATATTGAGGAATGACTTCGTCTCCC    | 725                         |
| OY                     | 1632   | OrthleuPheArgValIleIleArgLeu-AlaArgIle-GlyArgIleLeuArg-IleuIleLy | 1651                        |
| Dd                     | 726  | GACCCATTATTCGCGCATCCGATTCGATGGGCCGCGATGGGGCGCATCTTCGTTCATCA      | 785                         |
| OY                     | 1651   | sglValAlaysgIleArg---ThrlleuPheAlalaueMetSetleuPro---Al          | 1669                        |
| Dd                     | 786  | AGGCCCCCAAGAGATCCGCCACCCCTGCTCTTGGCCCTTAATGATGTCCGCGCCGCC        | 845                         |
| OY                     | 1669   | aleuPheasnIleGlyLeuLeuLeu---PheLeuValMetPheIleTyr                | 1684                        |
| Dd                     | 846  | CTGTTTCACAATCGGCGCTCCGCTCCTTCCTGGNCATGTTCATCTT                   | 894                         |
| RESULT 6               |  |  |                             |
| LOCUS                  | Bg342331   | 674 bp   | mRNA linear EST 27-FEB-2001 |
| DEFINITION             | 603374246r1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4481819 5'..  |  |                             |
| ACCESSION              | Bg342331   |  |                             |
| VERSION                | Bg342331.1   |  |                             |
| KEYWORDS               | EST.   |  |                             |
| SOURCE                 | house mouse.   |  |                             |
| ORGANISM               | Mus musculus   |  |                             |
| REFERENCE              | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  |  |                             |
| AUTHORS                | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.   |  |                             |
| TITLE                  | 1 (bases 1 to 674)   |  |                             |
| JOURNAL                | NIH-MGC http://mgc.ncl.nih.gov/.   |  |                             |
| COMMENT                | National Institutes of Health, Mammalian Gene Collection (MGC)<br>Unpublished (1999)<br>Contact: Robert Strausberg, Ph.D.<br>Email: cgaps@remail.nih.gov<br>Tissue Procurement: The Ceeko Laboratory<br>cDNA Library Preparation: Life Technologies, Inc.<br>DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)<br>Genome Sequencing by: Incyte Genomics, Inc.<br>Clone distribution: MGC clone distribution information can be<br>found through the I.M.A.G.E. Consortium/LLNL at:<br>http://image.llnl.gov<br>Plate: LAM10317 row: 1 column: 12<br>High quality sequence stop: 672.<br>Location/Qualifiers<br>1..674<br>/organism="Mus musculus"<br>/db_xref="taxon:10090"<br>/clone="IMAGE:4481819"<br>/clone_lib="NIH MGC_94"<br>/tissue_type="retina"<br>/lab_host="DH10B (phage-resistant)"<br>/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;<br>Site_2: SalI; Cloned unidirectionally; oligo-dr primed,<br>Average insert size 3.3 kb. library enriched for<br>full-length clones and constructed by Life Technologies.<br>Note: this is a NIH_MGC library." |  |                             |
| BASE COUNT             | 146 a 167 c 161 g 200 t  |  |                             |
| ORIGIN                 |  |  |                             |
| Alignment Scores:      |  |  |                             |
| Pred. No.:             | 1,65e-97   | Length:  | 674                         |
| Score:                 | 1100.00  | Matches:   | 220                         |
| Percent Similarity:    | 98.67%   | Conservative:  | 2                           |
| Best Local Similarity: | 97.78%   | Mismatches:  | 1                           |
| Query Match:           | 10.58%   | Indels:  | 1                           |

DB: 12 Gaps: 0

US-09-930-871-12 (1-2009) x BG342331 (1-674)

OY 1532 GlyMetValPheAspPheValThrArgLysValPheAspIleSerIleMetIleLeu 1551

DB 1 GGAATGGTTTTGACTTTTGCTTAACCGAAGAAGTTTGATATCAGATCATGATCTCTCATC 60

OY 1552 CysLeuAsnMetValThrMetLeuValGluThrAspAspGlnSerGluTyrValThrThr 1571

DB 61 TGTCTGAACATGATGTACCATGATGTGTGGAAGACGATGACCAAGAGCATATATGTGACAAAGC 120

OY 1572 IleLeuSerArgIleAsnLeuValPheIleValLeuPheMetIleGlyGluCysValLeuLys 1591

DB 121 ATTTTGTCACGGATCAACCTGGTGTGTCTGCTCCGTGTCACCGGGAGTGTGTGCTCAAG 180

OY 1592 LeuIleSerLeuArgHisTyrTyrPheThrIleGlyTyrPasnIlePheAspPheValVal 1611

DB 181 CTCATCTGCTCCCTCCCATATATATTTTCACCATGSGATGGAACATTTTGCAATTTTGATG 240

OY 1612 ValIleLeuSerIleValGlyMetPheLeuValGluLeuIleGluLysTyrPheValSer 1631

DB 241 GTCATCTCTCCATGTATGAGGATGTGTTCTTGCGGAGGCAATATGAAAGAATTTTGTGCT 300

OY 1632 ProThrLeuPheArgValIleArgLeuValAspArgIleGlyArgIleLeuArgLeuIleLys 1651

DB 301 CCTACCTGTTCCGAGTATCCGCTCATCCGCTGGCCAGAGATTTGACGAAATCTTACGGCTGATCAA 360

OY 1652 GlyAlaLysGlyIleArgThrLeuLeuPheAlaLeuMetSerLeuProAlaLeuPhe 1671

DB 361 GGTGGCAAGGGGATCCGACAGCTGCTGTTGGTCGATGATGATCCCTTCCTGGCTGTTT 420

OY 1672 AsnIleGlyLeuLeuLeuPheLeuValMetPheIleTyrAlaIlePheGlyMetSerAsn 1691

DB 421 AACATCGGCGTCCCTCTTTTCTGCTCATGTTCATCTACGCCATCTTTGGATGTGCCAAC 480

OY 1692 PheAlaTyrValLysArgGluValGlyIleAspAspMetPheAsnPheGluThrPheGly 1711

DB 481 TTGGCTTATGTTAAAGAGGAAGTGTGGATGTATGATCATGTTCACACTTGTGAGACCTTGGCC 540

OY 1712 AsnSerMetIleCysLeuPheGlnIleLeuThrSerAlaGlyTyrAspGlyLeuLeuAla 1731

DB 541 AACACATGATCTGCTCTTCCAAATTCACACATCTCGGGCGTGGAGATGATGCTGGCC 600

OY 1732 ProIleLeuAsnSerLysProProAspCysAspProAsnLysValAsnProGlySerSer 1751

DB 601 CCCATCTCCCAAAAGGAACCCCTACGTCTGACCTTAATAAGTTAACCTTGGAAGCTCG 659

OY 1752 ValLysGlyAspCys 1756

DB 660 GTGAAGGAGACTGT 674

RESULT 7

LOCUS AL533359 951 bp mRNA linear EST 13-FEB-2001

DEFINITION AL533359 LTI\_FLO15\_Brn1 Homo sapiens cDNA clone CS0ND004YF22 5

ACCESSION AL533359

VERSION prime, mRNA sequence.

KEYWORDS AL533359.1 GI:12796852

EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 951)

AUTHORS Li,W.B., Gruber,C., Jesssee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 Evry cedex - France

Email: seque@genoscope.cns.fr, web : www.genoscope.cns.fr.

Location/Qualifiers

FEATURES

**Source**

```

source
1. .951
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/db_xref="taxon:9606"
/clone="CS0DN004YR22"
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/sex="male"
/tissue_type="Adult brain"
/notice="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by life technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA fax : (1) 301 610 8371 Email : fliang@lifestech.com URL : http://fulllength.invitrogen.com"
189 c 203 g 247 t 9 others

```

|  |                 |
|--|-----------------|
| Alignment Scores:                            |                 |
| Pred. No.:                                   | 1,29e-96        |
| Score:                                       | 1093.00         |
| Percent Similarity:                          | 96.43%          |
| Best local Similarity:                       | 95.98%          |
| Query Match:                                 | 10.51%          |
| DB:  | 9               |
| US-09-930-871-12 (1-2009) x AL533359 (1-951) |                 |
|  | Length: 951     |
|  | Matches: 215    |
|  | Conservative: 1 |
|  | Mismatches: 8   |
|  | Indels: 0       |
|  | Gaps: 0         |

|    |      |   |      |
|----|------|---|------|
| QY | 1786 | LeuLysuSpheSerValAlaIthrGluLysuSerAlaGluProLeuSerGluuSpAspHe    | 1805 |
| Db | 3    | CTGGAGAACTTCMKWTGTTGGCTACTGAAGAAGTCGACACCTCTCAKGTAGGATACCTT     | 62   |
| QY | 1806 | GluuMetPheTyrGluValITrpGluLysPheAspProAspAlaThrGluPheMetGluDhe  | 1825 |
| Db | 63   | TAGATGTTCTATGAGCTGTTGGAGAAAGTTGATCCGATGCAACTCATGTTCAAGATT       | 122  |
| QY | 1826 | GluLysLeuSerGluPheAlaAlaAlaLeuGluProProLeuAsnLeuProGluProAsn    | 1845 |
| Db | 123  | GAATAATTAATCTCGTTTGAGCGTGGCGTTGAACCGCCCTCTCAATCTGCCAACAAAC      | 182  |
| QY | 1846 | LysLeuGluLeuLeuAlaMetAspLeuProMetValSerGluYAspArgIleHisCysLeu   | 1865 |
| Db | 183  | AAATCTCAGGCTCATTTGGCAGATGGATTTGCCATGTAAGTGAAGTCGAGATCCACGTCT    | 242  |
| QY | 1866 | AspIleLeuPheAlaPheThrLysArgValLeuGlyGluSerGlyGluMetAspAlaLeu    | 1885 |
| Db | 243  | GATATCTTAATTTGCTTTTACAAAGCGGCTCTGTAGAGAAAGTGGAGAGATGATGCTCTA    | 302  |
| QY | 1886 | ArgIleGluMetGluLysArgPheMetAlaSerAsnProSerLysValSerTyrGluPro    | 1905 |
| Db | 303  | CGAATACAGATGAGAAAGCCATTCATGCTTCCAAATCCTTCCAAGCTCTCCTATACGCA     | 362  |
| QY | 1906 | IleThrThrThrLeuLysArgLysGluGluGluValSerAlaValIleIleIleAlaArgAla | 1925 |
| Db | 363  | ATCACTACTACTTAAACAGAAAAACAGAGAGAGTATCTGCTGCTATTCACAGGTGCT       | 422  |
| QY | 1926 | TyrTrpArgHisLeuLeuLysArgThrValLysGluAlaSerPheThrTyrAsnLysAsn    | 1945 |
| Db | 423  | TACAGAGCCACCTTTTAAAGCCAGACTGTAAACAAGCTTCCTTACGATCAATTAAC        | 482  |
| QY | 1946 | LysIleLysGlyLysAlaAsnLeuLeuIleLysGluAspMetIleLeuAspArgIleAsn    | 1965 |
| Db | 483  | AAATCAAGAGTGGGCTAATCTTCTTATTAAMAKAAGACATGATTAATTACAGATAAT       | 542  |
| QY | 1966 | GluAsnSerIleIleThrGluLysThrAspLeuThrMetSerThrAlaAlaCysProProSer | 1985 |
| Db | 543  | GATAACTCTATTACAGNAAAAAACGATCGACATCGACATGCCACGACCTTGCCACCTTCC    | 602  |
| QY | 1986 | TyrAspArgValIThrLysProIleValGluLysHisGluGluGluGlyAspLysLys      | 2005 |
| Db | 603  | TATATCCGGGGACAAAGCCAAATTTGTGGAAAAACATGACACAGAAAGCCAAAGATATAAAA  | 662  |

| QY | 2006 | AlaLysGlyLys | 2009 |
|----|------|--------------|------|
|    |      |              |      |
| Db | 663  | GCCAAAGCGAA  | 674  |

|            |   |
|------------|---|
| RESULT     | 8   |
| BG761119   |   |
| LOCUS      |   |
| DEFINITION | 902 bp mRNA linear EST 15-MAY-2001                              |
| ACCESSION  | 60271745F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4841124 5', |
| VERSION    | mRNA sequence.  |
| KEYWORDS   | BG761119  |
| SOURCE     | BG761119 1 GI:14071772  |
| ORGANISM   | EST.  |
| REFERENCE  | Human . . . 54200   |

## FEATURES

Romo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
1 (Bases 1 to 902)  
NIH-MGC <http://mgc.ncl.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapds-remail.nih.gov](mailto:cgapds-remail.nih.gov)  
Tissue Procurement: ATCC/DCTD/DRP  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LINC1673 row: g column: 13  
High quality sequence gap: 750.  
Location/Qualifiers  
1..902

|            |       |       |       |       |
|------------|-------|-------|-------|-------|
| BASE COUNT | 251 a | 174 c | 215 g | 262 t |
| ORIGIN     |       |       |       |       |

|                        |          |
|------------------------|----------|
| Alignment Scores:      |          |
| Pred. No.:             | 5,64e-95 |
| Score:                 | 1076.00  |
| Percent Similarity:    | 81.33%   |
| Best Local Similarity: | 72.47%   |
| Query Match:           | 10.35%   |
| DB:                    | 12       |
| Length:                | 902      |
| Matches:               | 229      |
| Conservative:          | 28       |
| Mismatches:            | 43       |
| Indels:                | 23       |
| Gaps:                  | 1        |

US-09-930-871-12 (1-2009) x BG761119 (1-902)

[illegible]



| FEATURES                                      |   | Location/Qualifiers   |      |
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| source  | 1..778  |   |      |
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|   | /strain="C57BL"   |   |      |
|   | /db_xref="taxon:10090"  |   |      |
|   | /clone_1lb="MCD-0634"   |   |      |
|   | /clone_1lb="Sugano mouse brain mncb"  |   |      |
|   | /sex="female"   |   |      |
|   | /dev_stage="adult"  |   |      |
|   | /lab_host="TOP10"   |   |      |
|   | /note="Organ: brain; Vector: pME18S-F13; 1st strand cDNA was primed with an oligo(dT) primer AATGGCCCTTTTATTTTATTTT; double-stranded cDNA was ligated to a DraIII adaptor (TGTGGCCATCGG), digested into distinct DraIII sites of the pME18S-F13. XbaI sites just outside the DraIII sites can be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5 kb. Library was constructed by Sugano et al. (University of Tokyo, Institute of Medical Science) Custom primer used for sequencing: 5' end primer [CTTCTGCTTAAAGCTGGG], 3' end primer [CGACTCGACGCTCGACGACA]." |   |      |
| BASE COUNT                                    | 196 a 192 c 165 g 223 t   | 2 others  |      |
| ORIGIN  |   |   |      |
| Alignment Scores:                             |   |   |      |
| Pred. NO.:                                    | 1..1e-93  | Length:   | 778  |
| Score:  | 1062.00   | Matches:  | 228  |
| Percent Similarity:                           | 90.04%  | Conservative:   | 7    |
| Best Local Similarity:                        | 87.36%  | Mismatches:   | 21   |
| Query Match:                                  | 10..21%   | Indels:   | 6    |
| DB:   | 9   | Gaps:   | 2    |
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| OY  | 1459  | MetTyrLeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPhe    | 1478 |
| DB  | 2   | ATGATCTGTACTTGTGCATCTTCATCATCTTTGGGTCTTCTTCACTTAATCTATTC        | 61   |
| OY  | 1479  | IleGlyValIleIleAspAsnPheAsnGlnGlnLysLysLysPheGlyGlnAspIle       | 1498 |
| DB  | 62  | ATCGCGCTCATACAGACCACTTCAACACGACGACAAAGAAATTTGGAGCTCAACATC       | 121  |
| OY  | 1499  | PheMetThrGlnGlnGlnLysLysTyrTyrAsnAlaMetLysLysIleGlnSerLys       | 1518 |
| DB  | 122   | TTTATGACAGAGGCGAGAAAGTACTCAAAATGACATAGAAAGAACTGGCTCCAAAAA       | 181  |
| OY  | 1519  | ProGlnLysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheVal    | 1538 |
| DB  | 182   | CCTGAGAAAGCCCATCCTCGACCTGCAACCAATTTCAAGAAATGCTTTTACTTTGTA       | 241  |
| OY  | 1539  | ThrArgGlnValPheAspIleSerIleMetIleIleGlnLysLeuAsnMetValThrMet    | 1558 |
| DB  | 242   | ACCGAGACAAGTGTGACATCAGCATCATGATCTCATCTGAGCTCAACATGATGACATG      | 301  |
| OY  | 1559  | MetValGlnThrAspAsnGlnSerGlnTyrValThrThrIleLeuSerArgIleAsnLeu    | 1578 |
| DB  | 302   | ATGGTGGAAACGGACGACGACGACCAATATCATCCCTGTGTTGTGCCGAATCAACCTG      | 361  |
| OY  | 1579  | ValPheIleValLeuPheThrGlnGlyGlnLysValIleLysLeuIleSerLeuThrGlnTyr | 1598 |
| DB  | 362   | GTAATTCATCGTCCCTTTCATCTGGGAGATTCTCTCTAAGCTATCTCTTCAGATACAC      | 421  |
| OY  | 1599  | TyrPheThrIleGlyTyrAsnIlePheAspPheValValIleLeuSerIleValGly       | 1618 |
| DB  | 422   | TACTTCACGATGTGGCTGACATCTTGACTTTGTGTGTGATTCCTCATTTGATAGAA        | 481  |
| OY  | 1619  | MetPheLeuAlaGlnLeuIleGlnLysTyrTyrPheValSerProThrLeuPheArgValIle | 1638 |
| DB  | 482   | ATGTTCTCTGCTGAGAGAGAGATTTTGTCTCTCCACCTGTGTCGAGCTATTC            | 541  |



| QY         | 1982  | ValVallieusantlePheleuAlaleuenu**SerSerPheSerAlaAspAntleuAla | 1001 |
|------------|---|--|------|
| Db         | 541   | GTGGGCGTGAACCTATTATTTCTGCGCTTCTGAGCTCTTCACGGCAGACAAATCTGGCG  | 600  |
| QY         | 1002  | AlaThrAspAspAspAsngluMetAsnAsnleuGlnIleValaVal               | 1016 |
| Db         | 601   | GCACGGACGACGACGAGGGGAATGAAACAACCTGCAGATATCGGTG               | 645  |
| RESULT 11  |   |  |      |
| LOCUS      | BB622500  | 618 bp   | mRNA |
| DEFINITION | BB622500 RIKEN full-length enriched, adult male olfactory brain Mus musculus CDNA clone 6430408L10 5', mRNA sequence.   |  |      |
| ACCESSION  | BB622500  |  |      |
| KEYWORD    | BB622500.1 GI:15397780  |  |      |
| SOURCE     | house mouse.  |  |      |
| ORGANISM   | Mus musculus  |  |      |
| REFERENCE  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 618)   |  |      |
| AUTHORS    | Arakawa,T., Carinci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hikawa,K., Horii,F., Ishii,Y., Ito,M., Kawai,J., Komno,H., Kouda,M., Koya,S., Matsuyama,T., Miyauchi,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasakhi,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,T., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M., and Hayashizaki,Y. |  |      |
|            | RIKEN MOUSE ESTS (Arakawa,T., et al. 2001)  |  |      |
|            | Unpublished (2001)  |  |      |
| COMMENT    | Contact: Yoshihide Hayashizaki  |  |      |

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The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gsc.riken.go.jp,  
URL: <http://genome.gsc.riken.go.jp/>  
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh  
, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new  
genes. Genome Res. 10 (10), 1617-1630 (2000)  
wagii, K., Fujiwaka, S., Inoue, K., Togawa, Y., Ikawa, M., Ohara, E.,  
Matsubaki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunura  
, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and  
Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system-384-format  
sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
10 (11), 1757-1771 (2000)  
Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara  
, Y. and Hayashizaki, Y.  
Computer-based methods for the mouse full-length cDNA  
encyclopedia: real-time sequence clustering for construction of a  
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
Tamanaka, I., Kiyosawa, H., Kondo, S., Saito, T., Shingawa, A., Aizawa  
, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., Arakawa, T.,  
Ishii, Y. and Hayashizaki, Y.  
Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.  
Funct. Genomics 2 pre, 172-186 (2001)  
Please visit our web site (<http://genome.gsc.riken.go.jp>) for  
further details.  
e mouse tissues.

```

FEATURES
  source
    location/Qualifiers
      1. .618
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        /db_xref="taxon:10090"
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        /sex="male"

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/tissue-type="olfactory brain"
/dev-stage="adult"
/lab-host="DHI0B"
/notes="Site_1: SalI; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer 15',
GAGGAGAGAGAGCGGCCGCAACTCGAGTTTTTTTTTTTTTTNN 3', cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 10.0 and subtraction to Rot = 100.0. Second
strand cDNA was prepared with the primer adapter of
sequence 15' GAGAGAGAGATTCTGAGTATTAATTAATCCCCCCCCCC
3'. cDNA was cleaved with BamHI and XhoI. Vector: a
modified pluscript KS(+) after bulk excision from Lambda
FLC I."
BASE COUNT      133 a      155 c      157 g      173 t
ORIGIN
Alignment Scores:
Pred. No.:      1.36e-89      Length:      618
Score:          1019.00      Matches:      200
Percent Similarity: 98.06%      Mismatches: 2
Best Local Similarity: 97.09%      Indels: 0
Query Match:      9.80%      Gaps: 0
DB:
US-09-930-871-12 (1-2009) x BB622500 (1-618)

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| DB | 1    | CTCTCATTTGTAGGATGTTTCTCCGGAGCTGATAGAGAACTATTGCTGCCCTACCC      | 60   |
| OY | 1634 | IeuPheArgValIleArgLeuAlaArgIleGIYArgIleLeuArgLeuIleLysGLYAla  | 1653 |
| DB | 61   | CTGTCCGAGCATCATCCGCCCTGGCCAGGANTGGACGAATCTACGCCGTGATCAAGGCCGC | 120  |
| OY | 1654 | LysGLYIleArgThrLeuLeuPheAlaLeuMetMetSerLeuProAlaLeuPheAsnIle  | 1673 |
| DB | 121  | AAGGGGATCCGACACCTGCTCTTCTCTCTGATGAGATGCTCCCTCCGCGGTATTACATCC  | 180  |
| OY | 1674 | GLYLeuIleLeuPheLeuValMetPheIleThrAlaIlePheGLYMetSerAsnPheAla  | 1693 |
| DB | 181  | GGCTTCCTGCTTCTCTGCTCATGTTCATCTACGCCATCTTGGAGATGCCAATCTGGCC    | 240  |
| OY | 1694 | TyrValLysArgGluValGIYIleAspAspMetPheAsnPheGluThrPheGLYAsnSer  | 1713 |
| DB | 241  | TACGTTAAGAGCGAAGTTGGGATGTATGACATGTTCACTTGGACACCTTTGGCAACAC    | 300  |
| OY | 1714 | MetIleCysLeuPheGlnIleThrThrSerAlaGIYTrpAspGLYLeuAlaProIle     | 1733 |
| DB | 301  | ATGATCTGCTGCTTCCAAATCACCACTTCTCGGGCTGGAGTGCATGCTGGCCCTATA     | 360  |
| OY | 1734 | IeuAsnSerLysProProAspCysAspProAsnLysValAsnProGLYSerSerValLys  | 1753 |
| DB | 361  | CTAAATAGTGGACATCCGATTTGTACCTGAAAGATCATCTGGGAAGCTGGGTGAG       | 420  |
| OY | 1754 | GLYAspCysGLYAsnProSerValGIYIlePhePhePheValSerTrileIleIleSer   | 1773 |
| DB | 421  | GGAGCATGTGGGAACCATCTGTGGGGATTTCTTTTGTGACGTACATCATCTATACC      | 480  |
| OY | 1774 | PheLeuValValValAsnMetYrIleAlaValIleLeuGluAsnPheSerValAlaThr   | 1793 |
| DB | 481  | TTCCGTGTGTGTGTAACATGTACATTTGCTGTCACTCGAGAACTCAGACTGCCACA      | 540  |
| OY | 1794 | GIUGIuserAlaGluProLeuSerLysLysAspPheGluMetPheTyrGluValTrpGlu  | 1813 |
| DB | 541  | GAGGAATATGCAGACCTCTGATGAGGACGACTTTGAGATGTTCTTACGAATCTGGAG     | 600  |



High quality sequence stop: 425.  
Location/Qualifiers

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/dev\_stage="34 years old"  
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BASE COUNT 232 a 155 c 135 g 184 t

ORIGIN

Alignment Scores:

Pred. No.: 2.05e-86 Length: 706  
Score: 987.50 Matches: 201  
Percent Similarity: 86.72% Conservative: 8  
Best Local Similarity: 83.40% Mismatches: 20  
Query Match: 9.50% Gaps: 13  
Indels: 2

US-09-930-871-12 (1-2009) x AA984063 (1-706)

180 LeuGluAspPheThrPheLeuArgSPProtrPAsnTrpLeuAspPheThrValIleThr 199  
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200 PheAlaTrpValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArg 219  
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646 CTTCGATATGACAGATTTGTGACCCGCAATGTCTCAGCGTGGAACATTCACA 587  
220 ValLeuArgAlaLeu-LysThrIleSerValIleProGlyLeuLysThrIleValGlyAl 239  
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586 GTTCCTCCAGCATGAAACCAATTCAGTCATTCAGCCCTGAAGACCATGTG- 528  
239 AlaLeuIleIleSerValLysLeuSerAspValMetIleLeuThrValPheCysLeuSe 259  
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527 CCTGATCCAGTCAGTGAAGAACCTTGTGATGATGATCTGACTGCTGCTAG 468  
259 ValPheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleG 279  
467 CGTGTTCGCGCAATAGACATTCATGTCATGGCAACCTACCAAAATATGTTTGA 408  
279 nTrpProThrAsnAlaSerLeuGlnLysSerIleGlyLysAsnIleThr----- 297  
407 ATGGCTCCAGATTAATCT-----TCTTTGAATTAATATACATTCCT 363  
298 -----ValAsnTrpAsnGlyThrIleLeuAsnGlnThrValPheGluPheAs 313  
362 CTTTAACAATTCATTGAGGATGAGATGATCTTCAATAGACAGATGATATTAA 303  
313 TrpLysSerTrpIleGlnAspSerArgTrpIleIlePheLeuGlnGlyPheLeuAspAl 333  
302 CTGGGATGAATATATTAGGATAAAGACATTTATTTTATAGAGGGCAAAATGATCC 243  
333 AlaLeuLysCysGlyAsnSerSerAspAlaGlyLysCysProGlnGlyTrpMetCysVal 353  
242 TCTGCTTTGTGGCAACACTCAGATGACAGCGCAGTCTCTGAAGATACATCTGTGTGA 183  
353 AlaGlyLysArgAsnProAsnTrpGlyTrpThrSerPheAspTrpPheSerTrpAlaPhe 373  
182 GGCTGTGAGAAACCCCACTATGTCTACAGAGCTTTGACACCTTATGTTGGCTTTT 123

373 USerLeuPheArgLeuMetThrGlnAspPheTrpGlnAsnLeuTrpGlnLeuThrLeuAr 393  
|||||  
122 GTTCCTATTTTCCTCATCATCAGACATTCGGGAAAACCTTATCACTGACACTAG 63  
393 gAlaAlaGlyLysTrpThrTrpMetIlePhePheValLeuValIlePheLeuGlySerPhe 413  
62 TCCTCTGGGAAACGATCATATATTTTGTGTCGTCATTTCTTGGCTATTCYA 3  
413 r 413  
2 t 2  
RESULT 14  
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VERSION BF347024.1 GI:11294619  
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SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 689)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: David N. Louis, M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library: Arrayed by: The I.M.A.G.E. Consortium (ULM)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/ULM, at:  
http://image.llnl.gov  
Plate: LLM9431 row: f column: 06  
High quality sequence start: 3  
High quality sequence stop: 654.  
Location/Qualifiers

FEATURES

source

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Average insert size 2.3 kb. Constructed by Life  
Technologies. Note: this is a NCI\_CGAP library."

BASE COUNT 179 a 130 c 158 g 222 t

ORIGIN

Alignment Scores:  
Pred. No.: 2.4e-85 Length: 689  
Score: 976.50 Matches: 198  
Percent Similarity: 90.13% Conservative: 12  
Best Local Similarity: 84.98% Mismatches: 18  
Query Match: 9.39% Indels: 6  
Gaps: 1

US-09-930-871-12 (1-2009) x BF347024 (1-689)

1284 TrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThrAlaAsnAla 1303  
|||||  
3 TGTGCTGCTGCTGATTTCTGTGATCGT-GATGTTTCTTGGTTAGCCTGTACCAATGCT 61  
1304 LeuGlyTrpSerGlnLeuGlyAlaIleLysSerLeuArgThrLeuArgAlaLeuArgPro 1323  
|||||

Db 62 CTGGCTACACGAGACTGCGCATCAATCATTAAGACATTAAAGACCT 121  
 QY 1324 LeuArgAlaLeuSerArgPheGluGlyMetArgValValAlaAlaLeuGluVala 1343  
 Db 122 CTAAAGACCTTATCCCGGTTGAAGGCAATGAGGGGTGGTGAATGCTCATATGTCGAGCA 181  
 QY 1344 IleProSerIleMetAlaValLeuLeuValCysLeuIlePheThrPheIlePheSerIle 1363  
 Db 182 ATTCCTCTATCATGAAATGCTGCTGTGCTCATCTTCTGCTATCTTAAACATC 241  
 QY 1364 MetGlyValAlaLeuPheAlaGlyLysPheThrHisCysIleAsnThrThrGlyAsp 1383  
 Db 242 ATGGCTGATTTGTTGCTGCGCAAGTTTACACCTGTGTAACATGACAAAGGCTAAC 301  
 QY 1384 ArgPheAspIleGluAspValAlaAsnHisThrAspCysLeuValLeuIleGluArgAsn 1403  
 Db 302 ATGTTGACATTAGTATGATTAACAAATTGAGTACTGTCAGGCTCTT-----GCG 352  
 QY 1404 GluThrAlaArgTyrPheAspValLysValAlaAsnPheAspAsnValGlyPheGlyTyrLeu 1423  
 Db 353 AAGCAAGCTCGTGGAAGAAACGTGAAGTAACTTGAATATGTTGGCGCTGATCTT 412  
 QY 1424 SerLeuGluValAlaThrPheGlyGlyTyrMetAlaPheMetTyrAlaAlaValAsp 1443  
 Db 413 GCAGCTCTAAGTGGCCACATTTTAAGCGCTGATGATATATATATATACCTTTGAT 472  
 QY 1444 SerArgAsnValGluLeuGluProLysTyrGluGluSerLeuTyrMetTyrLeuTyrPhe 1463  
 Db 473 TCAGAGATGTTAACCTCAGCGCTATATGAAGAAATCTGTATCATGATTTATACCTT 532  
 QY 1464 ValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIleGlyValIleIle 1483  
 Db 533 GTCACTTTATCATCTTGGTGGTCACTTCACTGAAATCAATTCATGGTGTCAATCA 592  
 QY 1484 AspaAsnPheAsnGluGlyLysLysValPheGlyGlyGluAsnIlePheMetThrGluI 1503  
 Db 593 GATTAATCTTAACACGACAAACAAAGAGTTCGAGGTCAAGACATCTTATACAGAGCA 652  
 QY 1503 uGlnLys-LysTyrTyrAsnAlaMetLysLysLeu 1514  
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 AL706368 602 bp mRNA linear EST 22-MAR-2002  
 LOCUS DKFZp686H1140.5, mRNA sequence.  
 DEFINITION DKFZp686H1140.5, mRNA sequence.  
 ACCESSION AL706368  
 VERSION AL706368.1 GI:19689723  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 602)  
 Ansoerge,W., Winkner,U., Mewes,W., Well,B. and Wiemann,S.  
 EST (Ansoerge,W., Winkner,U., Mewes,H.W., Well,B. and Wiemann,S.)  
 Unpublished (1999)  
 JOURNAL Contact: Ansoerge W  
 COMMENT MDS  
 Am Klopferspitz 18a D-82155 Martinsried, Germany  
 This is the 5' sequence of the clone insert  
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
 sequenced by EMBL (European Molecular Biology Laboratories,  
 Heidelberg/Germany) within the cDNA sequencing consortium of the  
 German Genome Project.  
 No 5' sequence available.  
 This clone (DKFZp686H1140) is available at the RZPD in Berlin.  
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.  
 Location/Qualifiers  
 1. 602

FEATURES  
Source

/organism="Homo sapiens"  
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 /clone="DKFZp686H1140"  
 /clone\_lib="686 (synonym: hlcc3)"  
 /tissue\_type="human skeletal muscle"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /note="Vector: pTritipleX2; site\_1: sfIRA; site\_2: sfIRB;  
 cDNA-collection"  
 BASE COUNT 127 a 141 c 138 g 196 t  
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 Pred. No.: 3,51e-85 Length: 602  
 Score: 974.00 Matches: 188  
 Percent Similarity: 97.49% Conservative: 6  
 Best Local Similarity: 94.47% Mismatches: 5  
 Query Match: 9.37% Indels: 0  
 DB: Gaps: 0  
 US-09-930-871-12 (1-2009) x AL706368 (1-602)  
 QY 1584 PheThrGlyGluCysValLeuLysLeuIleSerLeuArgHisTyrTyrPheThrIleGly 1603  
 Db 5 TTCACCTGAGAGATTTGTGCTGAAGCTCTCTCCACAGACACTACTACTATAGGC 64  
 QY 1604 TrpAsnIlePheAspPheValValIleLeuSerIleValGlyMetPheLeuAlaGlu 1623  
 Db 65 TCGAACATCTTGAATTTGTGCTGGATTCCTCATATGATGATGATTTTGTGCTGAG 124  
 QY 1624 LeuIleGluLysTyrPheValSerProThrLeuPheArgValIleArgLeuAlaArgIle 1643  
 Db 125 AAGATGAAGAAATATTTTGTGCTCCCTACCTGTTCCGAGTATCCCTTGACAGATT 184  
 QY 1644 GlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLeuLeuPheAlaLeu 1663  
 Db 185 GCCCAATCTTACGTCTGATCAAGAGCAAGGGGATCCGACGCTGCTTGTGCTTG 244  
 QY 1664 MetMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuPheLeuValMetPheIle 1683  
 Db 245 ATGACGTCCCTTCCTGCTGTTTAAACATCGCGCTCTCTCTCTGTCATGTTATC 304  
 QY 1684 TyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgIleValGlyIleAspAsp 1703  
 Db 305 TATGCCATCTTGGGATGTCCAACTTGGCTATGTAAGAAAGAGCTGGAATGATGAC 364  
 QY 1704 MetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPheGluIleThrSer 1723  
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 QY 1724 AlaGlyTrpAspIleLeuAlaProIleLeuAsnSerLysProProAspCysAspPro 1743  
 Db 425 GCTGGCTGGAGATGATGCTAGACACTATCTTAATAGTCACACCGCAGCTGTGACCT 484  
 QY 1744 AsnLysValAlaAsnProCysLeuSerValLysGlyAspCysGlyAsnProSerValGlyIle 1763  
 Db 485 GACACATTCACCTCGGCGATTCAGTTAAGGGAGCTGTGGACCACTGTGGGATT 544  
 QY 1764 PhePhePheValSerTyrIleIleIleSerPheLeuValValAlaAsnMetTyrIle 1782  
 Db 545 TTCTTTTTCAGTTCATCATCATATATCTTCTGCTGTGTGTGAACATGTATCATC 601

Search completed: April 23, 2003, 02:38:17  
 Job time : 3720 secs



GenCore version 5.1.4-P5-A578  
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## OK protein - nucleic search, using frame\_plus.p2n model

Run on: April 22, 2003, 21:17:35 ; Search time 98 Seconds

(without alignments)  
6286.874 Million cell updates/sec

Title: US-09-930-871-12

Perfect score: 10397

Sequence: 1 MEQTVLPVPGDFSENFETRE.....TKPIVHEDEGKDEKAKGK 2009

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+g2n.model -DEV=xlh  
-O=/cg2n2.1/USPTO.spool/US09930871/runat.16042003.114839.8492/app\_query.fasta.1.2183  
-DB=Issued\_Patents.NA -QFMT=fastap -SUFFIX=p2n.rml -MINMATCH=0.1 -LOOPCL=0  
-LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR=SCORE-pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=plco -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09930871.ecgn.1.1.55.ernat.16042003.114839.8492 -MCP=6 -ICPU=3  
-NO\_XLPHY=NO -MAP= -LARGQUERY= -NEG\_SCORE=0 -WAIT -LONGIOG -DEV=TIMEOUT=120  
-MARK=TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELop=6 -DELEXT=7

Database :

Issued Patents.NA:\*  
1: /cg2n2.6/ptodata/1/lna/5A.COMB.seq:\*  
2: /cg2n2.6/ptodata/1/lna/5B.COMB.seq:\*  
3: /cg2n2.6/ptodata/1/lna/6A.COMB.seq:\*  
4: /cg2n2.6/ptodata/1/lna/6B.COMB.seq:\*  
5: /cg2n2.6/ptodata/1/lna/PCUTS.COMB.seq:\*  
6: /cg2n2.6/ptodata/1/lna/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score  | Query Match | Length | ID | Description                         |
|------------|--------|-------------|--------|----|-------------------------------------|
| 1          | 7913   | 76.1        | 6404   | 3  | US-08-836-325-14 Sequence 14, Appl  |
| 2          | 7877   | 75.8        | 6452   | 3  | US-08-836-325-9 Sequence 9, Appl    |
| 3          | 7861.5 | 75.6        | 6371   | 3  | US-08-836-325-13 Sequence 13, Appl  |
| 4          | 7755.5 | 74.6        | 6007   | 4  | US-09-024-020B-2 Sequence 2, Appl   |
| 5          | 7755.5 | 74.6        | 6007   | 4  | US-09-024-020B-2 Sequence 2, Appl   |
| 6          | 7720.5 | 74.3        | 5977   | 3  | US-09-024-020B-1 Sequence 1, Appl   |
| 7          | 7720.5 | 74.3        | 5977   | 3  | US-09-024-020B-1 Sequence 1, Appl   |
| 8          | 7720.5 | 74.3        | 6556   | 4  | US-09-024-020B-7 Sequence 7, Appl   |
| 9          | 7720.5 | 74.3        | 6556   | 4  | US-09-024-020B-7 Sequence 7, Appl   |
| 10         | 7712.5 | 74.2        | 6586   | 4  | US-09-024-020B-43 Sequence 43, Appl |
| 11         | 7712.5 | 74.2        | 6586   | 4  | US-09-024-020B-43 Sequence 43, Appl |
| 12         | 7525.5 | 72.4        | 6826   | 3  | US-09-024-020B-8 Sequence 8, Appl   |

|    |        |      |      |   |                  |
|----|--------|------|------|---|------------------|
| 13 | 7525.5 | 72.4 | 6826 | 4 | US-09-425-043-8  |
| 14 | 6312   | 60.7 | 6048 | 4 | US-09-634-920-3  |
| 15 | 5555   | 53.4 | 5874 | 4 | US-08-843-417-9  |
| 16 | 5437.5 | 52.3 | 6344 | 4 | US-08-843-417-1  |
| 17 | 5426   | 52.2 | 6527 | 4 | US-08-669-656A-7 |
| 18 | 5404   | 52.0 | 6524 | 4 | US-08-669-656A-1 |
| 19 | 5372.5 | 51.7 | 7052 | 4 | US-08-669-656A-5 |
| 20 | 4313.5 | 41.5 | 6513 | 1 | US-08-338-702-7  |
| 21 | 4313.5 | 41.5 | 6513 | 1 | US-08-337-339-7  |
| 22 | 4313.5 | 41.5 | 6513 | 1 | US-08-724-095-7  |
| 23 | 4313.5 | 41.5 | 6513 | 1 | PCR-US95-14262-7 |
| 24 | 4313.5 | 41.5 | 6513 | 5 | PCR-US95-14378-7 |
| 25 | 4309.5 | 41.4 | 6519 | 2 | US-08-808-793-24 |
| 26 | 4263   | 41.0 | 6315 | 2 | US-08-808-793-2  |
| 27 | 4263   | 41.0 | 6315 | 3 | US-08-772-512A-2 |
| 28 | 4262   | 41.0 | 6318 | 2 | US-08-808-793-1  |
| 29 | 4262   | 41.0 | 6318 | 3 | US-08-772-512A-1 |
| 30 | 4035.5 | 38.8 | 3033 | 3 | US-08-836-325-1  |
| 31 | 3952   | 38.0 | 5461 | 3 | US-07-998-282B-7 |
| 32 | 1739   | 16.7 | 2573 | 4 | US-08-669-656A-3 |
| 33 | 1558.5 | 15.0 | 8075 | 3 | US-08-374-077C-1 |
| 34 | 1558.5 | 15.0 | 8075 | 4 | US-08-895-590-1  |
| 35 | 1558.5 | 15.0 | 8075 | 4 | US-09-539-879A-1 |
| 36 | 1550.5 | 14.9 | 7741 | 4 | US-09-426-998-4  |
| 37 | 1550   | 14.9 | 6822 | 4 | US-09-426-998-3  |
| 38 | 1547   | 14.9 | 6575 | 3 | US-08-949-386-3  |
| 39 | 1547   | 14.9 | 6575 | 3 | US-08-450-562-3  |
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| 42 | 1541   | 14.8 | 5904 | 1 | US-08-455-543A-3 |
| 43 | 1541   | 14.8 | 5904 | 2 | US-08-193-078B-3 |
| 44 | 1541   | 14.8 | 5904 | 2 | US-08-223-305C-3 |
| 45 | 1541   | 14.8 | 5904 | 2 | US-08-149-097D-3 |

## ALIGNMENTS

RESULT 1  
US-08-836-325-14  
Sequence 14, Application US/08836325  
Patent No. 6110672

GENERAL INFORMATION:  
APPLICANT: Mandel, Gail  
APPLICANT: Halegoua, Simon  
TITLE OF INVENTION: Peripheral Nervous System Specific  
TITLE OF INVENTION: Sodium Channels, DNA Encoding Thereof, Crystallization  
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rationa  
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and I  
NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:  
ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 New York Ave., N. W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/836,325  
FILING DATE: 2-MAY-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/14251  
FILING DATE: 02-NOV-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/482,401  
FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/334,029  
 FILING DATE: 02-NOV-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ludm1g, Steven R.  
 REGISTRATION NUMBER: 36,203  
 REFERENCE/DOCKET NUMBER: 0917.0240002  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-371-2600  
 TELEFAX: 202-371-2540  
 INFORMATION FOR SEQ ID NO: 14:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6404 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: both  
 TOPOLOGY: both  
 MOLECULE TYPE: DNA (genomic)  
 US-08-836-325-14

Alignment Scores:  
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US-09-930-871-12 (1-2009) x US-08-836-325-14 (1-6404)

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OY 166 AAGAGATGATGATGAGAAAGCCCAAGCAAGTGAAGCTGGAAGCTGGCAAAACATCT 225
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DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 122 IleValIleIleuValIleSerIleuPheSerMetIleuIleMetysThrIleLeuThrAsn 141
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OY 406 ATTAAGATTATTAGTACCTCTTATTCATGATGCTCATGTCACATATTCGACAAAC 465
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 142 CysValPheMetThrMetSerAsnProProAspTyrThrLysAsnValGluTyrThrPhe 161
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 466 TGCATATTATATGACATGATTAACCCGCCGACTGAGCAAAAATGCGAGTACACTTTT 525
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OY 162 ThrGlyIleTyrThrPheGluSerIleuIleLysIleIleAlaArgGlyPheCysLeuGlu 181
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DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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OY 646 TATTTAACGAATTTGTAACCTTAGCAATGTTTCAGCTTTCGAACTTTCAGAGATTTG 705
  
```

```

OY 222 ArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeuIle 241
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DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 242 GlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerValPhe 261
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 262 AlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTyrPro 281
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 826 GCACATAATGAGTACAGCTGTTTCATGGAAGAACTGGAACCTTAATATGTTTTCGA----- 879
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 282 ProThrAsnAlaSerLeuGluGlnHisSerIleGluLysAsnIleThrValAsnTyrAsn 301
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 880 -----AATTCACCTTGAATAATGAACATATGAA----- 909
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 302 GlyThrIleuLeuAsnGluThrValPheGluPheAspThrLysSerTyrIleGlnAspSer 321
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 910 -----AGCATTAATGATTAACCTTAGAGAGTGAAGAAAGACTTTAGA----- 948
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 322 ArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSerAsp 341
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 1009 TCAGTCACTAGTCCAGAGGGGTACACCTGTGTGAAAATTTGGCAGAAACCCGATTAATGCG 1068
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OY 362 TyrThrSerPheAspThrPheSerThrPheLeuSerLeuPheArgLeuMetThrGln 381
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 382 AspPheThrPheGluAsnLeuTyrGlnLeuThrLeuArgAlaIleGlyLysThrTyrMetIle 401
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 1129 GATTACTGGGAAAACTTTTACCAACAGACCGTGGCTGCTGCTGCAAAACCTACATGATGTC 1188
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 402 PhePheValIleuValIlePheLeuGlySerPheTyrIleuIleAsnLeuIleAlaVal 421
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 1189 TTCCTTGTCTGATGATTTTCTGGGCTCCTTTATCTAATTAATCTGATCTGGCTGCTG 1248
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 422 ValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLysGlu 441
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 1249 GTTGCCATGTGCATATGAAAGAACAGAACCCAGCAAACTTGAAGAGCTTAACAAAGAA 1308
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 442 AlaGluPheGlnGluMetIleGluGlnLeuLysLysGlnGlnGluAlaGlnGlnAla 461
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 1309 TTAGAAATTTCAACAGATTTAGACCGCTTTAAAAAAGCAAGAAAGCAAGCTGAGCAATT 1368
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 462 AlaThrAlaThrAlaSerGluHisSerArgLysProSerAlaAlaGlyArgLeuSerAsp 481
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 1369 GCAGCGGACAGCGCTGAATATACAGATATTAGAGGAAGCAAGAAATTATGCGGCTTCAGAG 1428
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 482 SerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluAlaGlyArgAsnArg 501
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 1429 AGTTCTTCTGAAACATCCAACTGAGCTCTTAAGAGTCTTAAGAAAGAAAGAAAGAGA 1488
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 502 LysLysArgLysGlnLysGlnGlnSerGlyGluGlnLys---AspGluAspGluPhe 520
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 1489 AAAAAAAGAAATCAAAAAGAAAGCTCTCCAGTGGAGAGAGAAAGGAGATGCTGCAAAATTG 1548
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 1549 TCGAAATTCAGAAATCAGAGGACAGCATCAGAGAAAGAAAGTTCCACTTGGTGTGAGAGGG 1608
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 1609 CATAGCGAGACATGAAAGAGAGTTGTCTACCCCAATCAGTCAACCATCAGAGATTCGT 1668
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 561 GlySerLeuPheSerProArgArgAsnSerArgTyrThrSerLeuPheSerPheArgGlyArg 580
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 1669 GCGTCTTGTGTTCTGCAAGGCAAGCAGCAAGCAAGTCTTTTATTTCAAAAGGCGAGA 1728
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600
  
```



QY 1319 ArgAlaLeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsn 1338  
 DB 3925 AGAGCTTAAAGACCTCTAAAGACCTTATCTAGATTGAAAGAAAGAGGCTGTTGCAAT 3984  
 QY 1339 AlaLeuGluAlaLeuProSerIleMetAsnValLeuLeuValCysLeuIlePheTyr 1358  
 DB 3985 GCACCTATAGGACCAATTCCTTCATCATCAATGCTACTGCTGCTTATATCTGG 4044  
 QY 1359 LeuIlePheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsn 1378  
 DB 4045 CTGATATTCAGCAATCAGGAGATAATTTGTTGCTGGCAAGTTCTATAGCTGATTAAC 4104  
 QY 1379 ThrThrThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLys 1398  
 DB 4105 ACCACAGATGGGTCCAGCTTCTGCAAGTCCAAATGCTTCCGATTTTGGCC 4164  
 QY 1399 LeuIleGluArgAsnGluThrAlaArgTyrLysAsnValLysValAsnPheAspAsnVal 1418  
 DB 4165 CTATATGAAATCTTATGTCAAAATGTCGATGGAAGAAACCTGAAAGCACTTGATATGTC 4224  
 QY 1419 GlyPheGlyTyrLeuSerLeuLeuGluValAlaAlaThrPheLysGlyTyrPheLysIleMet 1438  
 DB 4225 GGACTTGCTACCATCTGCTTCAAGTTCGCAACTTTAAGGATGAGCATTTATATG 4284  
 QY 1439 TyrAlaAlaValAspSerArgAsnValGluLeuGluProLysTyrGluLysLeuTyr 1458  
 DB 4285 TATGACAGCATGGATCTGTTAATGTAGACACAGCCCAATATGAAATATAGCTCTAC 4344  
 QY 1459 MetTyrLeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPhe 1478  
 DB 4345 ATGTATATATTTATTTGCTGCTTATCATCTTGGGTCATCTTCACTTGAACCTTCTTC 4404  
 QY 1479 IleGlyValIleIleAspAsnPheAsnGluGluLysLysPheGlyGlyGluAsnIle 1498  
 DB 4405 ATTTGCTCATCATATGATTTTCAACCAACAGAAAGAGCTTGGAGCTCAAGCATC 4464  
 QY 1499 PheMetThrGluGluGluLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLys 1518  
 DB 4465 TTATATGACAGAAAGCAAGAAATCTATATGATGAAAGAGCTGGGCTCCAAAG 4524  
 QY 1519 ProGluLysProIleProArgProGlyAsnLysPheGluGlyMetValPheAspPheVal 1538  
 DB 4525 CCACAAAAGCAATCTCTCAACAGGAGCAAAAATCCAAAGATGATATTTGACCTAGTG 4584  
 QY 1539 ThrArgGluValPheAspIleSerIleMetIleCysLeuAsnMetValThrMet 1558  
 DB 4585 ACAATATCAAGCCTTGTATATAGATCATGCTTCTATCTGCTCAACATGATGATCATG 4644  
 QY 1559 MetValGluThrAspAspGlnSerGluTyrValThrThrIleLeuSerArgIleAsnLeu 1578  
 DB 4645 ATGTATGAAAGAGAGGCTCAAGTCAACATATGATGATTTATTTGATGATTAATGTCG 4704  
 QY 1579 ValPheIleValLeuPheThrGlyGluCysValLeuLysLeuIleSerLeuAsnHisTyr 1598  
 DB 4705 GTTTTATATATCTTCTTCACTGAGATGTGCTTAAACATGATCTCCCAACACTATC 4764  
 QY 1599 TyrPheThrIleGlyTyrAsnIlePheAspPheValValIleLeuSerIleValGly 1618  
 DB 4765 TACTTCACTAGAGATGATATTTGATTTGCTGCTTGTATATCTCATCTGATGATGCT 4824  
 QY 1619 MetPheLeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPheArgValIle 1638  
 DB 4825 ATTTTCTTACTGATTTGATGAAACATATTTTGTGCTCCCTCAAGCTTCCAGATGATC 4884  
 QY 1639 ArgLeuAlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThr 1658  
 DB 4885 CGTCTTCCAGAGATGGCCAAATCTAGTCTAGTCAAAAGAGCAAAAGGGATCCGACG 4944  
 QY 1659 LeuLeuPheAlaLeuMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPhe 1678  
 DB 4945 CTGCTCTTCTTGTGATGATGATGCTCTCTGCTGCTTGTATTAACATGCGCTCTCTCTTC 5004

QY 1679 LeuValMetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgGlu 1698  
 DB 5005 CTGCTCATGTTCATCTACGCCATCTTGGAAATGTCAACTTGGCTATGTTAAAGGAA 5064  
 QY 1699 ValGlyIleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPhe 1718  
 DB 5065 GATGGAATTAATGACATGTTCAATTTTGACACCTTTGGCAACAGTATGATTTGCTGTTC 5124  
 QY 1719 GluIleThrSerAlaGlyTyrAspGlyLeuLeuAlaProIleLeuAsnSerLysPro 1738  
 DB 5125 CAATTTCAACCTCTGCTGGCTGGAGATGATGATGATGATGATGATGATGATGATGATGAT 5184  
 QY 1739 ProAspCysAspProAsnLysValAsnProGlySerValLysGlyAspCysGlyAsn 1758  
 DB 5185 CCCGACTGTGACCCAAAAAGTTCACTTGGAGATTCAGTTGAAGAGAGACTGTGTATAC 5244  
 QY 1759 ProSerValGlyIlePhePheValSerTyrIleIleIleSerPheLeuValVal 1778  
 DB 5245 CCATCTGTGGAAATTTCTTCTTGTATGATATATCATATATCTTCTCTGCTGCTGCTGCTG 5304  
 QY 1779 AsnMetTyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGlu 1798  
 DB 5305 AACATGATACATGACATCATCTGAGATTTTATGCTGTGCTGCTGCTGCTGCTGCTGCTG 5364  
 QY 1799 ProLeuSerGluAspAspPheGluMetPheTyrGluValTyrGluLysPheAspProAsp 1818  
 DB 5365 CCTGTGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5424  
 QY 1819 AlaThrGlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaLeuGluProPro 1838  
 DB 5425 GCGACCCAGTTTAAAGATTTCTTAAACCTCTGATTTTGAAGCTGCTGCTGCTGCTGCTG 5484  
 QY 1839 LeuAsnLeuProGlnProAsnLysLeuGluLeuLeuIleAlaMetLysPheProMetValSer 1858  
 DB 5485 CTCTCTCATGACAAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 5544  
 QY 1859 GlyAspArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGlu 1878  
 DB 5545 GGTATCCGAGATCCATGCTGCTGATCATCTTATTTGCTTTTAAAGAGCTGTTGGTGAG 5604  
 QY 1879 SerGlyGluMetAspAlaLeuArgIleGluMetGluGluArgPheMetAlaSerAsnPro 1898  
 DB 5605 AGTGGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5664  
 QY 1899 SerLysValSerTyrGlnProIleThrThrThrLeuLysArgLysGluGluValSer 1918  
 DB 5665 TCCAAAATGCTCTTGAACCATCATCAACCAACCAACCAACCAACCAACCAACCAACCAAC 5724  
 QY 1919 AlaValIleIleGluArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGluAla 1938  
 DB 5725 GCTATCTGATTCATGAGCTGCTTATAGAGCTTACGCTTAAGCAAAATGTCAAAATATA 5784  
 QY 1939 SerPheThrTyrAsnLysAsnLysIleLysGlyLys-----AlaAsnLeuLeuIle 1955  
 DB 5785 TCAAGTATATATC-----ATAAAGATGAGACAGACAGATGATGATTTACTCAAT 5832  
 QY 1956 LysGluAspMetIleIleAspArgIleAsnGluAsnSerIleThrGluLysThrAspLeu 1975  
 DB 5833 AAAAAGATATGCTTTGATATATGATATATGATATATGATATATGATATATGATATATG 5892  
 QY 1976 ThrMetSerThrAlaAlaCysProProSerTyrAspArgValThrLysProIleValGlu 1995  
 DB 5893 ACTTCATCCACACACCTCT---CCACCTTCAATATGATGATGATGATGATGATGATGATG 5949  
 QY 1996 LysHisGluGluGluGluLysAspGluLysAlaLysGlyLys 2009  
 DB 5950 AAATATGAAACAGACAGAAAGCAAGAAAGCAAGAAAGCAAGAAAGCAAGAAAGCAAGAA 5991

RESULT 2  
 US-08-836-325-9  
 ; Sequence 9, Application US/08836325  
 ; Patent No. 6110672  
 ; GENERAL INFORMATION:

|    |      |  |      |
|----|------|--|------|
| Db | 443  | AAAGATGATGAGGAAGAAGAGCCCAAGGCCACAGCTACTGGAAAGCTGGAAACAGCTC       | 502  |
| QY | 62   | ProPheIleTyrlGlyaspIleProPogIuethValIserGIuPProLeuGIuaspLeuasp   | 81   |
| Db | 503  | CCCTTCATCATATGAGACATTCCTCCCTGGAAAGGCTGACAGCCCTGGAGAGACCTTGAC     | 562  |
| QY | 82   | ProGlyTyrlIleasnIysIstThrPheIleValIleasnIysGIyIAsIallePheary     | 101  |
| Db | 563  | CCATACATCTGTGACAAAACCTTTATAGATTGAACAAAGGAAAAAGCACTTCCTGG         | 622  |
| QY | 102  | PheSerAlaThrSerAlaLeuTyrlIleLeuThrProPheasnProLeuargIyIleAla     | 121  |
| Db | 623  | TTTCAGGCCACCTCCTGCTTTGTATACATAGCTGTCTCCCTCACTCTCAAGAGAAATATCT    | 682  |
| QY | 122  | IleIysIleLeuValHisSerLeuPheSerMetLeuIleMetIysThrIleLeuThrAsn     | 141  |
| Db | 683  | ATTATAGATCTTAGAGCACTCTTATTCACCAATGCAATCATGTGCACAAATTCAGCAGAC     | 742  |
| QY | 142  | CysValPheMetThrMetSerAsnProPoaSPTrPThrIysAsnValGIuTyTrhPhe       | 161  |
| Db | 743  | TGCATATTCAGACCTTGAGCAACCTCCAGATGAGACCAAAATGTAGATACCTTTT          | 802  |
| QY | 162  | ThrGIyIleTyTrhPheGIuSerLeuIleIysIleIleAlaArgIyPheCysLeuGIu       | 181  |
| Db | 803  | ACTGGGATATATACTTTTGAATACCATTAATAAATCCTTGCAAGAGCTTTGGCTGGGA       | 862  |
| QY | 182  | AspPheThrPheLeuArgaspProTrpasnTrPleuaspPheThrValIleThrPheAla     | 201  |
| Db | 863  | GAATTCACCTTCCTCCCTGACCTTGGAACCTGGCTGGACCTTGTTGTATGTTTGGCG        | 922  |
| QY | 202  | TyTrValThrGIuPheValaspIleuGIyAsnValIserAlaLeuArgTrhPheArgValLeu  | 221  |
| Db | 923  | TATTTATACAAATTTGTAAACCTAGGCAGATAGTTTACGCTTCGAACTTGACAGCTTG       | 982  |
| QY | 222  | ArgAlaLeuIysTrhIleSerValIleProGIyLeuIysTrhIleValGIyAlaLeuIle     | 241  |
| Db | 983  | AGAGCTTTGAAATATATTCTGTATATCCAGAGCTAAAGACATCGTGGGGGCTGATC         | 1042 |
| QY | 242  | GlnSerValIysIysIleuSerAspValMetIleLeuThrValPheCysLeuSerValPhe    | 261  |
| Db | 1043 | CAGTCAGTGAAGAAGCCTCTCTGACGTGATGATCCTACAGTGTCTGTCTGATAGTGTGT      | 1102 |
| QY | 262  | AlaLeuIleGIyLeuGIuIleuPheMetGIyAsnLeuArgAsnIysCysIleGIuThrPro    | 281  |
| Db | 1103 | GCATTAATTTGACATACAGCTGTTATATGGGCACTTAACACATTAATGTTTCAGC          | 1156 |
| QY | 282  | ProThrAsnAlaSerLeuGIuGIuHisSerIleGIuIysAsnIleThrValAsnTrAsn      | 301  |
| Db | 1157 | -----AAGCACTCGAAGAAATGAACATTAGAA-----                            | 1186 |
| QY | 302  | GlyThrLeuIleasnGIuThrValPheGIuPheaspTrPlySerTrIleGIuIaspSer      | 321  |
| Db | 1187 | ---ACTATCATGATACTGCTGAGACGTGAAGAAGAAATTGAA-----                  | 1225 |
| QY | 322  | ArgTyrlHisIstYrPheLeuGIuGIyPheLeuAspAlaIleuMetCysGIyAsnSerSerasp | 341  |
| Db | 1226 | AAATATTTTATATATCTTGGAGGGATCCAAAGATGCTCTACTCTGGCGCTTGACGACATAT    | 1285 |
| QY | 342  | AlaGIyGlnCysProGIuGIyTyMetCysValIysAlaGIyArgAsnProAsnTrGIyI      | 361  |
| Db | 1286 | TCAGGGAGATGCCAAGAGGCTACATCTGTGTGAAGGCTGCAGAAACCCGGATTAATGCG      | 1345 |
| QY | 362  | TyTrhSerPheaspThrPheSerTrPAlaPheLeuSerLeuPheArgIuMetThrIln       | 381  |
| Db | 1346 | TTCAGAGACTTGTGACACATTCAGCTGGGCTTCTTGCGCTGTGTTTGGCTAATATGACTAG    | 1405 |
| QY | 382  | AspPheTrpGIuAsnLeuTyrlGlnLeuThrLeuArgAlaAlaGIyIstYrThrIleTle     | 401  |
| Db | 1406 | GACTACTGGGAGAACCTTTACCAACAGACATCTGCGTGTCTGTGGCAAAACCTACATGAT     | 1465 |
| QY | 402  | PhePheValIleValIlePheLeuGIySerPheTyrlLeuIleasnLeuIleValIleVal    | 421  |
| Db | 1466 | TTCCTTGTCTGTGTATTTTCTGGGCTCTTTTACTGTATTAACCTGTATCTCTGCTGTG       | 1525 |

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|----|------|--|------|
| OY | 422  | ValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLysGlu       | 441  |
| Db | 1526 | GTACCCATGTGGCTGTATGTAGGAACACAGCCCAATCATGAAGAAGTAAACAGAAAG          | 1589 |
| OY | 442  | AlaGluPheGlnGlnMetIleGlnGlnLeuLysGlnGlnGlnGlnAlaIleGlnGlnAla       | 461  |
| Db | 1586 | TTTGAATTTACGATGATGTATGACCGCATCAAAAAGGACGAGAAAGAGCTGAGCGCATC        | 1645 |
| OY | 462  | AlaThrAlaThrAlaSerGlnHisSerLysArgGluProSerAlaIleAlaGlyArgLeuSerAsp | 481  |
| Db | 1646 | GCTGACAGCTCTCTCTGTAGTTCACAGAGTATAGGGCGGAGCAGATCATGGACCTCTCTGAG     | 1705 |
| OY | 482  | SerSerSerGlnLysSerLysLeuSerSerLysSerAlaLysGluArgAsnArgArg          | 501  |
| Db | 1706 | ACGCTTTCAGAAACCTCCAGCGGTGAGCTCAAGAAGTGTCCAAAGAGACAGAAACCGAAGA      | 1765 |
| OY | 502  | LysLysArgGlySerGlnLysGlnGlnSerGlyGlyGluGluLysAspGluAspGluPheGln    | 521  |
| Db | 1766 | AAAGAAAAGAAACAGAAAGATGTCAGAGTGGGAGAGAAAAGGTGTACGATGAGAACCTGTCC     | 1828 |
| OY | 522  | LysSerGlnLysSerGlnAspSerIleArgArgLysGlyPheArgPheSerIleGluGlyAsn    | 541  |
| Db | 1826 | AACTCAGGATCAAGAGAAACATCCGAAACAAAGCTTCATCTCGGTGTGGAAAGGCGAC         | 1885 |
| OY | 542  | ArgLeuThrTyrGlnLysArgTyrSerSerProHisGlnSerLeuSerIleArgGly          | 561  |
| Db | 1886 | CACCGGACCGGGGAAAAAGAGCGTGTCCACCCCAACCAAGTCCGCACATTCGCGGG           | 1945 |
| OY | 562  | SerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArgAla       | 581  |
| Db | 1946 | TCCCTTTTTCCTCCAGCGGCACACAGACAGACAGACAGTCTTTCAGTTTAAAGGGCGAGA       | 2005 |
| OY | 582  | LysAspValGlySerGlnLysAsnAspPheAlaAspAspGlnHisSerThrPheGluAspAsn    | 601  |
| Db | 2006 | ACGAGTCTGGATCTAGACAGATTCGCGATGATGATGATGATGATGATTTTGGAGAAC          | 2065 |
| OY | 602  | GlnSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSerAsn       | 621  |
| Db | 2066 | GAGAGCAGAAAGGGCTTCACATTCGTATCCCAATAGACCCCGGAGCGGCCAGCAGTAAC        | 2125 |
| OY | 622  | LeuSerGlnThrSerArgSerArgMetLeuAlaValPheProAlaAsnGlyLysMet          | 641  |
| Db | 2126 | ATCAGTCAGCCAGTGAAGTCCCG-----CCAGTGTACCGGTGAACGGGAAGATG             | 2176 |
| OY | 642  | HisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValProThr       | 661  |
| Db | 2177 | CACAGTCAGTGGATGCATATGAGAGTCGTGCTGCTGTGATGGACCCCTCAGCCCTCATG        | 2236 |
| OY | 662  | SerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAspAsn       | 681  |
| Db | 2237 | CTCCCCAATGGACAGCTTTCTCCACAGCGATATGATATGATATGATATGATATGATATGAT      | 2296 |
| OY | 682  | GlyThrThrThrGluThrGluMetArgLysArgArg-----SerSerSerPheHisValSer     | 700  |
| Db | 2297 | GGCAGAGACT-----AATCAGATGGCGAAAAAAGCGCTCTAGTCTTACTTCTTGTCT          | 2350 |
| OY | 701  | MetAspPheLeuGlnAspProSerGlnArgGlnArgAlaMetSerIleAserIleLeu         | 720  |
| Db | 2351 | GAGGACATGCTGAATGACCGCATCTCCAGCAAAAGGCGCATGAGCGGCGAGCATATCTG        | 2410 |
| OY | 721  | ThrAsnThrValGluGluLeuGlnGlnSerArgGlnLysCysProProCysTrpPyrLys       | 740  |
| Db | 2411 | ACCAACACTGTGGGAAGAACTTAAAGAAATCTTAACACAAAATGTCCACCAATGAGGTACAA     | 2470 |
| OY | 741  | PheSerAsnIlePheLeuIleTyrAspCysSerProTyrTyrLeuLysValIysHisVal       | 760  |
| Db | 2471 | TTTGCTCACACATTTTATCTGGAATTGCTCTCATATGTGATATAAATTCAAAAAGCTC         | 2530 |
| OY | 761  | ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu       | 780  |
| Db | 2531 | ATCATATTTATGTATGATGATCTTTGTGTAGATCTTGGCAATACCATTTGCATAGATTTA       | 2590 |

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|----|------|---|------|
| OY | 781  | AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu    | 800  |
| Db | 2591 | AAACCCCTTATTAAAGGCTATGGACACCCACCAATGACTGAAAGATCAAAATAATGCTCT    | 2650 |
| OY | 801  | ThrValGlyAsnLeuValPheThrGlyTLeuPheThrAlaGluMetPheLeuLysLeile    | 820  |
| Db | 2651 | GCACTGGGGAACCTGATCTTACAGGGATCTTCGCACCTGAAAGTACTCAAGTTAATA       | 2710 |
| OY | 821  | AlaMetAspProTyrTyrTyrPheGlnGluGlyTyrAsnLilePheAspGlyPheLeileVal | 840  |
| Db | 2711 | GCCATGAGACCCGATAGTAGTATTTCACAGTAGAGGGGAAATATTTTGGACAGCTAATTGTG  | 2770 |
| OY | 841  | ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer    | 860  |
| Db | 2771 | ACCGTGAGTTTGGATAGAGCTTTTCCPAGCAGATGTGAAAGGATTAATCAGTTCTCGGGCA   | 2830 |
| OY | 861  | PheArgLeuLeuArgValPheLysLeuAlaLysSerTyrProThrLeuAsnMetLeuile    | 880  |
| Db | 2831 | TTGAGATTGCTCCGAGCTTCAAGTTGGCAAAAGTCCGGGCCACACTGACATCTCATYT      | 2890 |
| OY | 881  | LysLilelleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaileile   | 900  |
| Db | 2891 | AAATATATCGGCACACTCGGGGGCGCACTGGCGCACTTGACCCCTGGGTGGCCATATATC    | 2950 |
| OY | 901  | ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal    | 920  |
| Db | 2951 | GTCCTCATTTTTGCCGTGGCGGCATGACACTGTTTGGAAGAAGCTACAAAGATGTGTTC     | 3010 |
| OY | 921  | CysLysLileleAsnSerPysGlnLeuProArgTyrHisMetAsnSppheHisSer        | 940  |
| Db | 3011 | TGCAGATCAATGTGAGACTGCACAGCTCCGCGCTGGCACATGAAACGACTTCCATCTCC     | 3070 |
| OY | 941  | PheLeuileValPheArgValLeuGlyGlyGlnTyrIleGluThrMetTyrPaspCysMet   | 960  |
| Db | 3071 | TTCCTCATCTGTGTCCGAGCTGCTGTGGGAGTGGATGAAAGACCATGTGGAGCTGATG      | 3130 |
| OY | 961  | GluValAlaGlyAlaMetCysLeuThrValPheMetMetValMetValileGlyAsn       | 980  |
| Db | 3131 | GAGGTGCGGGGCCAGACCATGTGCTTATTGTTACATGATGTCTCATGTGATTTGGGAC      | 3190 |
| OY | 981  | LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu    | 1000 |
| Db | 3191 | CTTGTTGCTCTGAACCTGTTTGGCTCTTCTGAGTCTCTTGTAGTTCTGCACATCTT        | 3250 |
| OY | 1001 | AlaAlaThrAspAspAsnSppGluMetAsnLeuGlnIleAlaValAspArgMetHis       | 1020 |
| Db | 3251 | ACAGCAATTGAGGAAGACACCGATGCAAAACATCTCAATGCTCCATGGCCAAATTAAG      | 3310 |
| OY | 1021 | LysGlyValAlaTyrValLysArgLysLileTyrGluPheIleGlnInsPheIleArg      | 1040 |
| Db | 3311 | AGGGGAATCAATTAAGTGAAGACAGACCCGCGGATTAATCTTAATAATCATTTTCCAAA     | 3370 |
| OY | 1041 | LysGlnLysLileLeuAspGluileLysProLeuAspAspLeuAsnLysLysAspSer      | 1060 |
| Db | 3371 | AGCCAAAGGCTCCAGAGCACAAAACAGACAGATCCCAACAAACAAGAAAGAAAC          | 3430 |
| OY | 1061 | CysMetSerAsnHisThr***GluIleGlyLysAspLeuAspTyrLeuLysAspVal       | 1079 |
| Db | 3431 | TATATTTCAAACCGTACCTTATCATTAACCCAGCCATCAGTAGTGCACATTCACACT       | 3490 |
| OY | 1080 | AsnGlyThrThrSerGlyLileGlyThrGlySerSerValGluLysTyrLileleAspGlu   | 1099 |
| Db | 3491 | GATAGAGATCAGT*****GGTTATGGCACAGCTTAGACAAAACCTTATTTGGATGAA       | 3541 |
| OY | 1100 | SerAspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaVal    | 1119 |
| Db | 3542 | AATGATTACACGCTCTTATCATTAACCCAGCCATCAGTAGTGCACATTCACACT          | 3601 |
| OY | 1120 | GlyGlnSerAspPheGlnAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGlu    | 1139 |
| Db | 3602 | GGGAGGCTGTGATTTGGACATTAATGAACACAGAAGAGCTTAAAGTACACACAGTAC       | 3661 |
| OY | 1140 | GluSerLysGluLysLeuAsnGluSerSerSerSerSerGlnGlySerThrValAsnIle    | 1159 |



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||||| 3662 TACAGAAAGAGAAAGAGAAAGCA---TCAGCTCTTGAGTGGACGACACTGTTGACAAAC 3718
||||| 1160 G1yAlaProValGluGluInProValGluProGluGluThrLeuGluProGluAla 1179
||||| 3719 CCTCGCCAGGAGAGAGAGAGGCTGAGAGAGCCGTAAAGCAGATGAGCTGAAGCC 3778
||||| 1180 CysPheThrGluGluGlyCysValGluThrPheGlyCysCysGluIleAsnValGluGluGly 1199
||||| 3779 TCCCTTACAGATGCTGTGTGAGAGATTCATGCTGCCAAGTTATGATGAGACTGTGG 3838
||||| 1200 ArgGlyLysGluIleThrPheAsnLeuArgThrCysPheArgIleValGluHisAsnThr 1219
||||| 3839 AAGGGAAGGTTGGTGGACCATCAGAGAAAGCTGCTACAGGATAGTTGACACACACTGG 3898
||||| 1220 PheGluThrPheIleValPheMetIleLeuLeuSerSerGlyValAlaLeuAlaPheGluAsp 1239
||||| 3899 TTGAAAGGTTCACTGCTTCATGATCCTGCTCAGCAGTGGAGCTCTGGCTTTGAAGAT 3958
||||| 1240 IleThrIleAspGluArgLysThrIleLysThrMetLeuGluIleValAlaAspLysValPhe 1259
||||| 3959 ACTATATTTGAAAGAGAGAAAGACCATTAAGATATCTCTGAGATGCTGCAAGATATTC 4018
||||| 1260 ThrThrIlePheIleLeuGluMetLeuLeuLysThrValAlaThrGlyIleGluThr 1279
||||| 4019 ACCATCATCTTCACTTCTGGAATGCTTCAAAATGGGTGCATATGGGTATTAACATAT 4078
||||| 1280 PheThrAsnAlaIlePheCysThrPheAspPheLeuIleValAlaAspValSerLeuValSerLeu 1299
||||| 4079 TTCACATAAGCCCTGGTGGTGGCTGACCTTCTTAATGTTGATGCTGCTCAGTACTTGA 4138
||||| 1300 ThrAlaAsnAlaLeuGlyIleThrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArg 1319
||||| 4139 GTAGCCAAACACTCTGGCTACTCAGACCTGGCCCATTAATCTACGAGACACTGAGG 4198
||||| 1320 AlaLeuArgProLeuArgAlaLeuSerArgPheGluGlyMetLargValValAlaAsnAla 1339
||||| 4199 GCCCTAAGACCCCTAAGAGCTTGTCTAGATTGAAAGGATGAGGAGTGGTCAACGCA 4258
||||| 1340 LeuLeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheThrLeu 1359
||||| 4259 CTCATAGAGACATCCCTTCATCATGAGACGCTCTCTGCTGCTTATATTCGCTGA 4318
||||| 1360 IlePheSerIleMetGlyValAlaLeuPheAlaGlyLysPheThrLysCysIleAsnThr 1379
||||| 4319 ATATTAGATCATGAGGAGCATCTGTTGCTGGCAAGTTCTATGATGTCACACACC 4378
||||| 1380 ThrThrGlyAspArgPheAspIleGluAspValAlaAsnHisIleThrAspCysLeuLeu 1399
||||| 4379 ACCGATGGGTCAAGATTTCTCATCTCAAGTTGCAAAACGGTCTGAGTCTTGGCCCTG 4438
||||| 1400 IleGluArgAsnGluThrAlaArgThrPheLysAsnValLysValAsnPheAspAsnValGly 1419
||||| 4439 ATGACGTTATGGAATATGCGCATGGAATAAACTGAAATTAACCTCGACACACTGGG 4498
||||| 1420 PheGlyThrLeuSerLeuLeuGluValAlaIleThrPheLysGlyIlePheLysIleMetThr 1439
||||| 4499 CTGGTTACCTGCTGCTGCTCAAGTTGCAACATTCGAAGGCTGAGATGATATATGAT 4558
||||| 1440 AlaAlaValAspSerArgAsnValGluLeuGluProLysThrGluLeuSerLeuThrMet 1459
||||| 4559 GCGACAGTTGACCTGTTAATGTAATGAACACGCGAAATACGAATACACTCTCTACATG 4618
||||| 1460 TyrLeuThrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIle 1479
||||| 4619 TACATTTACTTGTGATCTTCATCATCTTGGCTCATCTTCACGTTGAACCTGTTCAAT 4678
||||| 1480 GlyValIleIleAspAsnPheAsnGluGluLysLysLysPheGlyGlyGluAspIlePhe 1499
||||| 4679 GGATGATCATATATATTTCAACCAACAGAAAAAAGCTGGAGCTGCAAGATATCTTT 4738
||||| 1500 MetThrGluGluGluLysLysLysThrAsnAlaMetLysLysLeuGlySerLysLysPro 1519
|||||
||||| 4739 ATGACAGAGAGAGAGAAATACTATATGATGACATGAGAGAGCTGGGTCCAAAAACCA 4798
||||| 1520 GlnLysProIleProArgProGlyAsnLysPheGluGlyMetValIleAspPheValThr 1539
||||| 4799 CAATAACCAATTCACAGGCGAGAGAACAAATTCACAGAGATGATTAATGACTGATGACA 4858
||||| 1540 ArgGluValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMetMet 1559
||||| 4859 AACCAAGCTTTATATACCATCATGATGTTCTTATATGCTCCCAACATGATGATGATG 4918
||||| 1560 ValGluThrAspAspGlnSerGluThrValThrIleLeuSerArgIleAsnLeuVal 1579
||||| 4919 GTAGAAAGAGGCGAACAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4978
||||| 1580 PheIleValLeuPheThrGlyGluCysValLeuLysLeuIleSerLeuArgHisLysThr 1599
||||| 4979 TTCATATCTGTTCACTGAGGAGTGTGCTGAGCAATATCTCCACAGCATATCTAC 5038
||||| 1600 PheThrIleGlyThrPheAsnIlePheAspPheValValIleLeuSerIleValGlyMet 1619
||||| 5039 TTCATGCTGGTGGAGCAATTTTGTATTTGTGTGATGATGATGATGATGATGATGATGATG 5098
||||| 1620 PheLeuAlaGluLeuIleGluLysThrPheValSerProThrLeuPheArgValIleArg 1639
||||| 5099 TTTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5158
||||| 1640 LeuAlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLeu 1659
||||| 5159 CTGGCCAGATGAGTGGAGCAATCTTACGCTGATCAAGAGGCGCAAGGGATCCGACACTG 5218
||||| 1660 LeuPheAlaLeuMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuPheLeu 1679
||||| 5219 CTTTGTGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5278
||||| 1680 ValMetPheIleThrAlaIlePheGlyMetSerAsnPheAlaThrValLysArgGluVal 1699
||||| 5279 GTCATGTTATCTAGAGCATCTTTGGATGATGATGATGATGATGATGATGATGATGATGATG 5338
||||| 1700 GlyIleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPheGln 1719
||||| 5339 GGAATTAATGATCATGTTCACTTGAAGACCTTGTGCAACACATCATCTGCTTCCAA 5398
||||| 1720 IleThrThrSerArgIleGlyThrPheGlyLeuLeuAlaProIleAsnSerLysPro 1739
||||| 5399 ATACACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5458
||||| 1740 AspCysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsnPro 1759
||||| 5459 GACTGTACCTTAATAAAGTTCAACCCAGAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAG 5518
||||| 1760 SerValGlyIlePhePhePheValSerThrIleIleIleSerPheLeuValValAsn 1779
||||| 5519 TCCGTGGGATTTTCTTCTGAGTACATCATATATCTTCTGCTGCTGCTGCTGCTGCTGCTG 5578
||||| 1780 MetThrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGluPro 1799
||||| 5579 ATGTACATCGCTGATCTGAGACACTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5638
||||| 1800 LeuSerGluAspAspPheGluMetPheThrIleValThrGluLysPheAspProAspAla 1819
||||| 5639 CTGAGTAGAGACGACTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5698
||||| 1820 ThrGlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaLeuGluProLeu 1839
||||| 5699 ACTGATGATATAGATCTGCAAGCTGCTGACTTGTGAGCGCTGCTGCTGCTGCTGCTGCTG 5758
||||| 1840 AsnLeuProGlnProAsnLysLeuGluLeuIleAlaMetAspLeuProMetValSerLys 1859
||||| 5759 CTCATGCCAAAGCCAAAGAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAG 5818
||||| 1860 AspArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyLys 1879
||||| 5819 GACCGCATCCACTGCTGAGCATCTTGTGCTTTCATTAAGAGGCTGCTGCTGCTGCTGCTGCTG 5878

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|    |      |   |      |
|----|------|---|------|
| QY | 1880 | GLVGLMETASPAIALAIAATGTLIEGIMETGUNGUARPhMETALASERsnpProser     | 1893 |
|    |      |   |      |
| Db | 5879 | GGAGNATGATTTCTCTTCGTCACAGATGGAAGAAAGTTCATGTCACCCCATCTTCT      | 5938 |
| QY | 1900 | LysValSerTyrGlnProlIerThrThrLeuLysArgLysGlnGluLysSerIa        | 1919 |
| Db | 5939 | AAAGTGTCTATGAAACCCATCAGACACACTGAAGAAAACAGAGAGAGTGTCCCG        | 5998 |
| QY | 1920 | ValIleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGlnIaIaSer | 1939 |
|    |      |   |      |
| Db | 5999 | ACTATTCATTACGCTGCTTACAGACGGTATCGCTCAGACAACAGTCAAGATATATCG     | 6058 |
| QY | 1940 | PheThrTyrAsnLysAsnLysIleLysGlyLys-----AlaAsnLeuLeuLys         | 1956 |
|    |      |   |      |
| Db | 6059 | AGTATATATC-----ATATAAGATGGAGACAGGAGATGATGATTTGCCCATATAA       | 6106 |
| QY | 1957 | GluAspMetIleIleAspArgIleAsnGluAsnSerIleThrGluLysThrAspLeuThr  | 1976 |
|    |      |   |      |
| Db | 6107 | GAAATCTACAGTTTGTATACGTAACGGAACGAACTCAAGTCGCGGAAAAGCAGATTTACT  | 6166 |
| QY | 1977 | MetSerThrAlaAlaCysProProSerTyrAspArgValThrLysProIleValGluLys  | 1996 |
|    |      |   |      |
| Db | 6167 | GCCCTCAACCATCTCG---CCACCTTCTCTATGACAGTGTACAAACCCAGATCAACAGANA | 6223 |
| QY | 1997 | HisGlnGlnGluLysAspGluLysAlaLysGlyLys                          | 2009 |
|    |      |   |      |
| Db | 6224 | TATCAAAACAGCAAAACAGAGAGGAAGCAACAAAGANA                        | 6262 |

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US-09-930-871-12 (1-2009) x US-08-836-325-13 (1-6371)
;
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6371 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: DNA (genomic)
US-08-836-325-13
;
Alignment Scores:
Pred. No.: 0
Score: 7861.50
Percent Similarity: 85.60%
Best Local Similarity: 76.12%
Query Match: 75.61%
DB: 3
Gaps: 14
Length: 6371
Matches: 1533
Conservative: 191
Mismatches: 241
Indels: 49

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Db 2884 CTGGGCTCTTAACCTATTCTGGCTTATTATGAGCTCATTTAGTTCACAGCAATCTT 2943
Oy 1001 AAlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 2944 ACAGCAATTGAAGAGAACCCCTATGCMAAACACCTCCAGATTCGACTGCATGAATTA 3003
Oy 1021 LysGlyValAlaIleValValLysArgLysIleTyrGluPheIleGlnInSerPheIleArg 1040
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 3004 AAGGAAATTAATTAATGTAACCAACCTACGTGAATTTATTTCTAAACATTTTCCAA 3063
Oy 1041 LysGlnLysIleLeuAspGluIleLysProLeuAspPheAsnLysAspSer 1060
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 3064 AAGCCAAAGATTTCCAGGAGATTAAGACAGCAAGAAATCTGAATCTAAGTAAGGAAGAAC 3123
Oy 1061 CysMetSerAsnHisThr---**GluIleGlyLysAspLysAspTyrIleLysAspVal 1079
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 3124 TATATTCTCAACCATACACTCTCTGAATAGCAAAAGTCACAAATTTCTCAAGCAAAA 3183
Oy 1080 AsnGlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGlu 1099
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 3184 GATTAATACTAGT-----GGTTTGGAGCAGCTGGACAAACACTTGATGAGAAC 3234
Oy 1100 SerAspTyrMetSerPheIleAsnAsnProSerIleuThrValThrValProIleAlaVal 1119
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 3235 AGTGATGCTCAATCTATTATTTACAAATCCACCTCAGCTCAGTACAGTGCATTTGCACCT 3294
Oy 1120 GlyGlnSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGlu 1139
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 3295 GGGGAATCCGATTTGGAAAAATATGAAATGCTGAGGAACCTTAGACAGTATTCGGATAGTGA 3354
Oy 1140 GluSerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIle 1159
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 3355 TACAGCAAAAGTGAGATTAAACCG--TCAAGCTCTCCTGAGATGCAGCACTTGATAC 3411
Oy 1160 GlyAlaProValGlu---GluGlnProValValGluProGluGluThrLeuGluProGlu 1178
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 3412 CCTTGGCTGGAGAAAGAAAGAACAGAGAGCTGAACCTATGAATCCATGACATGACGAG 3471
Oy 1179 AlaCysPheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGlu 1198
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 3472 GGCTGTTTCACAGATGCTGTGTGTACGAGAGCTCTCATGCTGCCAAGTTACATAGACTCA 3531
Oy 1199 GlyArgGlyLysGluThrPheAsnLeuArgArgThrCysPheArgIleValGluHisAsn 1218
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 3532 GGGAAAGCAAAATCTGGGCAACATCAGAAACCTGCTACAGATTTGTTAAACACAGT 3591
Oy 1219 ThrPheGluThrPheIleValPheMetIleLeuLeuSerSerGlyValAlaLeuAlaPheGlu 1238
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 3592 TGGTTTGAAGGCTCATTTGTCTCATGATCTGCTCAGAGTGTGCTGCTGCTTTTGA 3651
Oy 1239 AspIleTyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysVal 1258
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 3652 GATATTATTAATGAAGAAAGAAAGAACATTAAGATTATTCCTGAGATGCACAAAGATC 3711
Oy 1259 PheThrTyrIlePheIleLeuGluMetLeuLeuLysTyrPheValAlaTyrGlyThr 1278
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 3712 TTCATTTCATCTCATCTCGAAATGCTTAAATGATGATGATGATGATGATGATGATGATGAT 3771
Oy 1279 TyrPheThrAsnAlaTyrCysThrLeuAspPheLeuIleValAlaValSerLeuValSer 1298
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 3772 TATTTTACCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3831
Oy 1299 LeuThrAlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeu 1318
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 3832 TTAGTGGCAACACCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3891
Oy 1319 ArgAlaLeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValAlaValAsn 1338
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 3892 AAGGCTTAAAGACCTTAAGAGCCCTTAATCTAATTTGAAGGAATGAGGCTGCTGGAAT 3951
Oy 1339 AlaLeuLeuGlyAlaIleProSerIleMetAsnValIleLeuValCysLeuIlePheThr 1358
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 3952 GCAGCTCATAGGACAAATCTTCATCATGAAATGCTACTTGTGTATTTATTTCTG 4011
Oy 1359 LeuIlePheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsn 1378
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 4012 CTGATATTGAGCATATGGAGCAATTAATTTGTTGCTGGCAATTTCTATCAGTATTAAC 4071
Oy 1379 ThrThrThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLys 1398
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 4072 ACCACAGATGGCTCAGGCTTCTCTCAAGTCAAGTCCAAATCGTTCCGAATGTTTGGCC 4131
Oy 1399 LeuIleGluArgAsnGluThrAlaArgTyrLysAsnValIleValAsnPheAspVal 1418
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 4132 CTATGAAATGTAATCAAAATGCGATGGAAGAAACCTGAAGTAACTTGATATATGTC 4191
Oy 1419 GlyPheGlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTyrPheAspIleMet 1438
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 4192 GGACTTGGTTACTTATCTCTGCTTCAAGTGCACCTTTAAGGATGAGCATTTATATG 4251
Oy 1439 TyrAlaAlaValAspSerArgAsnValGluLeuGlnProLysTyrGluGluSerLeuTyr 1458
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 4252 TATGCAGAGCTGATTTGTTATGTAGCAAGACCCCAATATGAAATATAGCTCTAC 4311
Oy 1459 MetTyrIleuThrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPhe 1478
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 4312 ATGTATATTTATTTGTCCTTTATCATCTTTGGGTCATCTTCACTTGAACTTGCTTC 4371
Oy 1479 IleGlyValIleIleAspAsnPheAsnGlnGlnLysLysValPheGlyGlyGlnAspIle 1498
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 4372 ATTTGGTTCATATGATATTAATTTCAACCAACCAAGAAAGACCTTGAGCTCAACATC 4431
Oy 1499 PheMetThrGluGluGlnLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLys 1518
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 4432 TTATAGCAGAAAGAAAGAAATATCTATATGCAAGAAAGAAAGAAAGCTGGGCTCAAGAG 4491
Oy 1519 ProGlnLysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheVal 1538
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 4492 CCACAAAGCCAAATCTCTGACAGGAAACAAACCAAGATGATATTTGATTCAGTAGTG 4551
Oy 1539 ThrArgGlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMet 1558
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 4552 ACRATCAAGCTTTGATATTTGATATCATGATGTTCTTATCTGCTCAACATGATACCATG 4611
Oy 1559 MetValGluThrAspAspGlnSerGluTyrValThrThrIleLeuSerArgIleAsnLeu 1578
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 4612 ATGTAGAAAGAGAGGCTCAAGTCAACATATAGACTGAAGTTTATATGATTAATG 4671
Oy 1579 ValPheIleValLeuPheThrGlyGlyCysValIleLysLysLeuIleSerLeuArgHisTyr 1598
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 4672 GTTTTATATATCTTTTCACTGGAAGATGCTGTAAGAACTGATCTCCTCAGACATAC 4731
Oy 1599 TyrPheThrIleGlyTyrAsnIlePheAspPheValValIleLeuSerIleValGly 1618
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 4732 TACTTCACGTAGAGATGGAATTTTGTATTTTGTGTTGTGTATATATCTCCATTTAGCT 4791
Oy 1619 MetPheLeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPheArgValIle 1638
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 4792 ATGTTTCTGAGCTGATTTGATGAAGATTTTGTGCTCCCTACCTGTTCCGAGTATC 4851
Oy 1639 ArgLeuAlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThr 1658
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 4852 GGTCTTGGCCAGGATGGCCGAATCTCAGCTCAGCAAGGAAGGAGGATCCGCAAG 4911
Oy 1659 LeuLeuPheAlaLeuMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPhe 1678
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 4912 CTGCTCTTGTCTTGTATGATGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4971
Oy 1679 LeuValMetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgLys 1698
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 4972 CTGCTCATGCTATCATGACCATCTTGGAAATGCTCAACTTGCTATGTTAAAAAGGA 5031
Oy 1699 ValGlyIleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPhe 1718
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 5032 GATGGAATTAATGACATTTCAATTTTGAACCTTTGGCAACAGTATGATTTGCTGCTG 5091
```

1719 GlnIleThrSerAlaGlyTrpAspGlyLeuAlaProIleLeuAsnSerLysPro 1738  
 1739 ProAspCysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsn 1758  
 5152 CCCGACTGTGACCCCAAAAAGTTCATCTCGAAGTTCGTTGAGGACAGCTGTGTAC 5211  
 1759 ProSerValGlyIlePhePhePheValSerTyrIleIleSerPheLeuValVal 1778  
 5212 CCATCTGTTGGATATATCTTGTAGTATATCATCATATCTCTCTGTTGGTGG 5271  
 1779 AsnMetTyrIleAlaValIleLeuGluAsnPheSerValAlaIleThrGluLeuSerAlaGlu 1798  
 5272 AACATGTACATTCAGTCACTGAGGAAATTTAGTGTGTCACCACTGAAGAAAGTACTGAA 5331  
 1799 ProLeuSerGluAspAspPheGluMetPheTyrGluValTyrGluLysPheAspProAsp 1818  
 5332 CCTGTAGTGGAGATGATCTTGATGATGTTCTATGAGGTTGGAGAGATTTGATCCCAT 5391  
 1819 AlaThrGlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaIleLeuGluProPro 1838  
 5392 GCGACCATTTATAGATTTCTTAAGCTCTGATTTGACAGCTGCCCTGGATCCTCT 5451  
 1839 LeuAsnLeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSer 1858  
 5452 CTTTCATATGCAAAACCAAAAGTCACATGATGATGATGATGATGATGATGATGAT 5511  
 1859 GlyAspArgIleIleGlySerLysAspIleLeuPheAlaPheThrLysArgValLeuGluGlu 1878  
 5512 GGTGACCGGATCCATGCTCTGACATCTATTTGCTTTTACAAAGGCTTTTGGGTGG 5571  
 1879 SerGlyGluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsnPro 1898  
 5572 AGTGGGGAATGATCTCTCTGTCACAGATGGAAGAAAGTTCATGCTGCAAAATCT 5631  
 1899 SerLysValSerTyrGlnProIleThrThrLeuLysArgLysGlnGluValSer 1918  
 5632 TCCAAAGTGTCCATGACCAACCAACACACACTAAACGGAAGAGGATGTGTCT 5691  
 1919 AlaValIleIleGlnArgIleArgArgGlnIleLeuLysArgThrGlnGlnAla 1938  
 5692 GCTACTGCTATTCAGCGCTGATATGACCTTACCGCTTACCAAAATGTCAAAATATA 5751  
 1939 SerPheThrTyrAsnLysAsnLysIleLysGlyGly-----AlaAsnLeuLeu 1955  
 5752 TCAGATATATC-----ATRAAAGATGGAGACAGAGATGATGATTTACTCAT 5799  
 1956 LysGluAspMetIleIleAspArgIleAsnGluAsnSerIleThrGluLysThrAspLeu 1975  
 5800 AAAAAGATATGCTTTGATATGTTAATGAGACTCAAGTCCAGAAAAAAGACAGATGCC 5859  
 1976 ThrMetSerThrAlaIleAspProProSerTyrAspArgValThrLysProIleValGlu 1995  
 5860 ACTTCTATCCACCCACTCT---CCACCTCATATGATAGTATCAAAAGCCAGCAAGAG 5916  
 1996 LysHisGluGlnGluLysAspGluLysAlaLysGlyLys 2009  
 5917 AATATGACAGACAGACAGAAAGAAAGAAAGAGGAAA 5958

## RESULT 4

US-09-024-020B-2  
 Sequence 2, Application US/09024020B  
 Patent No. 6030810

## GENERAL INFORMATION:

APPLICANT: DELGADO, STEPHEN G.  
 APPLICANT: DIETRICH, PAUL S.  
 APPLICANT: FISH, LINDA M.  
 APPLICANT: HERMAN, RONALD C.  
 APPLICANT: SANGAMESWARAN, LAKSHMI  
 TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE  
 TITLE OF INVENTION: SODIUM CHANNEL 1-SUBUNIT AND A SPLICED VARIANT THEREOF  
 NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: JANET PAULINE CLARK  
 STREET: 3401 HILVIEW AVENUE, MS A2-250  
 CITY: PALO ALTO  
 STATE: CA  
 COUNTRY: U.S.A.  
 ZIP: 94304-1397  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/024,020B  
 FILING DATE: 16-FEB-1998  
 CLASSIFICATION: 536  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/039,447  
 FILING DATE: 26-FEB-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: CLARK, JANET P.  
 REGISTRATION NUMBER: 34,799  
 REFERENCE/DOCKET NUMBER: R0020B-REG  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (650) 852-3097  
 TELEFAX: (650) 855-3522  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6007 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 US-09-024-020B-2

Alignment Scores:  
 Pred. No.: 0 Length: 6007  
 Score: 7755.50 Matches: 1338  
 Percent Similarity: 84.81% Conservative: 187  
 Best Local Similarity: 75.61% Mismatches: 227  
 Query Match: 74.59% Indels: 83  
 DB: Gaps: 24

US-09-930-871-12 (1-2009) x US-09-024-020B-2 (1-6007)  
 1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPheThrArgGlu 20  
 22 ATGGCAGCGGGCTGCTCGCACACAGCGCTGATGATTTCAAGCTTTCACCCCTGAG 81  
 21 SerLeuAlaIleGlnArgArgIleAlaGluLysAlaLysAsn---ProLysPro 39  
 82 TCGCTGGCAAAACATCGAGAGCGCTAATGCCGAGAGCAAGCTCAAGAAACCAAGAGCG 141  
 40 Asp-----LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGlu 56  
 142 GATGGCAGCCACCGCGGAGCGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 201  
 57 AlaGlyLysAsnLeuProPheIleTyrGlyAspIleProProGluMetValSerGluPro 76  
 202 GCTGGGAGAGATTGCTTTCATCTACGCGGAGACATCCCGCAAGCCCTGCTGGCTGCC 261  
 77 LeuGluAspLeuAspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGly 96  
 262 CTGGAGAGACTTTCACCTTCTATTTGAGCAGCAAGAAACCTTGTAGTATTAACAGAGG 321  
 97 LysAlaIlePheArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnPro 116  
 322 AAACCTCTTCAGATTAGTGGCACACCGCTTGTACATTTTAAGCCCTTTTAACCTG 381  
 117 LeuArgLysIleAlaIleLysIleLeuValIleSerLysSerMetLeuIleMetCys 136  
 382 ATAAGAGATATCTATTAATTTGATACCTGACTGATTTCAGCATGATCATCATGTGC 441

|    |      |                  |   |      |
|----|------|------------------|---|------|
| QY | 137  | ThrIleLeuThrAsn  | CysValPheMetThrMetSerAsnProProAspTrpPheIleAsn       | 156  |
| Db | 1442 | ACCATTCCTGACCA   | CGTGTGTTTCATGACCTTTAGTACCTCCCAAAATGCTCCAGAAAT       | 501  |
| QY | 157  | ValGluTyrThr     | PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArg    | 176  |
| Db | 502  | GTGGAGTACACATTC  | CACAGGATTTACACATTTGAAATCACTAGTAAATACATCGCAGAA       | 561  |
| QY | 177  | GlyPheCysLeuGlu  | AspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThr       | 196  |
| Db | 562  | GGTTCCTGATAGACGG | CTTCACTCTTTCGCGAGACCCGGGAACGTGGTATGACTTCAGT         | 621  |
| QY | 197  | ValIleThrPheAla  | TyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArg       | 216  |
| Db | 622  | GTCAATCATGATGGCA | TATATGTGACAGAGTTTGAGACCTGGCAATGTCTCAGCGCTGAGA       | 681  |
| QY | 217  | ThrPheArgValLeu  | ArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIle       | 236  |
| Db | 662  | ACATTCAGGGTCTCG  | AGACTTTGAAACCTATCTGTATATCCAGGCTGGAAGACATC           | 741  |
| QY | 237  | ValGlyAlaLeuIle  | GlnSerValLysLysLeuSerAspValMetIleLeuThrValPhe       | 256  |
| Db | 742  | GTGGGGCCCTAATCC  | AGTCCCGGAAGAGCTGTGCGAGCTGATGATCCGACAGTCTTC          | 801  |
| QY | 257  | CysLeuSerValPhe  | AlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLys       | 276  |
| Db | 802  | TGCCAGAGGTTCGCT  | CGCTCGATGCTGCACACTCTTCACTGGGGAACCTTCCAAACAG         | 861  |
| QY | 277  | CysIleGlnTrpPro  | ThrProThrAsnAlaSerLeuGluGlnIleHisSerIleGlyLysAsnIle | 296  |
| Db | 862  | TGTGTGTGTGCCC    | -----   | 876  |
| QY | 297  | ThrValAsnTyrAsn  | GlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSer       | 316  |
| Db | 877  | ---ATRAATTCAC    | AGACAGCTACCTCGAGAACCGGACCGACGAGGCTTTGACTGGAGAA      | 933  |
| QY | 317  | TyrIleGlnAspSer  | ArgTyrThrIleThrPheLeuGluGlyPheLeuAspAlaLeuCys       | 336  |
| Db | 934  | TATATCAACAA      | AAAAAACAACCTTTTACATGGTTCCTGGCAGCTGAGAACCTTGTCTGC    | 993  |
| QY | 337  | GlyAsnSerSerAsp  | AlaGlyGlnCysProGlnGlyTyrMetCysValLysAlaGlyArg       | 356  |
| Db | 994  | GGGAACAGTTCGAT   | CTGCTGGCATGCCACCGAGAGATCCAGTGCATGAAGACGAGAGG        | 1053 |
| QY | 357  | AsnProAsnTyrGly  | TyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPhe       | 376  |
| Db | 1054 | AACCCCACTAGGG    | TACACACACCTTTGACACTTCACGCGGGCCCTTTGGCATATATTC       | 1113 |
| QY | 377  | ArgLeuMetThrGln  | AspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGly       | 396  |
| Db | 1114 | CCCTTATACACCA    | CGACATATTTGGGAGAACTTATACAGCTGACCTTACAGCGCGCTGGG     | 1173 |
| QY | 397  | LysThrTyrMetIle  | PhePheValLeuValIlePheLeuGlySerPheTyrIleLeuAsn       | 416  |
| Db | 1174 | AAAGGTCATATAT    | CTTCTTGTGTGGTCACTCTGTGGGCTCTTTCATATGGGTGAAC         | 1233 |
| QY | 417  | LeuIleLeuAlaVal  | AlaValAlaMetAlaTyrGluGlnGlnAsnGlnAlaThrLeuGlnGlu    | 436  |
| Db | 1234 | TTGATCTTGCGCT    | GTGGTGCATGCTTATGAGAAACAGACAGCAACACTGGAGAGAG         | 1293 |
| QY | 437  | AlaGluGlnLysGlu  | AlaGluPheGlnGlnMetIleGlnGlnLeuLysLysGlnGlnGlu       | 456  |
| Db | 1294 | CGACAGCAAAAAG    | CGCCCACTTCAAGCAATGCTGAGCACTCAAGAGCAGCAGAGAG         | 1353 |
| QY | 457  | AlaAlaGlnGlnAla  | AlaAlaThrAlaThrAlaSerGlnHisSer-----                 | 470  |
| Db | 1354 | GAGGACACAGCTG    | CTGCATATGCGCACCTC-AGCGGACACTGTCTCGGAAGACCCATGA      | 1412 |
| QY | 471  | ArgGluProSerAla  | AlaAlaGlyArgLeuSerAsp-SerSerSerGlnAlaSerLysLeuSe    | 490  |
| Db | 1413 | ACAAGAAGGGGAAG   | ATGGGGGTAGCGCTCTCCGAGAGACTCTTCTGCACTGTCTAACTCAG     | 1472 |
| QY | 490  | rSerLysSerAlaLys | GluArgLysAsnArgLysLysArgLysGlnLysGlnLysGlnLysGln    | 510  |
| Db | 1473 | TTCCAAAGCGCGA    | AGAGCGGCGGAACCGACGAGGAAGAGGAAGGACGAGAGACTCTC        | 1533 |
| QY | 510  | rGlyGlyGlnGlu    | Lys---AspGlyAspGluPheGlnLysSerGlnSerGlnAspSerIle    | 529  |
| Db | 1533 | TGAAGCGGAGAGAA   | AGGAGACCCCGGAGAGAGGTGTTTAAGTCAAGGTGCGAGAGACGGTAT    | 1599 |
| QY | 529  | ArgArgLysGlyPhe  | ArgPheSerIleGlyLysAsnArgLeuThrTyrGlyLysArgTyr       | 549  |
| Db | 1593 | GAGAAAGAGCGCT    | TCCGG-----CTGCCAGACAACAGATA-----GGAGAGAGATT         | 1644 |
| QY | 549  | rSerSerProHisGln | SerLeuLeuSerIleArgGlySerLeuPheSerProArgArgAs        | 569  |
| Db | 1641 | TTCCATCATGATGA   | TATAGTGGTCCAGCATTCAGGCTCGCCCTCTCCCGCATATA           | 1700 |
| QY | 569  | AsnArgThrSerLeu  | PheSerPheArg-----GlyArgAlaLysAspValGlySerGln        | 587  |
| Db | 1701 | CAGCAAAAGCACT    | TTCACTTCACCTTCGGGAGCCGGGTGTGTCGGAGCCCGGCTCTGA       | 1766 |
| QY | 587  | AsnAspPheAla     | AspAspGlnHisSerThrPheGluAspAsnGlnSerArgArgAspSe     | 607  |
| Db | 1761 | GAATGAGTTGCGA    | ACAGATGAACAGACAGACCGGTGAGAGAGAGCGGCGCGTACCTC        | 1822 |
| QY | 607  | rLeuPheValPro    | ArgArgHisGlyLysArgAsn-----SerAsnLeu                 | 622  |
| Db | 1821 | GCCTTATATCCGAT   | CCGATCCGCGCGCGCGGAGCGCGGAGAGTACAGTGTGCTACACGCGCTA   | 1880 |
| QY | 622  | uSerGlnThrSer    | ArgSerSerArgMetLeuAlaValPheProAlaAsnGlyLysMetIle    | 642  |
| Db | 1881 | CAGCCAGTGCAGC    | CGCTGCTGCGCATCTTCCACGCTGCGCGCACGTCGAACCGCA          | 1944 |
| QY | 642  | sSerThrValAsp    | CysAsnGlyValAlaSerLeuValGlyLysProSerValProThrSe     | 662  |
| Db | 1941 | CAGACGCGTGAC     | TCGCAACGCGGTATGATCTACATCGG-----CCCGGCTC             | 1988 |
| QY | 662  | rProValGlyLeu    | LeuLeuProGluValIleIleAspLysProAlaThrAspAspAsnGln    | 682  |
| Db | 1989 | ACACATCGGGCG     | GGCTGCTGAGTGAATATGATTAAGCAGACTACGAGAC-----AG        | 2044 |
| QY | 682  | YThrThrThrGlu    | ThrGlnMetLysArgArgSerSerPheHisValSerMetAs           | 702  |
| Db | 2043 | CGCAACGACTGA     | GGTGAATTAAGAAAGAGCCCTGAGCTCTTTAGTTCTATGGA           | 2105 |
| QY | 702  | pPheLeuGluAsp    |   |      |



Db 2523 CCTAGTTTAATGAGCTGCTCCGACATGTGAGAGGGGCTCTCACTGCTGGGCTTT 2582  
 QY 861 eargleuAargValPheIysleuAlaIysSerTrpProIthrLeuAsnMetleuIlely 881  
 Db 2583 CCGACTGCTCCGAGTCTTCAAGCTGGCCAGATCTCTGGCCACCCCTGAAACATGTGATCA 2642  
 QY 881 stlleleIyAsnSerValIyAlaIeugIyAsnleuThrleuValleuAlaIleIle 901  
 Db 2643 GAATCAGCGGAGACTCCCTGGTGGTCCCTGGGCAACCTGACCTGGTGGTCCATCACTGT 2702  
 QY 901 lPheIlePheAlaValAlaIyMetGlnleuPheGlyLysSerTrpIyAspCyValCy 921  
 Db 2703 CTTCATCTTCCGCTGGTGGGATGACGCTGTTGGAAAGATTACAGAGAGTCCGCTG 2762  
 QY 921 stIyAlaIaSerAspCysGlnleuProArgTrpHisMetAsnAspPheHisSerPh 941  
 Db 2763 TAAGATCAACCAAGAGTCAAGCTCCGCGCTGGCACATGAACATCTTCCACTCTT 2822  
 QY 941 elauIleValPheArgValLeucysglYgluTrpIleGluThrMetTrpAspCysMetG 961  
 Db 2823 CCTCATCGTCTCCGAGTGTGTGTGGGAGTGTGATGAGACCATGTGGGACTGCTCATGA 2882  
 QY 961 uValAlaIaGlyAlaMetCysleuThrValPheMetMetValMetAlaIleGlyAsnle 981  
 Db 2883 GGTGGCCGAGCCAGCCATGTGCTCATTTGTTTATGATGATTAGTTCATTTGGCAACT 2942  
 QY 981 uValAlaIleuAsnleuPheleuAlaIleuLeu\*\*SerSerPheSerAlaAspAsnleuAl 1001  
 Db 2943 GGTGGTGTCAATCTATCTCTGGCTGCTGTGTGAGCTCTCTGACGCGACAGCAACCTGCC 3002  
 QY 1001 aAlaIthrAspAspAsnGluMetLysAsnleuGlnIleAlaValAspArgMetHisly 1021  
 Db 3003 GGGCAACAGAGAGAGAGCGGGAATGAACACCTGACATCTCATGTATCCGGATCAAGAA 3062  
 QY 1021 sglYValAlaIyValIyAsnArgIyIleYrGluPheIleGlnIleSerPheIleArgly 1041  
 Db 3063 GGGGCGGTGCTTGACCAAGTGAAGGTGACAGGCTTATGAGGCTCACTC-----AA 3116  
 QY 1041 sglIyAlaIleuAspIleuIleIyAsnProLeuAspAspLeuAsnIyAspSerCy 1061  
 Db 3117 GCAGCGGAGCGGATGATGAAGAAACCCCTGACGAGCTGATGAGAAAGAGCGCAACTG 3176  
 QY 1061 sMetSerAsnHisThr---\*\*GluIleGlyLysAspLeuAspTrpIleuIyAspValAs 1080  
 Db 3177 CACCGCCACACACCGGCGGTGATATCCACAGGAGCGGACACTTCCAGAAAGCGGAA 3236  
 QY 1080 nglYThrThrSerGlyIleGlyThrGlySerSerValGluIyTrpIleIleAspGluSe 1100  
 Db 3237 CGGAAACACAGCGGCGATC-----GGCAGCGGTGAGAGATCATCATCGACGAG-- 3288  
 QY 1100 rAspTrpMetSerPheIleAsnAsnProSerleuThrValThrValProIleAlaValAl 1120  
 Db 3289 -GACACATGTCCTTCAATTAACACCAACCAACCTGACCGTGGGTGGCCATTTGTGTGG 3347  
 QY 1120 ygluSerAspPheGluAsnleuAsnThrGluAspPheSerSerIySerAspIleuGlu 1140  
 Db 3348 CGAGTGTGACTTCGAGAACCTCAACACAGAGATGTTAGCGCAACACAGACCTCGAAG 3407  
 QY 1140 uSerIyGluIyLeuAsnGlnIySerSerSerSerSerGluIySerThrValAspIleG 1160  
 Db 3408 CACCAAAAGATTAACCTGACGAT--ACCAAGCTCTCAGAAAGAAATCCATCGACATCAA 3464  
 QY 1160 yAlaProValAlaIyGluIleProValAlaIyProGluIyIleuIyGluIyProGluAla 1180  
 Db 3465 GCCTGAGGTGGAAGAAATTCCTCCGCGAGCAACCTGAGAAATACCTTGATCCGAGCGCTG 3524  
 QY 1180 sPheThrGluIyCysValGlnArgPheIyCysCysGlnIleAsnValGluIyArg 1200  
 Db 3525 CTTCACAGAGAGGTGCTCCAGCGGTCAAGTGTCCAGAGGTCAACATCGAGAGGACT 3584  
 QY 1200 gglYIyGlnIyTrpTrpAsnleuArgArgTrpCysPheArgIleValGlnIyAsnTrpPh 1220  
 Db 3585 AGGCAAGTGTGTGTGATCTTGGGAAACCTGCTCTCATTTGTGGAGCAACAATTTGGTT 3644  
 QY 1220 egluThrPheIleValPheMetIleIleuLeuSerSerGlyAlaIleuAlaPheGluAsp 1240  
 Db 3645 TGAGACCTTATCATCTTCTTATGATTTGTGTCACACAGAGGGGCGCTGGCTTTAGAGCAT 3704  
 QY 1240 eYrIleAspGlnArgGlySerThrIleYsTrpMetleuGluIyAlaAspIyValPheTh 1260  
 Db 3705 CTACATTTGACAGAGAGAGAGCCATCCGACCAATCCTGTGATATGCGACAAAGTCTTAC 3764  
 QY 1260 rYrIlePheIleleuGluMetleuLeuIystrPValAlaIyArgIyGlnIyThrTrp 1280  
 Db 3765 CTACATCTTATCTCTGGAGATGTTGCTCAAGTGGAGACCGCTACGGCTTCTCAAGTCTT 3824  
 QY 1280 eThrAsnAlaTrpCysTrpLeuAspPheIleuIleValAspValSerIleuValSerIeuth 1300  
 Db 3825 CACCAATGCTGTGTGTGTGGTGGATCTCCATGTGTGGCTGTCTTACTGTACGCTTAT 3884  
 QY 1300 rAlaAsnAlaIeugIlyTrpSerGluIyGlnIyAlaIleIySerleuAsnThrArgAl 1320  
 Db 3885 AGCTAATGCCCTGGCTACTGAGAACTAGGTGCAATTAAGTCCCTTAGACCTTAGAGC 3944  
 QY 1320 aLeuArgProLeuArgAlaIeuserArgPheGluIyMetArgValAlaIyAlaIle 1340  
 Db 3945 TTTGAGACCTTAAGACCTTATCAGCATTTGAAGGATGAGGTTGGTGTGAATGCTT 4004  
 QY 1340 uLeuGlyAlaIleProSerIleMetAsnValleuLeuValCysleuIlePheTrpIleu 1360  
 Db 4005 GGTGGGCGCATCCCTCCATCATGAAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4064  
 QY 1360 ePheSerIleMetGlyAlaIyAsnleuPheAlaGlyLysPheTrpHisCysIleAsnThrTh 1380  
 Db 4065 TTTTACAGTATGAGGATTAACCTGTTGGGGAATACCATCTACTGCTTTATATGAGC 4124  
 QY 1380 rThrGlyAspArgPheAspIleGluAspValAsnHisIleTrpAspCysleuIyLeuI 1400  
 Db 4125 TTTGGAATCCGGTTCGAATTCGATTTGTCMACATTAACGACAGCTGTGAGAACTCAT 4184  
 QY 1400 egluArgAsnGluThr--AlaArgTrpLysAsnValLysValAsnIlePheAspAsnVal 1419  
 Db 4185 GAGCGGACCAACAGCAGGAGATCCGATGAGAAATGTCAAAATCACTTATCAATGCGG 4244  
 QY 1419 yPheGlyTrpLeuSerleuIyGlnIyAlaIyThrPheIyGlyTrpPheIyAspIleMetCy 1439  
 Db 4245 AGCAGGTACTGCGCTCTTCAAGTGGCAACCTTAAAGCTGGTGAATGACATCATGTA 4304  
 QY 1439 rAlaAlaValAspSerArgAsnValGluIyGlnIyTrpIyGluIySerleuIyTrpMe 1459  
 Db 4305 TGGCGGTGTGATTCGCGAAGACAGACAGACAGCTGACTAGAGGCAACATCTCAT 4364  
 QY 1459 tYrIleuTrpPheValIlePheIleIlePheGlySerPhePheThrleuAsnleuPheI 1479  
 Db 4365 GTACATCTACTGTCATCTTCAATCATCTTGGCTCTTCACTTCAACCTGCAACCTGTAT 4424  
 QY 1479 eglYValIleIleAspAsnIleAsnGlnIyLysLysLysPheGlyIyGlnIyAspIlePh 1499  
 Db 4425 CGGTGTATATTCACAACTTCAACAGCAAGAAATAAATTGGAGCTGACGACATCTT 4484  
 QY 1499 eMetThrGluIyGlnIyLysIyTrpAsnAlaMetIyLysLysLysIySerIyLysPr 1519  
 Db 4485 CATACAGAGAGAGAGAGAGATCTCATATGCCATATAAAGTGGGCTCCAAAGAACCC 4544  
 QY 1519 oGlnIyProIleProArgProGlyAsnIyPheGlnIyMetValPheAspPheValTh 1539  
 Db 4545 ACAGAACCCATCCCGCGACCTTGAACAAATAACCAAGGATGTCTTGAATTTGTCAC 4604  
 QY 1539 rArgGlnValPheAspIleSerIleMetIleIleuIleCysleuAsnMetValIyThrMet 1559  
 Db 4605 TCAACAAAGCTTGTACATTTGTATGATGATGATGATGATGATGATGATGATGATGAT 4664  
 QY 1559 tValGluTrpAspAspIleSerGluIyTrpValIyThrIleIleuSerArgIleAsnVal 1579  
 Db 4665 GGTGGAGACAGACACTGAGCAAGCAAGATGAGCAACATTTCTTACTGATTTAATCTGTT 4724

|    |      |  |      |
|----|------|--|------|
| OY | 1579 | lphnileValleuPheThrglyGluCysValleuLysleuIleSerLeuArghisIyTry   | 1599 |
| Db | 4725 | CTTGTGATCTTCTTACCGTCAAGAGTGCTGCTCAAAATGTTGGCTTGAGACACTACTA     | 4784 |
| OY | 1599 | rPhrThrlleGlyTTPraSnllePheSpheValValIleLeuSerIleValIglyme      | 1619 |
| Db | 4785 | TTTTACCACTGGCGGGAACATCTTTACATTTGGTGGGTCACTCTCCATCTTGGGAAT      | 4844 |
| OY | 1619 | tPheLeuAlaGluLeuIleGluLysTryPheValSerProThrlleuPheArghValIleAr | 1639 |
| Db | 4845 | GTTCCTGGCTGATATCTTATAGAAAGTACTTGGTCTCCCAACCTATTCGAGTATACG      | 4904 |
| OY | 1639 | gleuAlaArgIleGlyArqIleLeuArqIleuLysglValalysglIleArqThrlle     | 1659 |
| Db | 4905 | ATTGGCCCGATATTGGGGGCACTTTGGCTGTGATCAAGGGCGCAAAAGGATCGCACCT     | 4964 |
| OY | 1659 | uLeuPheAlaLeuMetMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuPheLe      | 1679 |
| Db | 4965 | GCTCTTTCGCTTATATGATGTCGCTGCCCGCTGTTCACATCGGCCCTCGCTCTTCT       | 5024 |
| OY | 1679 | uValMetPheIleTryAlaIlePheGlyMetSerSnPheArqValIlyArqGlyIuVa     | 1699 |
| Db | 5025 | CGTATCTTATCTCTTCTCCATTTTGGCAATGCAACTTCGATACGGAAGACAGAGGC       | 5084 |
| OY | 1699 | IglyIleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPheG    | 1719 |
| Db | 5085 | CGGATTTGAGACATGTTCAACTGCAAGCATTTGGCAACAGCATGCTGTTGTTCOA        | 5144 |
| OY | 1719 | nIleThrThrSerAlaGlyTTPraSpIlyLeuLeuAlaProIleLeuAsnSerLysProP   | 1739 |
| Db | 5145 | GATACACAACTCTGCTGGGAGTGCCTGCTGCTGCACATCCGCAAC---CGCCCCC        | 5201 |
| OY | 1739 | oAspCysAspProAsnIlyValAsnPheProLysSerValIlysgIlyAspCysGlyAsnPr | 1759 |
| Db | 5202 | TGACTGCAGCTTGAGCAAAAGACACCAAGAGAGTGCTTCAAAGGGGACTGTGGAAACC     | 5261 |
| OY | 1759 | oSerValIglyIlePhePhePheValSerTryIleIleSerPheLeuValIalValas     | 1779 |
| Db | 5262 | CTCGGTGGCATCTTCTTCTTGTGTGAGTACATCATCTTCCTCGATTTGTGGTAA         | 5321 |
| OY | 1779 | nMetTryIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGluPr   | 1799 |
| Db | 5322 | CATGTACATGCCATCATCTCTGGAGAACTTCAGCGTGGCCACCGAGAGAGCGCGCACCC    | 5381 |
| OY | 1799 | oLeuSerGluAspAspPheGluMetPheTryGluValIlyrGlyLysPheAspProAspAl  | 1819 |
| Db | 5382 | TCTAGAGAGAGATCTTGAGACTTCTTATAGATATCTGGAGAAATTTGTGCCACGACGC     | 5441 |
| OY | 1819 | athrGlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaIleGluGluProPole    | 1839 |
| Db | 5442 | CACCAATTCATAGAGACTGTAAGTGGCAACTTGGCCACGCGCTCGAGAGCACCCGCT      | 5501 |
| OY | 1839 | uasnLeuProGlnProAsnLysLeuGluLeuIleAlaMetAspLeuProMetValSerG    | 1859 |
| Db | 5502 | CCGAGTACCCCAACCCCAACACCATCCAGCTCATCCGCAATGAGACCTGCCATAGTGGACGG | 5561 |
| OY | 1859 | YAspArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArqValIleuGlyIuse   | 1879 |
| Db | 5562 | AGATCGCATCATGCTTGACATCTTTTGCGCTTCCACCAAGGAGAGTCCGTGGAGACAG     | 5621 |
| OY | 1879 | rGlyGluMetAspAlaLeuArqIleGluMetGluGluArqPheMetAlaSerAsnProse   | 1899 |
| Db | 5622 | TGGGGAATTGAGATCTGCGGGACAGATGAGAGAGGGTTCGTGGATCCATCTTCC         | 5681 |
| OY | 1899 | rLysValSerTryGlnProIleThrThrThrLeuLysArqIlysgIleGluGluValSerAl | 1919 |
| Db | 5682 | CAAAAGTCTTACAGACCATATCAACAACATCTGGCGGCAAGAGAGAGGTCTCTGC        | 5741 |
| OY | 1919 | avalIleIleGluAlaAlaTryArqThrGlyHisLeuLysArqThrVal-----Ly       | 1936 |
| Db | 5742 | AGTGTCTCTACAGCTGCTACAGGGAGACACTTGGCTAGCGGGGCTTCATCTCAGAAA      | 5801 |
| OY | 1936 | sglnAlaSerPheThrTryAsnLysAsnLysIleLysglGlyAlaAsnLeuLeuIleLy    | 1956 |

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Db      5802 GATGCGCTCC-----ACCAAGCTGAGATGGA-----5829
Qy      1956 scLusApMetIleIleAspArgIleAsnGluAsnSerIleThrGluValThrAspLeuTh 1976
Db      5830 -----GGCACACACAGACAGACACAAAGAGAGCC 5858
Qy      1976 rMetSerThrAlaAlaCyProSerThrAspArgValThrLysProIleValGluLys 1996
Db      5855 CCCGTCACAGCCTCCCTC---CCCTCTTACGACAGCGTCACAAAGCCAGACAGAGAGA 5915
Qy      1996 sHiscLu---GIngluGlyLysAspGluLysAlaIys 2007
Db      5916 CCAGCAGCGTCGGGAGAGAGGACGAAGAGGAAGAGCCAG 5955

RESULT 5
US-09-425-043-2
; Sequence 2, Application US/09425043
; Patent No. 6335172
GENERAL INFORMATION:
APPLICANT: DELGADO, STEPHEN G.
APPLICANT: DIETRICH, PAUL S.
APPLICANT: FISH, LINDA M.
APPLICANT: HERMAN, RONALD C.
APPLICANT: SANGAMESWARAN, IASHSMI
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: JANET PAULINE CLARK
STREET: 3401 HILVIEW AVENUE, MS A2-250
CITY: PALO ALTO
STATE: CA
COUNTRY: U.S.A.
ZIP: 94304-1397

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/425,043
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/024,020
FILING DATE: 16-FEB-1998
APPLICATION NUMBER: US 60/039,447
FILING DATE: 26-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,799
REFERENCE/DOCKET NUMBER: R0020B-RGS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-3097
TELEFAX: (650) 855-5322
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6007 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-425-043-2

Alignment Scores:
Pred. No.: 0
Score: 7755.50
Percent Similarity: 84.81%
Best Local Similarity: 75.61%
Query Match: 74.59%

Length: 6007
Matches: 1538
Conservative: 187
Mismatch: 227
Indels: 83
Gaps: 24

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US-09-930-871-12 (1-2009) x US-09-425-043-2 (1-6007)

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 DB 22 ATGGCAGGCGGCTCTGCACACACAGCCCTGATAGTTTCAACCTTTCACCCCTGAG 81  
 OY 21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluValAlaLysAsn---ProLysPro 39  
 DB 82 TCGCGGCAACATCAGAGGCGGTATGCGGAGCAGCCTCAACCAACCAACGAGGCG 141  
 OY 40 Asp-----LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGlu 56  
 DB 142 GATGCGACCGCAGGAGAGAGATGACAGCAGCAAGCCCAACGAGTACCTGAGG 201  
 OY 57 AlaGlyLysAsnLeuProPheIleTyrGlyAspIleProProGluMetValSerGluPro 76  
 DB 202 GCTGGAGAGTTGCTCTTCATCTACGGGAGATCCCGCAGAGGCTGTGCTGCTGCC 261  
 OY 77 LeuGluAspLeuAspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGly 96  
 DB 262 CTGGAGGACTTGGACCTTACTATTTGACGAGAAACCTTTGTGATTTAAACAGAGG 321  
 OY 97 LysAlaIlePheArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnPro 116  
 DB 322 AAACTCTCTTCAATTTAGTGCACACCTGCTGTGATTTTAAAGCTTTTAACTG 381  
 OY 117 LeuArgLysIleAlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCys 136  
 DB 382 ATAAAGATATGCTATTAATTTTGTATACACTGATTTTCAGATGATCATCATGTC 441  
 OY 137 ThrIleLeuThrAsnCysValPheMetThrMetSerAsnProProAspTyrThrLysAsn 156  
 DB 442 ACCATCCGTGACCAATGTTGTTGATGACCTTGTAGTAACTCCAGAAATGTCGCAAGAT 501  
 OY 157 ValGluTyrThrPheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArg 176  
 DB 502 GTGGAGTACATTCACAGAGATTTACATTTGAATCTAGTAAATTCATCGCAAGA 561  
 OY 177 GlyPheCysLeuGluAspPheThrPheLeuArgAspProTyrAsnTyrPheAspPheThr 196  
 DB 562 GCTTCTGATAGAGCGCTTCACTCTTCCGAGACCGGTGAGACGTGTAGCTTCACT 621  
 OY 197 ValIleThrPheAlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArg 216  
 DB 622 GTCAATCATGATGATATGATGACAGAGTTTGGACCTGGCAATGCTCAGCGCTGAGA 681  
 OY 217 ThrPheArgValLeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIle 236  
 DB 682 ACATTCAGGGTCTCGAGCTTTGAAACTATCTGTAAATTCAGGCTGAGAGACAAATC 741  
 OY 237 ValGlyAlaLeuIleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPhe 256  
 DB 742 GTGGGCGCCCTAATCCAGTCCGAGAGAGAGCTGTGAGATGATGATCTGACAGAGTTC 801  
 OY 257 CysLeuSerValPheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLys 276  
 DB 802 TCCCTGAGTGTTCGCTGATGCTGATGCTGACAGCTTCAATGCGGAACTTCCAAACAAG 861  
 OY 277 CysIleGlnTyrProProThrAsnAlaSerLeuGluGlnHisSerIleGluLysAsnIle 296  
 DB 862 TGTGCTGTGCTGCC----- 876  
 OY 297 ThrValAsnTyrAsnGlyThrLeuIleAsnGluThrValPheGluPheAspTyrLysSer 316  
 DB 877 -----ATTAATTCACAGAGAGCTACCTGAGAAACGAGCAAGAGCTTGTACCTGAGAGAA 933  
 OY 317 TyrIleGlnAspSerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLysCys 336  
 DB 934 TATATCAACAATAAACAACCTTTTACATGTTCTCTGAGATGCTAGAACCCCTGCTGCG 993  
 OY 337 GlyAsnSerSerAspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArg 356  
 DB 994 GGAACAGTTCTGATGCTGCGCAATGCCAGAGAGGATTCACATGAGAAAGAGAGAGG 1053

OY 357 AsnProAsnTyrGlyTyrThrSerPheAspThrPheSerTyrPheAlaPheLeuSerLeuPhe 376  
 DB 1054 AACCCCACTACAGGCTTACACCAAGCTTTGACACCTTCAGCTGCGCTTCTTGTGATTAATTC 1113  
 OY 377 ArgLeuMetThrGlnAspPheThrProLysAsnLeuTyrGlnLeuThrLeuArgAlaAlaGly 396  
 DB 1114 CGCTTATGACCCAGGAGACTATTTGGAGAACTTATACACTGACCTTACAGCGCTGAGG 1173  
 OY 397 LysThrTyrMetIlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsn 416  
 DB 1174 AAAAGTACATATATCTTCTTGTCTGTGCATCTTGTGGTCTTCTATCTGATGAGAC 1233  
 OY 417 LeuIleLeuAlaValAlaAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGlu 436  
 DB 1234 TTGATCTGTGCTGTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1293  
 OY 437 AlaGluGlnLysGluValGluPheGlnGlnMetIleGluGlnLeuLysGlnGlnGlu 456  
 DB 1294 GCAAGCAGAAAGAGGCGCGATTCAGAGCAATCTGAGCACTCAAGAGCAGCAGAG 1353  
 OY 457 AlaAlaGlnGlnAlaAlaThrAlaThrAlaSerGluHisSer----- 470  
 DB 1354 GAGCAGACAGGCTCTGCATAGCCACTC-AGCGGCACTGTCTCGAGAGCCCATTTGA 1412  
 OY 471 ArgGluProSerAlaAlaGlyArgLeuSerAsp-SerSerSerGluAlaSerLysLeuSe 490  
 DB 1413 AGAAGAGAGGAGAGATGAGGTAGGCTCTCGAGAGCTCTTGTGAACTGCTTAACTCAG 1472  
 OY 490 rSerLysSerAlaLysGluArgArgAsnArgArgLysArgLysGlnGlnGlnGln 510  
 DB 1473 TTCCAAGAGCGCAAGAGAGCGGAGAACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1532  
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 DB 1533 TGAAGCGAG 1592  
 OY 529 eArgArgLysGlyPheArgPheSerIleGluGlyAsnArgLeuThrTyrGluLysArgTyr 549  
 DB 1593 GAG 1640  
 OY 549 rSerSerProHisGlnSerLeuLeuSerIleAlaGlyLysLeuPheSerProArgArgAs 569  
 DB 1641 TTCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1700  
 OY 569 nSerArgThrSerLeuPheSerPheArg-----GlyArgAlaLysAspValLysSerG 587  
 DB 1701 CAGCAAAAGAGAGATCTTCACTTCCGGGAGACCCGCTGCTTCCGGGAGACCCGCTGCTGA 1760  
 OY 587 uAsnAspPheAlaAspAspGluHisSerThrPheGluAspAsnGluSerArgArgAspSe 607  
 DB 1761 GAATGAGTGTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1820  
 OY 607 rLeuPheValProArgArgIleGlyLysArgArgAsn-----SerAsnLe 622  
 DB 1821 GCTTCTTATCCCATCCAGCGCGCGCGAGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1880  
 OY 622 uSerGlnThrSerArgSerSerArgMetLeuAlaValPheProAlaAsnGlyLysMetHis 642  
 DB 1881 CAGCAGAGTGCAGCGCTGCTGCGGATCTTCCCGAGCTGCGGAGAGAGAGAGAGAGAGAGAG 1940  
 OY 642 sSerThrValAspCysAsnGlyValValSerLeuValGlyLysProSerValProThrSe 662  
 DB 1941 CAGAGAGTGTGAGTGCAG 1988  
 OY 662 rProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAspAsnG 682  
 DB 1989 ACACATGCGCGCGCTCTGCTGAG 2042  
 OY 682 yThrThrThrGluThrGluMetArgLysArgArgSerSerPheHisValSerMetHis 702  
 DB 2043 CGCAAGCACTGAGGTGAGAAATTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2102



Db 4245 AGCAGGGTACCTGGCCCTTCTTCAAGTGGCAACCTTCAAAAGCTGATGACATCATGTA 4304  
 QY 1439 TALAAlaValaSPSerFARaSPaValaGluleuGlnProLysTYrGluGluSerLeuTYrMe 1459  
 Db 4305 TCGGGCTGTAGATTCGCCGAAGCAGACAGACGCTGACTACAGGAGCCACATCTACAT 4364  
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 Db 4365 GTACATCTACTGCTGCTATCATCATCTTCGCTCCCTCTTCAACCTCAACCTGTTTCAT 4424  
 QY 1479 eGlyValaIleIleAspAsnPheAsnGlnGlnLysLysPheGlyGlyGlnAspIlePhe 1499  
 Db 4425 CGGTGATCATCATGACACTTCAACAGAGAGAAAGTTGGAGCTGACAGCATCTT 4484  
 QY 1499 eMetThrGluGluGlnLysLysTYrTYrAsnAlaMetLysLysLeuGlySerLysLysPr 1519  
 Db 4485 CATGACAGAGAACAGACAGACAGATCATCAATGCCAAGAAAGCTGGCTCCAGAACCC 4544  
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 Db 4545 ACAGAAAGCCCATCCCGGAGCCCTTGAACAAATCCAAAGGATGTCTTTGATTTTCGTAC 4604  
 QY 1539 rArgGlnValaPheAspIleSerIleMetIleLeuIleGlyLeuAsnMetValaThrMetMe 1559  
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 QY 1559 tValGlnThrAspAspGlnSerGlnLysValaIleThrIleLeuSerArgIleAsnLeuVa 1579  
 Db 4665 GGTGGAGACAGACACACAGACAGACAGATGAGAACATCTTTACGATTAATCGT 4724  
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 QY 1599 rPheThrIleGlyTYrAsnIlePheAspPheValaValaIleLeuSerIleValaGlyMe 1619  
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 Db 4905 ATTGGCCCGATATGGCGGCACTTGTGCTGATCAAGGGGCGCAAAAGGATCCGCAACCT 4964  
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 Db 4965 GCTCTTGTCTTATATGATGTCGCTGCCGCCGCTGTTCAACATGAGCCCTCTGCTCTCT 5024  
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 QY 1739 oAspCysAspProAsnLysValaAsnProGlySerSerValaLysGlyLysPcysGlyAsnPr 1759  
 Db 5202 TGACTGACAGCTTGACAAAGACACCCAGGAGATGGCTTCAAAAGGAGCATCTGGAAACC 5261  
 QY 1759 oSerValaGlyIlePhePhePheValaSerTYrIleIleIleSerPheLeuValaValaVala 1779  
 Db 5262 CTCGGGGGAGCATCTTCTTCTTGAGACTACATCATCATCTCTCTCTGATTTGGAGAA 5321  
 QY 1779 nMetTYrIleAlaValaIleLeuGlnAsnPheSerValaIleThrGlnLysSerAlaGluPr 1799  
 Db 5322 CATGTACATGCATCATCTCTGAGAACTTCAAGGTGCGCACCGAGAGAGAGCGCGACCC 5381

QY 1799 oLeuSerGlnAspAspPheGlnMetPheTYrGlnValaITrGlnLysPheAspProAspAl 1819  
 Db 5382 TCTGAGTGAAGAGACTTCCAGACTTCTATGATCATGTGGAGAAAGTTTGACCCAGACGC 5441  
 QY 1819 aThrGlnPheMetGlnPheGlnLysLeuSerGlnPheAlaAlaIleLeuGlnProProle 1839  
 Db 5442 CACCCAGTTATGATGACTGTAAAGCTTGAAGACTTGGCAGCCCTTGAGACACCCGCT 5501  
 QY 1839 uAsnLeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValaSerGln 1859  
 Db 5502 CCGAGTACCCAGACCCACACACATCGAGCATGATGCCATGAGCTGCCATGATGAGAGCG 5561  
 QY 1859 yAspArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValaLeuGlyLys 1879  
 Db 5562 AGATGCTCATCTGCTGTCGACATCCTTTTCGCTTCAACAGAGAGTCTGGAGAGACAG 5621  
 QY 1879 rGlyGlnMetAspAlaLeuArgIleGlnMetGlnLysArgPheMetAlaSerAsnProse 1899  
 Db 5622 TGGGAGTTGGACATCTCGGCGACAGATGAGAGAGCGTTCTGTCATCAATCTTC 5681  
 QY 1899 rLysValSerTYrGlnProIleThrThrThrLeuLysArgLysGlnGlnLysAlaSerAl 1919  
 Db 5682 CAAGTGTCTTACAGACTATACACACACTCTCGGCGCAGACAGAGAGAGTGTCTGC 5741  
 QY 1919 aValIleIleGlnArgAlaTYrArgArgHisLeuLeuLysArgThrVal-----Ly 1936  
 Db 5742 AGTGTCTCTCAGCTCTCCACAGGAGGACCTTGCTGAGCGGGCTTCATCTCAGAA 5801  
 QY 1936 sGlnAlaSerPheThrTYrAsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuIleLy 1956  
 Db 5802 GATGCTCTC-----AACACCTGAGAAATGA----- 5829  
 QY 1956 sGlnAspMetIleIleAspArgIleAsnGlnAsnSerIleThrGlnLysThrAspLeuTh 1976  
 Db 5830 -----GGCACACAGACAGACAGAAAGAGAGCAG 5858  
 QY 1976 rMetSerThrAlaAlaCysProProSerTYrAspArgValaThrLysProIleValaGly 1996  
 Db 5859 CCCGTCACAGCCCTCCCTC-----CCCTTACGACAGCTCTCAAAAGCCAGACAGAGAA 5915  
 QY 1996 sHisGlu-----GlnGlnGlyLysAspGlnLysAlaLys 2007  
 Db 5916 GCAGCAGCGTGGGAGGAGGCGCAGAGAGAGAGCCAG 5955

RESULT 6  
 US-09-024-020B-1  
 Sequence 1, Application US/09024020B  
 Patent No. 6030810  
 GENERAL INFORMATION:  
 APPLICANT: DELGADO, STEPHEN G.  
 APPLICANT: DIEHRICH, PAUL S.  
 APPLICANT: FISH, LINDA M.  
 APPLICANT: HERMAN, RONALD C.  
 APPLICANT: SANGAMESWARAN, LAKSHMI  
 TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE  
 TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF  
 NUMBER OF SEQUENCES: 43  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: JANET PAULINE CLARK  
 STREET: 3401 HILLVIEW AVENUE, MS A2-250  
 CITY: PALO ALTO  
 STATE: CA  
 COUNTRY: U.S.A.  
 ZIP: 94304-1397  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/024,020B  
 FILING DATE: 16-FEB-1998

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CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,447
FILING DATE: 26-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,799
TELEPHONE: (650) 852-3097
TELEFAX: (650) 855-5322
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5977 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-024-020B-1

Alignment Scores:
Pred. No.: 0 Length: 5977
Score: 7720.50 Matches: 1531
Percent Similarity: 84.46% Conservative: 187
Best Local Similarity: 75.27% Mismatches: 224
Query Match: 74.26% Indels: 93
DB: 3 Gaps: 24

US-09-930-871-12 (1-2009) x US-09-024-020B-1 (1-5977)

OY 1 MetLugIntrValLeuValProGlyProAspSerPheAsnPhetThrArgLlu 20
DB 22 ATGGCAGCGCGGCTCCGACACGACGCGCTGATGATTCACGCCCTTACCGCTTC 81
OY 21 SerLeuAlaIleGluArgGlyLeuGluGluLysAlaLysAsn---ProLysPro 39
DB 82 TCGCTGGCAACATCGAGAGCGGCTTCCGAGACGACGCTCAGAAACCAACCAAGCG 141
OY 40 Asp-----LysLysAspAspAspLysnGlyProLysProAsnSerAspLeuLlu 56
DB 142 GATGCGACGCCGCGGAGGAGCATGACAGACAGCAAGCCCAAGCCAAACAGTGCAG 201
OY 57 AlaLysAsnLeuProPheIleGlyLysLysLysLysLysLysLysLysLysLys 76
DB 202 GCTGGGAGAGCTTGGCTTTCATCATCGGAGACATCCGCAAGCGCTGCGCTTCCC 261
OY 77 LeuLluAspLeuAspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGly 96
DB 262 CTGGAGAGCTTGGACCTTACTATTGACGAGAAACCTTTGATGATTAACAGAGG 321
OY 97 LysAlaIlePheArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnPro 116
DB 322 AAACTCTCTTCAGATTAGTGCCACACCTGCTTGTACATTTTAAAGCCCTTTAACTG 381
OY 117 LeuArgLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 136
DB 382 ATAGAAGAAATAGCTATTAAATTTGTTACACATGTTTTCAGATCATCATGTC 441
OY 137 ThrIleLeuThrAsnCysValPheMetThrMetSerAsnProProAspTyrThrLysAsn 156
DB 442 ACCATCTCGACCAACTGTGTTCATGACCTTTAGTAACTCCAGATGCTCAAGAT 501
OY 157 ValGluTyrThrPheThrGlyIleTyrThrPheGluSerLeuIleLysLysLysLys 176
DB 502 GTGAGAGTACATTCACAGGAGATTACATGATTTGATCATGATGAAATCATGCAAGA 561
OY 177 GlyPheGlyLeuGluAspPheThrPheLeuArgAspProTyrPheAsnPhetThr 196
DB 562 GGTGTCGATAGAGCGGCTTCACTTCTTGGAGACCGCTGGAACCTGGTTAGCTTCAGT 621
OY 197 ValIleThrPheAlaTyrValThrGluPheValAspLeuGluLysValSerAlaLeuArg 216
DB 622 GTCATCATGATGAGCATATGTCAGAGATTGTGACCTGGGCAATGTCTCAGCGCTGAGA 681

OY 217 ThrPheArgValLeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIle 236
DB 682 ACATTCAGAGGTTCTCCGAGCTTGAAGAACTATCTGTAAATTCAGAGGCTGAAGCAATC 741
OY 237 ValGlyAlaLeuIleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPhe 256
DB 742 GTGGCGCGCTTAATCCATCCGCTGAGAGAGCTGCGAGCATGATCATCTGCACGTTC 801
OY 257 CysLeuSerValPheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLys 276
DB 802 TGCCGATGATGTTTGGCCCTGATTTGGCTGACGCTTTCATGAGGACCTTCGAAACAG 861
OY 277 CysIleGlnTyrProProThrAsnAlaSerLeuGluLysSerIleGluLysAsnIle 296
DB 862 TGTGTCGTGGGCCC-----3----- 876
OY 297 ThrValAsnTyrAsnGlyThrLeuIleAsnGluThrValPheGluPheAspTyrLysSer 316
DB 877 --ATMAACTTCAGAGAGCTACTGAGAACGCGACAGAGGCTTGTGACTGGAGAGAA 933
OY 317 TyrIleGluAspSerArgTyrHisTyrPheLeuGluGluPheLeuAspAlaLeuLys 336
DB 934 TATATCAACATTAATAACAACTTTTACATGCTCTGCGACGTAAGAACCTTGTCTGC 993
OY 337 GlyAsnSerSerAspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArg 356
DB 994 GGGAAACATTCGATGATGCGGGGCAATGGCCAGAGGATTCAGATGATGAAGACAGAAAG 1053
OY 357 AsnProAsnTyrGlyTyrThrSerPheAspThrPheSerTyrPalaPheLeuSerLeuPhe 376
DB 1054 AACCCCAACTCGGTTTACACAGCTTTCACACTTCAGCTGGGCTTTCGCAATTATTC 1113
OY 377 ArgLeuMetThrGlnAspPheTyrGluLysnLeuTyrGlnLeuThrLeuArgAlaIleGly 396
DB 1114 CGCCTTATGACCCAGCATTTATGGAGAACTTATACAGCTGACTGACCTTACAGCGCTGG 1173
OY 397 LysThrTyrMetIlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsn 416
DB 1174 AAAGCTCATGATCTCTTGTGTGTGTCATCTTCGAGGCTTCTTCTTATCTGTGTGAC 1233
OY 417 LeuIleLeuAlaValAlaIleMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGlu 436
DB 1234 TTGATCTTGGCTGTGGTGGCCATGCTTATGAGAAACAGAAACAGCAACTGAGAGAG 1293
OY 437 AlaGluGlnLysGluAlaGluPheGlnIleMetIleGlnIleLysGlnGlnGln 456
DB 1294 GCAGAGCAAAAGAGGCGGAGGTTCAAGGCATGCTGGAGCAACTCAAGACAGCAGAG 1353
OY 457 AlaAlaGlnGlnAlaAlaThrAlaThrAlaSerGluHisSer----- 470
DB 1354 GAGGACAGAGGCTGCGCAATGCGACCTC -AGCGGCGACCTGTCCGAAAGCCCATGCA 1412
OY 471 ArgGluProSerAlaAlaGlyArgLeuSerAsp-SerSerSerGluAlaSerLysLeu 490
DB 1413 AGAAGAAAGGAGAGTGGGAGAGGCTTCCGAGAGAGCTTCTGAACTGTTAAACTCAG 1472
OY 490 rSerLysSerAlaLysGluArgArgAsnArgArgLysLysArgLysGlnLysGlnLys 510
DB 1473 TTCCAGAGCGCGAAGAGCGCGGAGACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1532
OY 510 rGlyGlyGluLysLys---AspGluAspGluPheGlnLysSerGlnSerGluAspSerIle 529
DB 1533 TGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1592
OY 529 earArgArgLysGlyPheArgPheSerIleGluGlyAsnArgLeuThrTyrGluLysArgTy 549
DB 1593 GAGAAGAGAGAGCTTCGCG-----CTGCCAGACAAACAGGATA-----GGAGAGAGATT 1640
OY 549 rSerSerProHisGlnSerLeuLeuSerIleArgGlySerLeuPheSerProArgArgAs 569
DB 1641 TTCCATCATGATGATGCTGCTGCTGATTCAGAGCTCGCCCTTCTCTCCGACATTA 1700

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569 nserarthrserleupesrhearg-----glarvalalayspvaliglysercl 587  
1701 CAGCAAAAGCAGCATCTTCAGCTCCGGGAGCCGGTGGTCCGGAGCCCGCTCTGA 1760  
587 usnsrpphealaaspasgluhsrthrphelgluaspsangluserararapspe 607  
1761 GATATAGTTCGAGACGATGAAACAGCAGCCGTGAGAGAGAGCGCGCGTGCAGTC 1820  
607 rleupehalproarararhslgyluarararasn-----serasule 622  
1821 GCTTTCATCCGATCCGGCCCGGAGCGCGAGCCGACGTACGTGCTACGCGCTGA 1880  
622 usertlnhrserar 642  
1881 CAGCCAGTGCAGCCCGCTGCTCCGATCTCCCGAGCCGCGCGCGAGCGTGAACGCA 1940  
642 sserthrvalaspsasnglyvalasrleuvalalpheproalalasnlylysmethi 662  
1941 CAGCAGGAGTGCAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1988  
662 rprovalgllyleuvalleuvalleuvalleuvalleuvalleuvalleuvalleu 682  
1989 ACACATCCGGCGCTCCCTCCGAG----- 2013  
682 ythrthrthrthrthrthrthrthrthrthrthrthrthrthrthrthrthrthr 702  
2014 -GCAACGAGTGCAGGAAATTAAGAAAGCCCGTGCATCTCTTTGTTCTATGGA 2072  
702 pheleugluasprosersgluarararararararararararararararar 722  
2073 CCACCTCCGCTCCAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2132  
722 nthr---Valgluileuileuileuileuileuileuileuileuileuileuileu 741  
2133 CAGCGTGCAGGAG 2192  
741 esersnle 761  
2193 TCCCAACATCTTCATCTGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 2252  
761 lnsnleuvalleuvalleuvalleuvalleuvalleuvalleuvalleuvalleu 781  
2253 GACATTAATCGATGAG 2312  
781 nthrleupehalamegluhsrthrphelthralspshasnasnvalleu 801  
2313 TACGCTATTATGAG 2372  
801 rValgluasnleuvalpheThrThrThrThrThrThrThrThrThrThrThrThr 821  
2373 CAGAGAAATTCGTTGTCACGCGGATCTTCACGCGGAAATTCGTTGTCACGCTGAT 2432  
821 ahetasprotyrtyrtyrtyrtyrtyrtyrtyrtyrtyrtyrtyrtyrtyrtyr 841  
2433 CATTGACCCCTCTATTTATTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2492  
841 rleuvalleuvalleuvalleuvalleuvalleuvalleuvalleuvalleuval 861  
2493 CCTGATTTATGAG 2552  
861 eArglleuvalleuvalleuvalleuvalleuvalleuvalleuvalleuvalleu 881  
2553 CCGAGTCTCCGAGTCTTCAAGCTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2612  
881 stle 901  
2613 GATCATCGGAACTCCGAG 2672  
901 lphelilepalealavalgllymetgluileuileuileuileuileuileuileu 921  
2673 CTTCATCTTCGCGTGGTGGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2732  
921 slysllealaserapsygluileuvalleuvalleuvalleuvalleuvalleuval 941

2733 TAAAGTCAACAG 2792  
941 eleuilevalphear 961  
2793 CTTATCTGCTTCAG 2852  
961 uValalaglylnalameCysleuThrValphelelelelelelelelelelele 981  
2853 GGTGACCGGCGAG 2912  
981 uValalaglylnalameCysleuThrValphelelelelelelelelelelele 1001  
2913 GGTGAGTGCATCTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2972  
1001 aalThrAspAspAspAspAspAspAspAspAspAspAspAspAspAspAsp 1021  
2973 GGCACAG 3032  
1021 sgllyal 1041  
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1041 sgllyal 1061  
3087 GAGAGGAG 3146  
1061 smetserasnasrthr---\*gluileuileuileuileuileuileuileuileu 1080  
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3207 CCGAACACAG 3258  
1100 raspyrmetserphele 1120  
3259 -GACCAATGCTCTTATTAACCAACCAACCTGAGCGGCTCCGCTGCTGCTGCTG 3317  
1120 ygluileuvalleuvalleuvalleuvalleuvalleuvalleuvalleuvalleu 1140  
3318 CAGCTGAGTGCAG 3377  
1140 usertlsglyllyleuvalleuvalleuvalleuvalleuvalleuvalleuval 1160  
3378 CAGCAAAATTAACCTGAGAGAT---ACCAGCTCTCAGAGAGAGAGAGAGAGAG 3434  
1160 yAlaProvalgluileuvalleuvalleuvalleuvalleuvalleuvalleuval 1180  
3435 GCGTGAAGTGAAG 3494  
1180 spherthrgluileuvalleuvalleuvalleuvalleuvalleuvalleuvalleu 1200  
3495 CTTTACAG 3554  
1200 ggllylsgllyllyleuvalleuvalleuvalleuvalleuvalleuvalleuval 1220  
3555 AGCAGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGT 3614  
1220 egluileuvalleuvalleuvalleuvalleuvalleuvalleuvalleuvalleu 1240  
3615 TGAAGCTTCATATCTTCATGATGATGATGATGATGATGATGATGATGATGATG 3674  
1240 eYrllleaspglnar 1260  
3675 CTACATTAAG 3734  
1260 rYrllle 1280  
3735 CTACATCTTCATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3794  
1280 eThrasnalatrcysllyleuvalleuvalleuvalleuvalleuvalleuvalleu 1300

|    |      |   |      |
|----|------|---|------|
| Db | 3795 | CACCAATGCGTGGTGGTGGTGGTGGACTTCCATCTTGCGCTGTCCTCTTAATGACGACCTTAT | 3854 |
| Qy | 1300 | ralasnaalaleuuliyrisersguleugiyalaileysserleatqthrleuargal      | 1320 |
| Db | 3855 | AGCTAAATGCCCTGGGCTACTCGGAACTAGGTGCCATTAAGTCCCTTAGAGACCTTAAGAC   | 3914 |
| Qy | 1320 | aleuargProleuargalaleuSerargphegiuglymetarvalvalasnalale        | 1340 |
| Db | 3915 | TTTGAGACCTTAAGACCTTAACAGATTTCAGAGGAAGAGGAGGTGGTGAATGCTT         | 3974 |
| Qy | 1340 | uleugiyalaleproserlilektsanvalleuvalcysleuilepheprpleuile       | 1360 |
| Db | 3975 | GGTGGCGCCATCCCTCCATCATGATGAGTGGCGGTGTCTCATCTTCTGGCTCAT          | 4034 |
| Qy | 1360 | epheserlilemetllyalasnleuPhealaglylsPheYrHLSysIleasrThH         | 1380 |
| Db | 4035 | TTTCAGCATCATGGGAATTAACTGTTGGGGGAATAATACCACTACTGCTTAATGAAC       | 4094 |
| Qy | 1380 | rThglyhspargPheaspillegluaspvalasnasnhrsthraspCysleuysleuile    | 1400 |
| Db | 4095 | TTTCGAATCCGCTTCGAATCATGATTTGTCACATATAAACGGACTGTGAGAACCTCAT      | 4154 |
| Qy | 1400 | egluargasnluhr---alargtrpbyasnvallylsValasnPheaspasnalgl        | 1419 |
| Db | 4155 | GGAGGGCAGACGCGAGATGCGATGGAAATGTCAGAAATGCACAACTTTGACAAATGCGG     | 4214 |
| Qy | 1419 | yPheglYTyriserleuenginalaIatrrPelysglyTrrPmeAspIleMetY          | 1439 |
| Db | 4215 | AGCAGGCTACTGGCCTTTTAAATGGCCACCTTCNAAGCTGGATGAGCATCATATA         | 4274 |
| Qy | 1439 | ralaalaValasPserargasnvalgluleugInProlYsYrHglugIuserleuYrme     | 1459 |
| Db | 4275 | TGGCGCTGTAGATTCCGGAAGCCAGACGACGCGCTGACTCGAGGGCCACATCTACAT       | 4334 |
| Qy | 1459 | tTyrlentYrPhevalIlephelIleIepheglysrPhepethrleuasleuPheI        | 1479 |
| Db | 4335 | GTACATCTACTCTGCTCATCTTCATCATCTTCGCGCTCTCTTCAACCCCAACCTGTCAT     | 4394 |
| Qy | 1479 | eglYvalIleIleaspasnPheasnInglunlylsYrHsPheglYsglyInaspIleph     | 1499 |
| Db | 4395 | CGGTCTCATCTGCACACTTTCACACGACGAAAGAAAGTTTGGAGGTTCAGACATCTT       | 4454 |
| Qy | 1499 | emetrHglugluInlylsYrTyrrasnalameTlylsYsleuIglyserlysr           | 1519 |
| Db | 4455 | CATGACAGAGGAACAGAAAGATACATATGCGCATGAAAAAGCTGGGCTCCAGAAACCC      | 4514 |
| Qy | 1519 | oGlnlyrProIleProargProglYsnlysrPheglInglymetValPheasphevalTh    | 1539 |
| Db | 4515 | ACGAAACCCATCCCGGACCCCTTGAAACAAATCCAAAGGATGTCTTGATTCGCTAC        | 4574 |
| Qy | 1539 | rArgIlnalPheaspIleSerIleketIleuilecysleuasnmetValThrmeI         | 1559 |
| Db | 4575 | TCAACAAGCCTTGACATTGTGATCATGATGCTCATCTGCTTAACATGAGACAAATAT       | 4634 |
| Qy | 1559 | tValgluThrAspAspInserglunlyrThrHrIleuSerargIleasleuVal          | 1579 |
| Db | 4635 | GGTGGACAGACACCTCAGACGAAAGCAAGATGGAGAAACATTTTTCAGTGAATCTGGT      | 4694 |
| Qy | 1579 | lPheIleValleuPheThrglycysValleuIysleuIleSerleuargHsYrTy         | 1599 |
| Db | 4695 | CTTGTGTCTCTCTTCCTGACCGACAGTGTGCTCAAAATGTTGGCTTGACACACTACTA      | 4754 |
| Qy | 1599 | rPheThrIleglYrPasnIlePheaspheValvalIleuSerIleValagIyme          | 1619 |
| Db | 4755 | TTTTCACATTGGCTGGAACTCTTAACTTTGGGGGCGATCCCTCATCTGCGGAT           | 4814 |
| Qy | 1619 | rpheIlealaleuIleglunlysrYrPheValSerProthrIleuPheargValIlear     | 1639 |
| Db | 4815 | GTTCCTGGCGATATCATTTAGAAAGTACTGCTCCCAACCCATTCGAGTATTCG           | 4874 |
| Qy | 1639 | gleuIalargIleglYargIleuargleuIleYsglyalalysglyIlearghrle        | 1659 |
| Db | 4875 | ATTGTGCCGTATTGGGGCATCTTGGGTGTGATTCAGAGGGCGCAAGAGGATCCGACCTT     | 4934 |

|    |      |  |      |
|----|------|--|------|
| QY | 1659 | unuphleaaleumetketerleuproalaleupheasnilleglyleuleuleuphele      | 1679 |
| Db | 4935 | GCCTCTTCCCTTAATGATGTCGGCCGCCCGCTGTCAACATCGGCGCTCTCTCTCT          | 4994 |
| QY | 1679 | uValmerphellelyrralallepheglymetSerasnphlealalyrralylsArngluva   | 1699 |
| Db | 4995 | CGTCACTGTCACTCTTCACATTTTGGCAATGTCCAACTTCGATACGTGAACAGAGGC        | 5054 |
| QY | 1699 | lGlylleasphametheasnphelutrrhpeglyanSermetillecylsLeuphegl       | 1719 |
| Db | 5055 | CGGCATTGACGCACATGTTTCAACTTCAGACATTTGGCAACACACATGATCTGTTTGTCCA    | 5114 |
| QY | 1719 | nllerThrSeraleglyrrpaspglyleuleualaproilleuAasSerlysPropr        | 1739 |
| Db | 5115 | GATCAACAACGCTCTGCTGGGATGGCTGCTGCTGCCAATCTGAAC---CGCCCCC          | 5171 |
| QY | 1739 | oAsPCysasProasnllysalasnProglySerSerValylsglyaspCysglyasnpr      | 1759 |
| Db | 5172 | TGACAGCAGCTTGGACAAAGAGCACCAGGAGATGGCTTCAAAAGGGGACTGTGGGACCC      | 5231 |
| QY | 1759 | oSerValglyllephephehevalserlyrillelleSerphleuvalValas            | 1779 |
| Db | 5232 | CTCGGTGGCACTCTCTCTTGTGGAGCTACATCAATCAATCTCTTCGATGTGGTAA          | 5291 |
| QY | 1779 | nmetLyrrllealavalilleuenglunsnpheserValaIarhrglugluseralagLupr   | 1799 |
| Db | 5292 | CATGATCATGCGCCATATCCTTGGAGAACTTCACGCGTGGCCACCGAGAGAGCCCGACCC     | 5351 |
| QY | 1799 | oLeuSerGlunaspaspheglumethepetyrgluValIrrpglulyspheasProaspal    | 1819 |
| Db | 5352 | TCTGTGAGGAGATATCACTTCAGACTTTCATGAGATCTGGAGAGATTGGACCGAGAGC       | 5411 |
| QY | 1819 | aThrGlunphemglslnheglulysylSerSerGlunphealalaleuenglupProfole    | 1839 |
| Db | 5412 | CACCCAGTATCATCAGATCACTGAAGCTGGACAGCTTTCGGACGCCCTGGAGACCCGCT      | 5471 |
| QY | 1839 | uAsnLeuproglInproasnLysleuGlunleuIlealelameIaspleuPrometValSerGl | 1859 |
| Db | 5472 | CCGAGTACCCAGGCCAACACATCGAGCTCATCGCATGAGACTGCCCATGTGTAGCGG        | 5531 |
| QY | 1859 | yAspArgllleHisCysLeuaspilleuuphealaphethrlysarValleuuglyluse     | 1879 |
| Db | 5532 | AGATCGCATCCACAGCTTGGACATCTTTCGGCTTCAACAAGCAGAGCTGTGGAGACG        | 5591 |
| QY | 1879 | rglyGlumethaspalaleuargllleelmetglugluarphemetalaseranProse      | 1899 |
| Db | 5592 | TGGGAGATGGACATCCCTGGGAGAGATGAGAGGCGGTTCGGCATCAATCTCTTC           | 5651 |
| QY | 1899 | rLyValSerTyrglnProIleThrrhThrrheulysarGlysglnglugluvalSerAl      | 1919 |
| Db | 5652 | CAAGTGTCTTACGAGCTTTCACAAACCTCTGGGGGCAAGCAGGAGAGGTGTGTGC          | 5711 |
| QY | 1919 | avalilleeqlnarGlnIarTargllleHisLeuLeuLysarGthrVal-----Ly         | 1936 |
| Db | 5712 | AGTGTCTCGTAGAGGTCCACAGGGGACACTTGGCTAGGGGGGCTTCATCTCCAGAAA        | 5771 |
| QY | 1936 | seqlnAlSerPhethrTyrrasnLysnLyslleysetglyalalaenleuilely          | 1956 |
| Db | 5772 | GATGGCTCTC-----AACACGCTGAGAGATGA-----                            | 5799 |
| QY | 1956 | sGluAspmetllelelaspArgllleasnLunserilleThrgluysThraspleuth       | 1976 |
| Db | 5800 | -----GCCACACACAGAGCAAGAGAGAGACAC                                 | 5828 |
| QY | 1976 | rmetSerThrAlaAlaCysProProSerTyrraspArgValThrrysProIleValglyly    | 1996 |
| Db | 5829 | CCGCTCACAGCTCCCTC---CCCTCTACGACGCTTCACAAAGCCAGCAAGGAGAA          | 5885 |
| QY | 1996 | sHsSglu-----GlnGluGlyLysaspGluLysAlaLys                          | 2007 |
| Db | 5886 | GCACGACCGTGGCAGAGCGGACGAGCAAGAGAGACCAAG                          | 5925 |

RESULT 7  
 US-09-425-043-1  
 Sequence 1, Application US/09425043  
 Patent No. 635172  
 GENERAL INFORMATION:  
 APPLICANT: DELGADO, STEPHEN G.  
 APPLICANT: DIETRICH, PAUL S.  
 APPLICANT: FISH, LINDA M.  
 APPLICANT: HERMAN, RONALD C.  
 APPLICANT: SANGAMESWARAN, LAKSHMI  
 TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE  
 TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF  
 NUMBER OF SEQUENCES: 43  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: JANET PAULINE CLARK  
 STREET: 3401 HILVIEW AVENUE, MS A2-250  
 CITY: PALO ALTO  
 STATE: CA  
 COUNTRY: U.S.A.  
 ZIP: 94304-1397  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/425,043  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 09/024,020  
 FILING DATE: 16-FEB-1998  
 APPLICATION NUMBER: US 60/039,447  
 FILING DATE: 26-FEB-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: CLARK, JANET P.  
 REGISTRATION NUMBER: 34,799  
 REFERENCE/DOCKET NUMBER: R0020B-REG  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (650) 852-3097  
 TELEFAX: (650) 855-5322  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 5977 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 US-09-425-043-1

Alignment Scores:  
 Pred. No.: 0 Length: 5977  
 Score: 7720.50 Matches: 1531  
 Percent Similarity: 84.46% Conservative: 187  
 Best Local Similarity: 75.27% Mismatches: 224  
 Query Match: 74.26% Indels: 93  
 Gaps: 24

US-09-930-871-12 (1-2009) x US-09-425-043-1 (1-5977)

QY 1 MetGluGlnThrValLeuValProGlyProAspSerPheAsnPheThrArgGlu 20  
 Db 22 ATGGACACGGCGGTCTGCGACACCGACGCGCTGATGTTCAAGCCCTTCACCCCTGAG 81  
 QY 21 SerLeuAlaIleGluArgGlyIleAlaGluIleLysAlaLysAsn---ProLysPro 39  
 Db 82 TCGCTGGCAACATCGAGAGCGATATGCGGAGCAAGCTCAGAAACCAACCAAGGCG 141  
 QY 40 Asp-----LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGlu 56  
 Db 142 GATGGACGACCGGAGGAGGAGATGAAGACAGCAAGCCCAAGCAAGAGAGAGAGAG 201  
 QY 57 AlaGlyLysAsnLeuProPheIleTyrGlyLysIleProGluMetValSerGluPro 76

Db 202 GCTGGAGAGAGTTGCTTCATCTACGGGAGACATCCGACAGGCGCTGGTGGGTCC 261  
 QY 77 LeuGluAspLeuAspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGly 96  
 Db 262 CTGGAGAGACTTACCTTACTATTTGACCGCAAGAAACCTTTGTATTAACAGAGG 321  
 QY 97 LysAlaIlePheArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnPro 116  
 Db 322 AAACCTCTTCAGATTATGTCACACCTGCTTGTACATTTAAAGCCCTTTAAACCTG 381  
 QY 117 LeuArgLysIleAlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCys 136  
 Db 382 ATAAGAGAAATACCTATTAATAATTTGATACATCACTGTTTCAAGATGATCATGTCG 441  
 QY 137 ThrIleLeuThrAsnGlyValPheMetThrMetSerAsnProProAspTyrPheLysAsn 156  
 Db 442 ACCATCTGACCAAGCTGTGTTTCATGACCTTAGTAACTTCAGAAATGTCACAGAT 501  
 QY 157 ValGluTyrThrPheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArg 176  
 Db 502 GTGAGACACATTCACAGGAGATTACACATTTGAACACTAGTGAAGAAATCATCGCAGA 561  
 QY 177 GlyPheCysLeuGluAspPheThrPheLeuArgAspProTyrAsnTyrPheAspPheThr 196  
 Db 562 GGTTCCTGCAATACAGGCTTCACTTCTGCGAGACCCGTCGAGACTGTTAGCTTACGT 621  
 QY 197 ValIleThrPheAlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArg 216  
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 QY 217 ThrPheArgValLeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIle 236  
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 Db 802 TGCTGAGGTGTTTCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 861  
 QY 277 CysIleGlnIleProProThrAsnAlaSerLeuGluIleHisSerIleGluLysAsnIle 296  
 Db 862 TGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 876  
 QY 297 ThrValAsnTyrIleAsnGlyThrLeuIleAsnGluThrValPheGluPheAspTyrLysSer 316  
 Db 877 ---ATTAACCTTCAAGAGAGCTACCTGAGAAACGACCAAGAGGCTTTGACTGGAGAA 933  
 QY 317 TyrIleGlnAspSerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLysCys 336  
 Db 934 TATATCAACATAAACAACCTTTACATGTTCTGCGACATGCTAGAAACCTTCTCTGCG 993  
 QY 337 GlyAsnSerSerAspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArg 356  
 Db 994 GCGAACAGCTTCATGCTGCGCAATGCCAGAGAGATTCACAGTCAATGAAGACAGAGAG 1053  
 QY 357 AsnProAsnTyrGlyTyrThrSerPheAspThrPheSerThrPheLeuSerLeuPhe 376  
 Db 1054 AACCCCACTACAGGTATACACAGCTTGGACCTTCAAGCTGGGCTTCTTCAATATTC 1113  
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 QY 417 LeuIleLeuAlaValAlaIleMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGlu 436

Db 1234 TTGATCTTGGCTGTGGCCATGGCTTATGAGAACAGACAGCAACTGGAGAG 1293  
 Oy 437 AlagluglnylsgluAlagluPheglnglnmetileglnglnleuylsngln 456  
 Db 1294 GCAGAGCAAAAGAGCGGAGTTCAAGGAAATGCTGGAGCACTCAAGAGAGAGAG 1353  
 Oy 457 AlalaglnglnAlalathralathralaserghuhsier----- 470  
 Db 1354 GAGGACAGGCTGTGCTGATGGCCACTC-ACGGGGACCTCTCTCGAAGACGCATTGA 1412  
 Oy 471 ArggluProserAlalagluAlagluSerasp-SerSerSerghuhsierleu 490  
 Db 1413 AGAAGAGAGGAGAGATGGGATAGCTCTCGAGAGCTCTTGTGAAGTCTTAACCTAG 1472  
 Oy 490 rSerlySerAlalylsgluArgArgAsnArgArglylsArglysglnylsngln 510  
 Db 1473 TTCGAAGAGCGGAGAGAGCGGAGACCGAGAGAGAGAGAGAGAGAGAGAGAG 1532  
 Oy 510 rgllygllyglulys---AspGluAspGluPheglnglnylsSerghuhsier 529  
 Db 1533 TGAAGCGCGAG 1592  
 Oy 529 eArgArglysglyPheArgPheSerileglnglnylsAsnArgleuThrlyrgly 549  
 Db 1593 GAGAGAGAGAGCGCTTCCG-----CTGCGAGACAGAGAGATA-----GGAGAGAGCTT 1640  
 Oy 549 rSerSerProHlsInserleuSerleuSerleuSerleuSerleuSerleuSer 569  
 Db 1641 TTCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1700  
 Oy 569 nSerArgThrSerleuPheSerPheArg-----GlyArgAlalylsAspValgly 587  
 Db 1701 CAGCAAAAG 1760  
 Oy 587 uAsnAspPheAlaAspAspArgPheSerThrPhegluAspAsnGlnSerArgArg 607  
 Db 1761 GATAGATGTCGAG 1820  
 Oy 607 rLeuPheValProArgArgHlsGlyluArgArgAsn-----SerAsnle 622  
 Db 1821 GCTCTTCATCCGAGATCCGCGCGCGCGAGAGAGAGAGAGAGAGAGAGAG 1880  
 Oy 622 uSerGlnThrSerArgSerSerArgMetleuAlaValPheProAlaAsnGly 642  
 Db 1881 CAGCCAG 1940  
 Oy 642 sSerThrValAspAspAsnGlyValValSerleuValGlyGlyProSerVal 662  
 Db 1941 CAGCAGGAG 1988  
 Oy 662 rProValGlyGlnleuLeuProGluValAlleleAspLysProAlaThrAsp 682  
 Db 1989 ACACATCGGGCGGCTCTGCTCGAG----- 2013  
 Oy 682 yThrThrThrGlnThrGlnMetArgLysArgArgSerSerSerPheHlsVal 702  
 Db 2014 -GCAAG 2072  
 Oy 702 pPheleuGlnAspProSerGlnArgGlnArgAlaMetSerileleleleuThr 722  
 Db 2073 CCAACTGCGCTCTCTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2132  
 Oy 722 nThr---ValGlnGlnleuGlnGlnSerArgGlnLysCysProProCysP 741  
 Db 2133 CAGCGTATGAG 2192  
 Oy 741 eSerAsnilePheleuileuPhePAspCysSerProThrPheleuValLysHls 761  
 Db 2193 TGCCAGACTTCTCTCATCTGGAGAGTGTACCCCTAGTGAATAAAGAGAGAG 2252  
 Oy 761 lAsnleuValValMetAspProPheValAspLeuAlaIleThrIleCysIle 781  
 Db 2253 GAACCTTAATCGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2312

Oy 781 nThrleuPheMetAlaMetGlnHlsIleThrProMetThrAspHlsPheAsnVal 801  
 Db 2313 TACGCTATTATGAG 2372  
 Oy 801 rValGlyAsnleuValPheThrGlyIlePheThrAlaGlnMetPheleuylsle 821  
 Db 2373 CGTAGGAATCTGCTGCTCACCGGATCTTACGCGGAGAAATGTTCTGAGCTCA 2432  
 Oy 821 AsnAspProThrThrThrPheglnglnGlnLysPheAsnlePheleuVal 841  
 Db 2433 CAGGAG 2492  
 Oy 841 rLeuSerleuValGlnleuGlyLeuAlaAsnValGlnGlyLeuSerValleu 861  
 Db 2493 CCGTACGTTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2552  
 Oy 861 eArgleuLeuArgValPheLysleuAlaLysSerThrProThrleuAsnMet 881  
 Db 2553 CCGAGCTGCTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2612  
 Oy 881 silelleGlyAsnSerValGlyAlaLeuGlnLysleuThrleuValleuAla 901  
 Db 2613 GATCATCGGAG 2672  
 Oy 901 lPheilePheAlaValAlGlyMetGlnleuPhegllySerThrLysAspCys 921  
 Db 2673 CTTCATCTTCCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2732  
 Oy 921 sLysIleAlaSerAspCysGlnleuProArgThrPheAsnAspPhePheHls 941  
 Db 2733 TAAAGATCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2792  
 Oy 941 eLeuileValPheArgValleuCysGlyGluThrIleGlnThrMetPheP 961  
 Db 2793 CCTCATCTCTCTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2852  
 Oy 961 uValAlaGlyGlnAlaMetCysLeuThrValPheMetValMetValleu 981  
 Db 2853 GGTGCGCGGAG 2912  
 Oy 981 uValValleuAsnleuPheleuAlaLeuLeu\*\*SerSerPheSerAlaAsp 1001  
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 Oy 1001 AlaThrAspAspAsnGlnMetAsnAsnleuGlnIleAlaValAspArg 1021  
 Db 2973 GGCACAG 3032  
 Oy 1021 sGlyValAlaThrValLysArgLysIleThrGluPheIleGlnIleSerPhe 1041  
 Db 3033 GGGCTGCGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3086  
 Oy 1041 sGlnLysIleleuAspGlnIleLysProleuAspAsnAsnLysLysAsp 1061  
 Db 3087 GCAAGGAG 3146  
 Oy 1061 sMetSerAsnHlsThr-----GluIleGlyLysAspLeuAspThrLys 1080  
 Db 3147 CATGCGCAACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3206  
 Oy 1080 nGlyThrThrSerGlyIleGlyThrGlySerSerValGlnLysThrIleleu 1100  
 Db 3207 CCGAAGCAG 3258  
 Oy 1100 rAspThrMetSerPheIleAsnAsnProSerleuThrValThrValProIle 1120  
 Db 3259 -GACACATGTCCTTCATTAACCAACCAACCAACCAACCAACCAACCAACCA 3317  
 Oy 1120 yGluSerAspPheGlnleuAsnThrGluAspPheSerSerGlnSerAsp 1140  
 Db 3318 CGAGCTGACCTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3377

|    |      |   |      |
|----|------|---|------|
| QY | 1140 | uSerlysgluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleG | 1160 |
| QY | 1160 | YAlaProValGluGluGluProValValGluProGluGluThrLeuGluProGluLac  | 1180 |
| QY | 1180 | sPheThrGluGlyCysValAlaGlnPheLysCysGlnIleAsnValGluGluGly     | 1200 |
| QY | 1200 | gGlyLysGluTrpTrpAsnLeuArgTrpCysPheArgIleValGluHisTrp        | 1220 |
| QY | 1220 | eGluThrPheIleValPheMetIleLeuLeuSerSerGlyValAlaLeuAlaPheGlu  | 1240 |
| QY | 1240 | eTyrlIleAspGlnArgLysThrIleLysThrMetLeuGluTrpValAlaTrpGly    | 1260 |
| QY | 1260 | rTyrlIlePheIleLeuGluMetLeuLeuLysTrpValAlaTrpGlyTrpGlu       | 1280 |
| QY | 1280 | ePheAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerIleuValSer    | 1300 |
| QY | 1300 | rAlaAsnAlaLeuGlyLysSerGluLeuGlyAlaIleLysSerLeuArgThrLeu     | 1320 |
| QY | 1320 | aLeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValAla        | 1340 |
| QY | 1340 | uLeuGlyAlaIleProSerIleMetAsnValIleLeuValCysLeuIlePheTrp     | 1360 |
| QY | 1360 | ePheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTrpHisCysIleAsn     | 1380 |
| QY | 1380 | rThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeu        | 1400 |
| QY | 1400 | eGluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnAspAsnValG       | 1420 |
| QY | 1420 | yPheGlyTrpLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpPheAspIle     | 1440 |
| QY | 1440 | aGAGAGGACAGCAGCAGAGATCCGATGGAAGATGTCAATCACTTGCAATGTCG       | 1460 |
| QY | 1460 | TTTCAACATCATGAGGATTAACCTGTTGGGGGAAATACCACTACCTTATAGAC       | 1480 |
| QY | 1480 | TTTCAACATCATGAGGATTAACCTGTTGGGGGAAATACCACTACCTTATAGAC       | 1500 |
| QY | 1500 | TTTCAACATCATGAGGATTAACCTGTTGGGGGAAATACCACTACCTTATAGAC       | 1520 |
| QY | 1520 | TTTCAACATCATGAGGATTAACCTGTTGGGGGAAATACCACTACCTTATAGAC       | 1540 |
| QY | 1540 | TTTCAACATCATGAGGATTAACCTGTTGGGGGAAATACCACTACCTTATAGAC       | 1560 |
| QY | 1560 | TTTCAACATCATGAGGATTAACCTGTTGGGGGAAATACCACTACCTTATAGAC       | 1580 |
| QY | 1580 | TTTCAACATCATGAGGATTAACCTGTTGGGGGAAATACCACTACCTTATAGAC       | 1600 |
| QY | 1600 | TTTCAACATCATGAGGATTAACCTGTTGGGGGAAATACCACTACCTTATAGAC       | 1620 |
| QY | 1620 | TTTCAACATCATGAGGATTAACCTGTTGGGGGAAATACCACTACCTTATAGAC       | 1640 |
| QY | 1640 | TTTCAACATCATGAGGATTAACCTGTTGGGGGAAATACCACTACCTTATAGAC       | 1660 |
| QY | 1660 | TTTCAACATCATGAGGATTAACCTGTTGGGGGAAATACCACTACCTTATAGAC       | 1680 |
| QY | 1680 | TTTCAACATCATGAGGATTAACCTGTTGGGGGAAATACCACTACCTTATAGAC       | 1700 |
| QY | 1700 | TTTCAACATCATGAGGATTAACCTGTTGGGGGAAATACCACTACCTTATAGAC       | 1720 |
| QY | 1720 | TTTCAACATCATGAGGATTAACCTGTTGGGGGAAATACCACTACCTTATAGAC       | 1740 |
| QY | 1740 | TTTCAACATCATGAGGATTAACCTGTTGGGGGAAATACCACTACCTTATAGAC       | 1760 |
| QY | 1760 | TTTCAACATCATGAGGATTAACCTGTTGGGGGAAATACCACTACCTTATAGAC       | 1780 |
| QY | 1780 | TTTCAACATCATGAGGATTAACCTGTTGGGGGAAATACCACTACCTTATAGAC       | 1800 |
| QY | 1800 | TTTCAACATCATGAGGATTAACCTGTTGGGGGAAATACCACTACCTTATAGAC       | 1820 |
| QY | 1820 | TTTCAACATCATGAGGATTAACCTGTTGGGGGAAATACCACTACCTTATAGAC       | 1840 |
| QY | 1840 | TTTCAACATCATGAGGATTAACCTGTTGGGGGAAATACCACTACCTTATAGAC       | 1860 |
| QY | 1860 | TTTCAACATCATGAGGATTAACCTGTTGGGGGAAATACCACTACCTTATAGAC       | 1880 |
| QY | 1880 | TTTCAACATCATGAGGATTAACCTGTTGGGGGAAATACCACTACCTTATAGAC       | 1900 |
| QY | 1900 | TTTCAACATCATGAGGATTAACCTGTTGGGGGAAATACCACTACCTTATAGAC       | 1920 |
| QY | 1920 | TTTCAACATCATGAGGATTAACCTGTTGGGGGAAATACCACTACCTTATAGAC       | 1940 |
| QY | 1940 | TTTCAACATCATGAGGATTAACCTGTTGGGGGAAATACCACTACCTTATAGAC       | 1960 |
| QY | 1960 | TTTCAACATCATGAGGATTAACCTGTTGGGGGAAATACCACTACCTTATAGAC       | 1980 |
| QY | 1980 | TTTCAACATCATGAGGATTAACCTGTTGGGGGAAATACCACTACCTTATAGAC       | 2000 |
| QY | 2000 | TTTCAACATCATGAGGATTAACCTGTTGGGGGAAATACCACTACCTTATAGAC       | 2020 |
| QY | 2020 | TTTCAACATCATGAGGATTAACCTGTTGGGGGAAATACCACTACCTTATAGAC       | 2040 |
| QY | 2040 | TTTCAACATCATGAGGATTAACCTGTTGGGGGAAATACCACTACCTTATAGAC       | 2060 |
| QY | 2060 | TTTCAACATCATGAGGATTAACCTGTTGGGGGAAATACCACTACCTTATAGAC       | 2080 |
| QY | 2080 | TTTCAACATCATGAGGATTAACCTGTTGGGGGAAATACCACTACCTTATAGAC       | 2100 |
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| QY | 2140 | TTTCAACATCATGAGGATTAACCTGTTGGGGGAAATACCACTACCTTATAGAC       | 2160 |
| QY | 2160 | TTTCAACATCATGAGGATTAACCTGTTGGGGGAAATACCACTACCTTATAGAC       | 2180 |
| QY | 2180 | TTTCAACATCATGAGGATTAACCTGTTGGGGGAAATACCACTACCTTATAGAC       | 2200 |
| QY | 2200 | TTTCAACATCATGAGGATTAACCTGTTGGGGGAAATACCACTACCTTATAGAC       | 2220 |
| QY | 2220 | TTTCAACATCATGAGGATTAACCTGTTGGGGGAAATACCACTACCTTATAGAC       | 2240 |
| QY | 2240 | TTTCAACATCATGAGGATTAACCTGTTGGGGGAAATACCACTACCTTATAGAC       | 2260 |
| QY | 2260 | TTTCAACATCATGAGGATTAACCTGTTGGGGGAAATACCACTACCTTATAGAC       | 2280 |
| QY | 2280 | TTTCAACATCATGAGGATTAACCTGTTGGGGGAAATACCACTACCTTATAGAC       | 2300 |
| QY | 2300 | TTTCAACATCATGAGGATTAACCTGTTGGGGGAAATACCACTACCTTATAGAC       | 2320 |
| QY | 2320 | TTTCAACATCATGAGGATTAACCTGTTGGGGGAAATACCACTACCTTATAGAC       | 2340 |
| QY | 2340 | TTTCAACATCATGAGGATTAACCTGTTGGGGGAAATACCACTACCTTATAGAC       | 2360 |
| QY | 2360 | TTTCAACATCATGAGGATTAACCTGTTGGGGGAAATACCACTACCTTATAGAC       | 2380 |
| QY | 2380 | TTTCAACATCATGAGG  |      |





Db 1009 TGTGTCGTGGGCC----- 1023  
 Qy 297 ThrValAsnTyrAsnGlyThrLeuLeuAsnGluThrValPheGluPheAspTrrIysSer 316  
 Db 1024 ---ATTAACCTTCAACGAGAGCTACCTGGAGAGACGACACAGGCTTGTGAGTGGAGAGAA 1080  
 Qy 317 TyrIleGlnAspSerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuIys 336  
 Db 1081 TATATCAACATTAACAACACTTTTACATGGTCTCGCATGCTAATGAACCCCTGCTGTC 1140  
 Qy 337 GlyAsnSerSerAspAlaGlyGlnCysProGluGlyTyrMetCysValIysAlaGlyArg 356  
 Db 1141 GGGACAGCTTGTGATGCTGGCCATGCCCCAGAGGATTCACAGTGAATGAACAGAGAAAG 1200  
 Qy 357 AsnProAsnTyrGlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPhe 376  
 Db 1201 AACCCCACTACGTTACACAGCTTGTACACCTTCAGCTGGCTTGTGACATTAATTC 1260  
 Qy 377 ArgLeuMetThrGlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGly 396  
 Db 1261 CGCCTTAAGACCCAGAGACTATTGGAGAACTTAACACAGCTTACCTTACAGACCCGCTGG 1320  
 Qy 397 LysThrTyrMetIlePhePheValLeuValIlePheLeuGlySerPheTyrLeuLeuAsn 416  
 Db 1321 AAACGTCATGATCTTCTTGTCTTGTGCTCATCTTGTGGTCTTCTTATCTGATGAAC 1380  
 Qy 417 LeuIleLeuAlaValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGlu 436  
 Db 1381 TTGATCTTGGCTGGTGGCCATGGCTTATGAGAAACAGAACAGCAACACTGGAGAGAG 1440  
 Qy 437 AlaGluGlnIysGluAlaGluPheGluGlnMetIleGluGlnLeuIysGluGlnGlu 456  
 Db 1441 GCAGGCAAAAGAGCCGAGTTCAGAGCAAGCTGGAGCAACTCAGAGAGAGAGAGAGAG 1500  
 Qy 487 AlaAlaGlnGlnAlaIleThrAlaThrAlaSerGluHisSer----- 470  
 Db 1501 GAGGACAGAGCTGCTGATGACACCTTC-ACCGGGCACTGCTCTGGAGAGCCCATTTGA 1559  
 Qy 471 ArgGluProSerAlaAlaGlyArgLeuSerAsp-SerSerSerGluAlaSerIysLeuSe 490  
 Db 1560 AGAAGAGGGAGAGAGAGGGGTGAGCTCTCCGAGAGAGCTTCTGAACCTGTAACACTGAG 1619  
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 Db 1620 TTCCAGAGAGCCGAGAGAGCCGAGACCGAGAGAGAGAGAGAGAGAGAGAGAGAG 1679  
 Qy 510 rGlyGlyGluGluIys---AspGluAspGluPheGlnIysSerGluSerGluAspSerIle 529  
 Db 1680 TGAAGGCGAG 1739  
 Qy 529 eArgArgIysGlyPheArgPheSerIleGluIysAsnArgLeuThrTyrGluIysArgTyr 549  
 Db 1740 GAG 1787  
 Qy 549 rSerSerProHisGlnSerLeuLeuSerIleArgGlySerLeuPheSerProArgArgAs 569  
 Db 1788 TTCCATCTCATGATCATGCTCTCTGATGATCCAGAGCTGCGCTCTCTCCGACATATA 1847  
 Qy 569 nSerArgThrSerLeuPheSerPheArg-----GlyArgAlaIysAspValGlySerG 587  
 Db 1848 CAGCAAAAGACAGATCTTACGCTTCCGGGAGCCGGTGGTCCGGGAGCCCGGAGCTCTGA 1907  
 Qy 587 uAsnAspPheAlaAspAspGluHisSerThrPheGluAspAsnGluSerArgArgAspSe 607  
 Db 1908 GAATAGATTCGAG 1967  
 Qy 607 rLeuPheValProArgArgHisGlyGluArgArgAsn-----SerAsnLe 622  
 Db 1968 GCTTTCATCCGAGATCCGCGCGCGAGCGCGAGACAGCTACAGTGGCTACAGCGCGCTA 2027  
 Qy 622 uSerGlnThrSerArgSerSerArgMetLeuAlaValPheProAlaAsnGlyIleMetIle 642  
 Db 2028 CAGCCAGTGCAGCGCTGCTGCGAGCATTTCCCAAGCTCTGGGCGGAGGTGAAGGCGCAA 2087

Qy 642 sSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValProThrSe 662  
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 Qy 662 rProValGlyGlnLeuLeuProGluValIleIleAspIysProAlaThrAspAsnGln 682  
 Db 2136 ACACATGCGGCGGCTCTGCTGAG----- 2160  
 Qy 682 yThrThrThrGluThrGluMetArgIysArgArgSerSerPheHisValSerMetAs 702  
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 Qy 702 pheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeuThrAs 722  
 Db 2220 CCAACCTGCGCTCTTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2279  
 Qy 722 nThr---ValGluGluLeuGluGluSerArgGlnIysCysProProCysTrpTyrIysSPH 741  
 Db 2280 CACGCTAGTGAAGAGACTGGAAGAGTCTCAGAGAAAGTGCACCTGCTGCTGATTAAGT 2339  
 Qy 741 eSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuIysValIysHisValVa 761  
 Db 2340 TGCACCACTTTCCTCATCTCGGAGTGCACCCCTGATGATTAACAGAGAGATGCT 2399  
 Qy 761 IAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeuAs 781  
 Db 2400 GAACCTTAATCGTATGATGACCCCTTCTAGACTTACCATCATCATCTGCTTCTGGA 2459  
 Qy 781 nThrIlePheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeuThr 801  
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 Qy 801 rValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuIysIleAla 821  
 Db 2520 CGTAGAATATCTGCTTACACGGAGACTTCAAGGGGAGAAATTTCTGAAAGTCAATAC 2579  
 Qy 821 aMetAspProTyrTyrTyrPheGlnGluGlyTyrPasnIlePheAspGlyPheIleValTh 841  
 Db 2580 CATGAGACCCCTACTATTATTCCAGAGAGCTGCAACATTTTTCACGATTTATTCCTC 2639  
 Qy 841 rIleuSerLeuValGluGluGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSerPh 861  
 Db 2640 CCTCAGTTTATGAGAGCTGAGTCTCCAGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 2699  
 Qy 861 eArgLeuLeuArgValPheIysLeuAlaIysSerTrpProThrLeuAsnMetLeuIleIy 881  
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 Qy 881 sIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIleVa 901  
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 Qy 901 lPheIlePheAlaValAlaGlyMetGlnLeuPheGlyIysSerTyrIysAspCysValCy 921  
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 Db 2880 TAAGATCAACCAAG 2939  
 Qy 941 eLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMetG 961  
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 Qy 981 uValValLeuAsnLeuPheLeuAlaLeuLeu\*\*\*SerSerPheSerAlaAspAsnLeuAl 1001  
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STREET: 3401 HILLVIEW AVENUE, MS A2-250
CITY: PALO ALTO
STATE: CA
COUNTRY: U.S.A.
ZIP: 94304-1397
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/425,043
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/024,020
FILING DATE: 16-FEB-1998
APPLICATION NUMBER: US 60/039,447
FILING DATE: 26-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,799
REFERENCE/DOCKET NUMBER: R0020B-REG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-3097
TELEFAX: (650) 855-5322
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 6556 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-425-043-7

Alignment Scores:
Pred. No.: 0 Length: 6556
Score: 7720.50 Matches: 1531
Percent Similarity: 84.46% Conservative: 187
Best Local Similarity: 75.27% Mismatches: 224
Query Match: 74.26% Indels: 93
Gaps: 24

US-09-930-871-12 (1-2009) x US-09-425-043-7 (1-6556)
QY 1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhetheThrArgGlu 20
Db ||| ::||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 169. ATGGCAGCGGGCGCGTCGCGCACACGAGCCCGCTGATGTTCAAGCCCTTGACCCCTGAG 22
Db ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 21 SerLeuAlaIalIleGluIaGArgIleAlaIaGluIuLysAlaLysAsn---ProLysPro 39
Db ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 229 TCGCTGGCAAAACATCGAGGCGCTATTGCCGAGGACCAAGCTCAAGAAACCAACCAAGCGC 281
Db ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 40 ASP-----LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGlu 56
Db ||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
QY 289 GATGCGACGCCACCGGGAGGAGATGAGACAGCAAGCCCAAGCCCAAGACGATGACTGGAG 341
Db ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 57 AlaGlyLysAsnLeuProPheIleTyrGlyAspIleProProGluMetValSerGluPro 76
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 349 GCTGGGAAGATTTGGCTTTCATCTAGCGGGGACATCCCGCAAGCGCTGGTGGGTTCC 400
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 77 LeuGluAspLeuAspProTyrTyrTlleAsnLysLysThrPheIleValLeuAsnLysGly 96
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 409 CTGAGAGCATTTGACCCCTTACTATTGACGACGAGAAACCTTGGTATTAACAGAGGG 461
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 97 LysAlaIlePheIaGpHeSerSerIaIaThrSerIaLeuTyrIleIaThrProPheAsnPro 111
Db ||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
QY 469 AAAACTCTCTTCAATTTAGTGGCACACCTCTGTCATTTTAAGCCCTTTTAACCTG 521
Db ||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
QY 117 LeuArgLysIleAlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCys 131
Db ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
QY 529 ATAAGAGAAATAGCTATTAAATTTTGATTACACATCAGTTTCACAGCATGATCATCATGTC 581
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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QY 137 ThrIleuThrAsnCysValPheMetThrMetSerAsnProProAspThrThrIysAsn 156  
 |||||  
 Db 589 ACCATCTCGACCACTGCTGTTCATGACCTTAGTAACCCCTCGAAGAGGTCACGAAT 648  
 QY 157 ValGluTyrThrPheThrGlyTyrThrPheGluSerLeuIleIysIleIleAlaArg 176  
 |||||  
 Db 649 GGGAGCTACACTTCACAGAGGATTTACACATTGGAATCTGTAATAATCTATCCGAGA 708  
 QY 177 GlyPheCysLeuGluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThr 196  
 |||||  
 Db 709 GGTTCCTGATAGACGGCTTCACTTCCTTGCAGACCCGTGGACCTGGTTACACTCACT 768  
 QY 197 ValIleThrPheAlaTyrValThrGluPheValAspLeuGlyAsnValSerIleAlaLeuArg 216  
 |||||  
 Db 759 GTCATCATGATGGCATATGTGACAGATTTGGACCTGGGCAATCTCTCACGCGTAGA 828  
 QY 217 ThrPheArgValIleuArgAlaLeuIysThrIleSerValIleProGluIleuIysThrIle 236  
 |||||  
 Db 829 ACATTCAGGGTCTCGACACTTGTAAACTATCTGTATATTCAGGCTCGAAGACAAATC 888  
 QY 237 ValGlyAlaLeuIleGlnSerValIlyIysIysLeuSerAspValMetIleLeuThrValPhe 256  
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 Db 889 GGGGCGCCCTAATCCAGTCGTAAGAAGCTGTGGAGCTGATGATCTGACAGCTTC 948  
 QY 257 CysLeuSerValPheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnIys 276  
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 Db 949 TCCCGATGTTTTCGCCCTGATGTGGCTGCGACCTTCATGGGACCTTCGAAACAAG 1008  
 QY 277 CysIleGlnTrpProThrAsnIleSerLeuGluGlnIleSerIleGluIysAsnIle 296  
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 Db 1009 TGTGCTGTGGCC----- 1023  
 QY 297 ThrValAsnTyrAsnGlyThrLeuIleAsnGlnThrValPheGluPheAspTrpIysSer 316  
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 Db 1024 ---ATAAACTTCACAGAGAGCTACCTGGAGAACGGCACAGGCTTTCACCTGGAGGAA 1080  
 QY 317 TyrIleGlnAspSerArgTyrHisTyrPheLeuGlnGlyPheLeuAspAlaLeuLeuIys 336  
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 Db 1081 TATATCAACAATAAACAACATTTATACATGTTCTCGCATCTGAGAACCTTGTGCTGC 1140  
 QY 337 GlyAsnSerSerAspAlaGlyGlnCysProGluGlyTyrMetCysValIlyIysAlaArg 356  
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 Db 1141 GGGAAAGTCTGATGCTGGGCAATGCCAGAGGATCCATCCATGAAACACAGAGAAAG 1200  
 QY 357 AsnProAsnTyrGlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPhe 376  
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 Db 1201 AACCCCACTACGCTTACACAGCTTGTGACCTTCAGCTGGGCTTCTGTGCATTATTC 1260  
 QY 377 ArgLeuMetThrGlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGly 396  
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 Db 1261 CGCCTTATAGACCAGAGACTATTTGGAGAACTATACAGCTGACTACGACCCGCTGGG 1320  
 QY 397 LysThrTyrMetIlePhePheValIleuValIlePheLeuGlySerPheTyrLeuIleAsn 416  
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 Db 1321 AAAAGCTATGATATCTTCTTGTGTGTCATCTCTGTGGGCTTTCTTATCTGTGGTAAAC 1380  
 QY 417 LeuIleLeuAlaValAlaMetAlaTyrGlnGluGlnIleAsnGlnAlaThrLeuGlnIle 436  
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 Db 1381 TTGATCTTGGCTGTGGTGGCCATGGCTTATAGGAACAGAACACAGCAACTGGAGGAG 1440  
 QY 437 AlaGluGlnIysGluAlaGluPheGlnGlnMetIleGluGlnLeuIysIysGlnIleGln 456  
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 Db 1441 GCAGAGCAAAAAGAGCGGAGTTCAAGCAATGTGGAGCACTCAAGAGCAGAGAGG 1500  
 QY 457 AlaAlaGlnGlnAlaAlaThrAlaThrAlaSerGluHisSer----- 470  
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 Db 1501 GAGGCAAGCGCTGTGCAATGTGCACCTC-ACCGGGCACTGTCTCGAAGACCCATTCGA 1559  
 QY 471 ArgGluProSerAlaAlaGlyArgLeuSerAsp-SerSerSerGluAlaSerIysLeuSe 490  
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 Db 1560 AGAAGAAGGGGAAGATGGGCTAGGCTCTCCAGAGAGCTCTTGTGAACGTCTAAACTCAG 1619  
 QY 490 rSerIysSerAlaIysGluIleArgAsnArgIysIysArgIysGlnIysGluGlnSe 510

Db 1620 TTCCAAGACGGGGAAGAGCGCGGGAACCGACAGGAAGAGAGCAAGCAAGACCTCTC 1679  
 QY 510 rGlyGlyGluGlnIys---AspGluAspGluPheGlnIysSerGluSerGluAspSerI 529  
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 Db 1680 TGAAGCGGAGGAAAGAGGAGCACCAGAGAGGTGTTAAGTCAAGCTCGGAAGCGGTAT 1739  
 QY 529 eArgArgIysGlyPheArgPheSerIleGluIysAsnArgLeuThrTyrGluIysArgTy 549  
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 Db 1740 GAGAAGGAAGGCTTCGCG-----CTGCCACACAAGAGANA-----GGAGAGAGTT 1787  
 QY 549 rSerSerProAsnGlnSerLeuLeuSerIleArgGlySerLeuPheSerProArgArgAs 569  
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 Db 1788 TTCATATCATGAAATCATGCTCCTCTCAGCAATCCAGGCTCGCCCTTCCTCCGACATGA 1847  
 QY 569 nSerArgThrSerIleuPheSerPheArg-----GlyArgAlaIysAspValGlySerG 587  
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 Db 1848 CAGCAAAACACACATCTTCAGCTCCGGGACCCGGTGGTTCCGGAGCCCGGCTCTGA 1907  
 QY 587 uAsnAspPheAlaAspAspGlnHisSerThrPheGluAspAsnGluSerArgArgAspSe 607  
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 Db 1908 GATAGATTCGAGAGAGATGAACACAGACACCTGGAGAGAGAGAGCGGCGGCTGACTC 1967  
 QY 607 rLeuPheValProArgArgHisGlyGluArgArgAsn-----SerAsnLe 622  
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 QY 622 uSerGlnTrpSerArgSerSerArgMetLeuAlaValPheProAlaAsnGlyLysMetI 642  
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 QY 642 sSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValProThrSe 662  
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 Db 2088 CAGCAGCGTGCAGCTCAGACGCGGTAGCTCATCTCATCGG-----CCGGGCTC 2135  
 QY 662 rProValGlyGlnLeuLeuProGluValIleIleAspIysProAlaThrAspAspAsnG 682  
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 Db 2136 ACACATCGGCGCGCTCTCTCTGAG----- 2160  
 QY 682 yThrThrThrGluThrGluMetArgIysArgArgSerSerSerPheHisValSerMetAs 702  
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 Db 2161 -GCACAGACTGTAGGTGAATAAAGAAAGAGCCCTGTGATCTCTTAACTTAACTGA 2219  
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 QY 722 nThr---ValGluGlnLeuGluLeuSerArgGlnIysCysProProCysTrpTyrLysPh 741  
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 QY 741 eSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuIysValIysHisValVa 761  
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 Db 2460 TACGCTATTATGGAATGAGACACATCCATGACACACAGTTCGAACAGCTTGTGGC 2519  
 QY 801 rValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuIysIleIleAl 821  
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 Db 2520 CGTAGAAATCTGTGTTACACCGGATCTTCACGCGGAGAAAGTTTCTGAAGCTCATAGC 2579  
 QY 821 aMetAspProTyrTyrTyrPheGlnGluGlyTyrAsnIlePheAspGlyPheIleValTh 841  
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 Db 2580 CATGACCCCTACTTATTTTCAAGAGAGCTGGAGAACATTTTGTGCGGATTTATTTGTCTC 2639  
 QY 841 rLeuSerLeuValGluLeuGlyLeuAlaAsnValGluIysLeuSerValLeuArgSerPh 861  
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Db 2640 CCTGATTATGAGCTGAGCTGCGAGATGTGAGGGGCTTCATGCTGGCTTT 2699  
Qy 861 eargleuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIlely 881  
Db 2700 CCGACTGCTCGGAGCTTCAAGCTGGCCAGATCTGCGCCACCCGAAACATCTGATCA 2759  
Qy 881 ailleleLysAsnSerValAlaLeuGlyAsnLeuThrLeuValIleAlaIleIleVal 901  
Db 2760 GATCATTCGGGAATCTCGGGGGTCCCTGGCAACCTGAGCTGGCTCATATGCT 2819  
Qy 1PheIlePheAlaValAlaGlyMetGlnPheGlyLysSerTrpLysAspCysValCy 921  
Db 2820 CTTCATCTTCGCGGTGGGGGATCAGCTGTTTGGAAGACTTCAAGAGATGGCTCG 2879  
Qy 921 slyslsIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPheHisSerPh 941  
Db 2880 TAAAGTCAACAGCAGAGCTGCAAGCTCCGCGGCGCAGATGAAAGCATCTTCACCT 2939  
Qy 941 eleuIleValPheArgValLeuCysGlyLeuTrpIleGluThrMetTrpAspCysMet 961  
Db 2940 CCTCATCTCTCCAGAGCTGTGGGGAGTGGAGATCGAGACCATGTGGGACTGATGA 2999  
Qy 961 uValAlaGlyAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsnLe 981  
Db 3000 GTGGCGGCGCAGGCGCATGTGCTCATTTCTTCATGATGATGATGATGATGCAACT 3059  
Qy 981 uValAlaLeuAsnLeuPheLeuAlaLeuLeu\*\*SerSerPheSerAlaAspAsnLeuAl 1001  
Db 3060 GGTGGTGTGATCTATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3119  
Qy 1001 aAlaThrAspAspAsnGlnMetCysAsnLeuGlnIleAlaValAlaAspArgMetHisLy 1021  
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Qy 1021 sglValAlaTrpValLysArgLysIleArgLysPheIleGlnGlnSerPheIleArgLy 1041  
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Qy 1041 sglLysIleLeuAspGlnIleLysProLeuAspAspLeuAsnAsnLysLysAspSerCy 1061  
Db 3234 CGAGCGGAGCGGATGAAAGTAAACCCCTGACAGAGCTGTATGAAAGAGGCCAACAGT 3293  
Qy 1061 sMetSerAsnHisThr-----\*GluIleGlyLysAspLeuAspTrpLysAspValAs 1080  
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Qy 1080 nglThrThrSerGlyIleGlyThrGlySerSerValGlyLysTrpIleIleAspLeu 1100  
Db 3354 CGGAACCAACACGCGGCTATC-----GGCAGCAGCGTGGAGAGTATCATCATGACGAG-- 3405  
Qy 1100 rAspTrpMetSerPheIleAsnAspProSerLeuThrValTrpValProIleAlaValG 1120  
Db 3406 -GACCAACATGCTTCATTAACAACCAACCAACTGACCGGCGGATGCTGCTGAG 3464  
Qy 1120 yGlnSerAspPheGlnAsnLeuAsnThrGlnAspPheSerSerGlnSerAspLeuGln 1140  
Db 3465 CGAGCTGACTTTCGAGAACCTCAACACAGAGATGTTAGACAGCATCAGACCCCTGAAG 3524  
Qy 1140 uSerLysGlyLysLeuAsnGlnLysSerSerSerSerGlnLysSerThrValAspIle 1160  
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Qy 1160 yAlaIleProValGlnGlnGlnProValAlaGlnProGlnGlnGlnGlnGlnGln 1180  
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Qy 1180 sPheThrGlnGlyCysValGlnArgPheLysCysGlnIleAsnValGlnGlnGly 1200  
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Qy 1200 gGlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgTrpIleValGlnHisAspTrp 1220  
Db 3702 AGGCAAGTCTGTGTGATCTCGGAAACCTGCTTCATTTGTGAGACCAATTTGTT 3761  
  
Qy 1220 eglThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGlnAsp 1240  
Db 3762 TGAGACTTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 3821  
Qy 1240 eTrpIleAspGlnArgLysThrIleLysThrMetLeuGlnGlyTrpAlaAspLysValPhe 1260  
Db 3822 CTACATTGAGCAG 3881  
Qy 1260 rTrpIlePheIleLeuGlnMetLeuLeuLysTrpValAlaTrpGlyTrpGlnThrTrp 1280  
Db 3882 CTACATCTTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 3941  
Qy 1280 eThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAlaAspValSerLeuValSerLeu 1300  
Db 3942 CACCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4001  
Qy 1300 rAlaAsnAlaLeuGlyTrpSerGlnLeuGlyAlaIleLysSerLeuArgTrpThrLeuArg 1320  
Db 4002 ACCTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4061  
Qy 1320 aLeuArgProLeuArgAlaLeuSerArgPheGlnGlnMetArgValAlaValAlaAla 1340  
Db 4062 TTTGAGACCTTAAGACCTTAACAGATTTGAAGAGAGAGAGAGAGAGAGAGAGAG 4121  
Qy 1340 uLeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeu 1360  
Db 4122 GGTGGGCGCATCCCTTCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 4181  
Qy 1360 ePheSerIleMetGlyValAlaAsnLeuPheAlaGlyLysPheTrpHisCysIleAsnThr 1380  
Db 4182 TTTACACATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 4241  
Qy 1380 rThrGlyAspArgPheAspIleGlnAspValAlaAsnHisTrpAspCysLeuLysLeu 1400  
Db 4242 TTTCTGAATCCGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 4301  
Qy 1400 egluArgAsnGlnThr---AlaArgTrpLysAsnValLysValAsnPheAspAsnVal 1419  
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Qy 1439 rAlaAlaValAspSerArgAsnValAlaLeuGlnProLysTrpGlnGlnSerLeuTrp 1459  
Db 4422 TGCGCTGTGATTCGCGAAGCAGACAGCAGCAGCTGATGAGAGGCAACATCATCAT 4481  
Qy 1459 eTrpLeuTrpPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPhe 1479  
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Db 4662 ACAG 4721  
Qy 1539 rArgGlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrPhe 1559  
Db 4722 TCACAG 4781  
Qy 1559 tValGlnThrAspAspGlnSerGlnLysValThrThrIleLeuSerArgIleAsnLeu 1579  
Db 4782 GGTGGAG 4841





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OY 1 MetGluInThrValLeuValProProGlyProAspSerPheAsnPhetheThrArgGlu 20
DB 169 ATGGACGCGCGGCTGTCGACACCGAGCCCTGATGATGTTCAAGCCCTTCAACCCCTGAG 228
OY 21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluValAlaLysAsn---ProLysPro 39
DB 229 TCGCGGCAACATCGAGGCGGATGTCGAGAGCAGACCTCAAGAACCAACCAAGGCGG 288
OY 40 Asp-----LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGlu 56
DB 289 GATGGACACCGGAGAGAGAGATGAGACAGCAAGCCCAAGCAAGAGTGCCTGGAG 348
OY 57 AlaGlyLysAsnLeuProPheIleTyrlGlyAspIleProProGluMetValSerGluPro 76
DB 349 GCTGGAGAGAGTTCCTTCATCTACCGGGGACATCCCAAGGCGCTGGCTGGCTCC 408
OY 77 LeuGluAspLeuAspProTyrlTyrlLysAsnLysTyrlPheIleValLeuAsnLysGly 96
DB 409 CTGGAGGACTTGGACCTTACTATTGAGCGAGAAAACTTGTGATATTAAACACAGG 468
OY 97 LysAlaIlePheArgPheSerAlaThrSerAlaLeuTyrlIleLeuThrProPheAsnPro 116
DB 469 AAAATCTCTTCAGATTGATGTCACACCTGCTTGTACATTTTAAGCCCTTTTAAC 528
OY 117 LeuArgLysIleAlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCys 136
DB 529 ATAAGACAGATAGCTATTAAATTTGATACACTCATGTTTACATGATCATCATGTC 588
OY 137 ThrIleLeuThrAsnCysAlaPheMetThrMetSerAsnProProAspThrThrLysAsn 156
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OY 157 ValGluTyrlThrPheThrGlyIleTyrlThrPheGluSerLeuIleLysIleAlaArg 176
DB 649 GTGGAGTACACATTCACAGAGATTACATTTGATCATCTAGTAAATCATCGAGAG 708
OY 177 GlyPheCysLeuGluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThr 196
DB 709 GGTTCCTGATAGAGCGGCTTCACTCTTTCGAGACCCGCGTGAACGTGTAGACTCAG 768
OY 197 ValIleThrPheAlaIleTyrlThrGluPheValAspLeuGlyValAsnValSerAlaLeuArg 216
DB 769 GTCATCATGATGATGATATGACAGAGTTGTGGACCTGGGCAATGTCCTGAGCGTGA 828
OY 217 ThrPheArgValLeuArgAlaLeuLysTyrlIleSerValIleProGlyLeuLysTyrlIle 236
DB 829 ACATTCAGGGTCTTCGAGACTTGAATACTATCTGTATTCAGAGCCCGAGAGACATC 888
OY 237 ValGlyAlaLeuIleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPhe 256
DB 889 GTGGGCGCCCTATCCAGTCCGAGAGAGCTGTGAGAGCTGATGATCCGACAGCTGC 948
OY 257 CysLeuSerValPheAlaLeuIleGlyLeuGlnLeuPheMetCysLysLeuArgAsnLys 276
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DB 1009 TGTGTCGTGTGCGCC----- 1023
OY 297 ThrValAsnTyrlAsnGlyLysLeuIleAsnGluThrValPheGluPheAspTrpLysSer 316
DB 1024 ---ATAAATCTCAACAGAGACTACTGAGAGAACGGCAGCAGAGAGCTTGTGAGAGAA 1080
OY 317 TyrlIleGlnAspSerArgTyrlIleTyrlPheLeuGluGlyPheLeuAspAlaLeuLys 336
DB 1081 TATATCAACAAATAAACAACTTTTACATGTTCTGCGCATGCTTAACACCTGCTCTGC 1140
OY 337 GlyAsnSerSerAspAlaGlyLysCysProGluGlyTyrlMetCysValLysAlaGlyArg 356
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OY 417 LeuIleLeuAlaValAlaIleMetIleAtyrlGluGluGlnAsnGluAlaThrLeuGluGlu 436
DB 1381 TTGATCTTGGCTGTGTGTGTCATGTTGTTGAGAACACACACAGCAACACAGCGAGAG 1440
OY 437 AlaGluGlnLysGluAlaLeuPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGlu 456
DB 1441 GCGAGCCAAAAGAGGCGGAGTTCAAGGCAATGCTGAGCACTCAAGAACGACGAGAG 1500
OY 457 AlaAlaGlnGlnAlaIleThrAlaThrAlaSerGluHisSer----- 470
DB 1501 GAGCGACAGCTGCTCATATGAGCACCTC-AGCGGCGACTGTCTCGAAGAGCCATTTGA 1559
OY 471 ArgGluProSerAlaAlaIleArgLeuSerAsp-SerSerSerGluAlaSerLysLeuSe 490
DB 1560 AGAAGAGGAGGAGATGGGGTAGGCTCCGAGGACTTCTTGAACTGTCTTAACCTCAG 1619
OY 490 rSerLysSerAlaLysGluArgArgAsnArgArgLysArgLysGlnLysGlnLysGln 510
DB 1620 TTCAGAGAGCGGAGAGAGAGCGGAGACCGGAGAGAGAGAGAGAGAGAGAGAGAG 1679
OY 510 rGlyLysGlnGluLys---AspGluAspGluPheGlnLysSerGluSerGluAspSerI 529
DB 1680 TGAAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1739
OY 529 eArgArgLysGlyPheArgPheSerIleGluGlyAsnArgLeuThrTyrlGluLysArg 549
DB 1740 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1787
OY 549 rSerSerProHisGlnSerLeuLeuSerIleArgGlySerLeuPheSerProArgArgAs 569
DB 1788 TTCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1847
OY 569 nSerArgThrSerLeuPheSerPheArg-----GlyArgAlaLysAspValGlySerG 587
DB 1848 CAGCAAAACAGAGATCTTCAAGTTCGCGGAGACCGGCTGCGTCCGAGACCCCGCTCTGA 1907
OY 587 uAsnAspPheAlaAspAspGluHisSerThrPheGluAspAsnGlnSerArgArgAspSe 607
DB 1908 GATGATGTTCCGAGAGATGAGACACAGACCGTGGAGAGAGAGAGAGAGAGAGAGAG 1967
OY 607 rLeuPheValProArgArgHisGlyLysArgArgAsn-----SerAsnLe 622
DB 1968 GCTCTTCATCTCCGATGCTCGGCGCGGAGAGCGGCGAGCTACAGTGGCTACAGCGGCTA 2027
OY 622 uSerGlnThrSerArgSerSerArgMet-----LeuAlaValPhe 635
DB 2028 CAGCCAGTGCAGCGGCTGCGCGGTAATAAGATAGAGAGAGTACGAGAGAGAGAGAG 2087
OY 635 eProAla-----AsnGlyLysMetHisSerThrValAspCysAsnGlyValValSe 652
DB 2088 CCCACCTTCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2147
OY 652 rLeuValGlyGlyProSerValProThrSerProValGlyGlnLeuLeuProGluValI 672
DB 2148 ACTCATGAGG-----CCGCGCTACACATCGAGGCGGCTCTCTGCTGAG----- 2190
OY 672 eIleAspLysProAlaThrAspAspAsnGlyThrThrGlnGluThrGluMetArgLysAr 692
DB 2191 -----GCAACGACTGAGGTGGAATTAAGAAAGAA 2219
OY 692 gArgSerSerSerPheHisValSerMetAspPheLeuGluAspProSerGlnArgGlnAr 712

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Db 2220 AGGCCCTGATCTTTTATTCTATGAGCAACTGCGCTCTACGAGCGAAGACAG 2279  
QY 712 GAlMeSerIleAlaSerIleLeuThrAsnThr---ValGluGluLeuGluSerAr 731  
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QY 851 nValGluGlyLeuSerValLeuArgSerPheArgLeuLeuArgValPheLysLeuAla 871  
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QY 871 sSerTrpProThrLeuAsnMetLeuIleLysIleIleGlyAsnSerValGlyAlaLeuG 891  
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QY 891 yAsnIleuThrLeuValLeuAlaIleIleValPheIlePheAlaValAlaGlyMetGlu 911  
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QY 911 uPheGlyLysSerTrpLysAspCysValCysLysIleAlaSerAspCysGluLeuProAr 931  
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QY 1051 uAspAspLeuAsnLysLysAspSerCysMetSerAsnHisThr---\*\*GluIleG 1070  
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 OY 1789 eservalalathrgluinsleralagluinslergluinslergluinsler 1809

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 OY 1929 sleuanslyargthral-----lyslnalaserphethrtyrasnlyasly 1946  
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 DB 5964 GCTGGAGATGAG----- 5976  
 OY 1966 unsnerlethrghlysttyrthraspleuansleuansleuansleuansleuansleu 1986  
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 OY 1986 raspergvalthrlysprolllevalgluinslyshlsu-----glingluinslyaspl 2004  
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 OY 2004 ulysalylys 2007  
 DB 6093 AAGAGCCAG 6102  
 DB 6093 AAGAGCCAG 6102  
 RESULT 11  
 US-09-425-043-43  
 ; Sequence 43, Application US/09425043  
 ; Patent No. 6335172  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DELGADO, STEPHEN G.  
 ; APPLICANT: DIETRICH, PAUL S.  
 ; APPLICANT: FISH, LINDA M.  
 ; APPLICANT: HERMAN, RONALD C.  
 ; APPLICANT: SANGAMESWARAN, LAKSHMI  
 ; TITLE OF INVENTION: NOVEL CLONED TETRODOXIN-SENSITIVE  
 ; TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF  
 ; NUMBER OF SEQUENCES: 43  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: JANET FAULINE CLARK  
 ; STREET: 3401 HILLVIEW AVENUE, MS A2-250  
 ; CITY: PALO ALTO  
 ; STATE: CA  
 ; COUNTRY: U.S.A.  
 ; ZIP: 94304-1397  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/09/425,043
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/024,020
FILING DATE: 16-FEB-1998
APPLICATION NUMBER: US 60/039,447
FILING DATE: 26-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,799
REFERENCE/DOCKET NUMBER: R0020B-REG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-3097
TELEFAX: (650) 855-5322
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 6586 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-425-043-43

Alignment Scores:
Pred. No.: 0 Length: 6586
Score: 7712.50 Matches: 1533
Percent Similarity: 84.20% Conservative: 188
Best Local Similarity: 75.00% Mismatches: 221
Query Match: 74.18% Indels: 103
Db: 4 Gaps: 26

US-09-930-871-12 (1-2009) x US-09-425-043-43 (1-6586)
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Db 229 TCGCTGCGCAACATCGAGAGGCGGTATGCCGAGACCACTCAAGAAACCAACCAAGGCG 288
Oy 40 Asp-----LysLysAspAspAspGluAsnGlyProLysProAsnSerAspIleuGlu 56
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Oy 57 AlaGlyLysAsnLeuProPheIleTyrlGlyAspIleProProGluMetValSerGluPro 76
Db 349 GCTGGGAAGAGTTGCTTCACTACGAGGACATCCCGCAAGGCGCTGCTGCGGTTCCC 408
Oy 77 LeuGluAspLeuAspProTyrlTyrlIleAsnLysLysThrPheIleValIleuAsnLysGly 96
Db 409 CTGGAGGACTTGGACCTTACTATTTGACGCAAGAAACCTTTGTATATTAACACAGG 468
Oy 97 LysAlaIlePheArgPheSerAlaThrSerAlaLeuTyrlIleuThrProPheAsnPro 116
Db 469 AAAACTCTCTTCAAGATTGATGCCACACCTGCTTACATTTTAACCTTTTAACTG 528
Oy 117 LeuArgLysIleAlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCys 136
Db 529 ATAAAGAGATAGCTATTAATAATTTGATACACTGTTTTCAGCATGATCATCATGTC 588
Oy 137 ThrIleLeuThrAsnCysValPheMetThrMetSerAsnProProAspThrPheLysAsn 156
Db 589 ACCATCTCGACACACTGTGTGTTCATGACCTTAGTAACCTTCACAAAGATGCTCAAGAT 648
Oy 157 ValGluTyrlThrPheThrGlyIleTyrlThrPheGluSerLeuIleLysIleIleAlaArg 176
Db 649 GTGGGTCACACATTCACAGGAGTTTACACATTTGAATCACTAGTGAATAATCATCGCAAG 708
Oy 177 GlyPheCysIleuGluAspPheThrPheLeuArgAspProTyrlAsnThrPheAsnPhenThr 196
Db 709 GATTTCGATACGAGCGCTTCACTTCTTGGACAGACCGGTGAACGTGTAGACTTCACT 768

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Oy 197 ValIleThrPheAlaTyrlThrGluPheValAspLeuGlyAsnValSerAlaLeuArg 216
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Oy 217 ThrPheArgValLeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIle 236
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Oy 417 LeuIleLeuAlaValAlaIleMetAlaTyrlGluGluGlnAsnGlnAlaThrLeuGluGlu 436
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Db 1501 GAGGACACAGGCTGCTCAAGGCGCACCTC-AGCGGCGACTGTCTCGAAGACCCCATTTGA 1559
Oy 471 ArgGluProSerSerAlaAlaGlyArgLeuSerAsp-SerSerSerGluAlaSerLysLeuSe 490
Db 1560 AGAAGAGAGGGAAGATGGGTAGGCTCTCCGAGACCTTCTGAACTGTCTAAACTCAG 1619
Oy 490 rSerLysSerAlaLysGluArgArgAsnArgGlyLysArgLysGlnLysGluGlnSe 510
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| Oy | 549  | rSeSerProHisGlnSerLeuLeuSerLleAaRgLySerLeuPheSerProAaArgAs       | 569  |
| Db | 1788 | TTCCATCATGAAACAGTCGGCTGTCTGAGCATTCACAGCTGGCCCTCTCTCCGACATTA      | 1847 |
| Oy | 569  | nSeArGrThSerLeuPheSerPheArg-----GlyAaGalAtyAsAaValGlySergI       | 587  |
| Db | 1848 | CAGCAAAAGACGATCTTCAGCTTCGCGGGGAGCCGGTCGGTTCGCGGACCCCGCTCTGA      | 1907 |
| Oy | 587  | uAsnAsPheAlaAspAspLuiHisSerThrPheGluAaPaasnGluSerAArgArgAspSe    | 607  |
| Db | 1908 | GAATGAGTTCGACAGCATGACATGACACAGCACCGGTGAGGAGACGAGCGCGCGTGA        | 1967 |
| Oy | 607  | rLeuPheValProAaArgHisGlyLuarArgAsn-----SerAsnLe                  | 622  |
| Db | 1968 | GCTTCATCCCATCCATCCGCGCCCGCAGCGCGCGACACTACGTGCTACAGCGGCTGA        | 2037 |
| Oy | 622  | uSeGlnThSerAArgSerSerArgMet-----LauAlaValPh                      | 635  |
| Db | 2028 | CAGCAATGCGACCGCGCTCTCGCGCTGAAAAATAGATAAGCAGCTACGAGCACCGCATTT     | 2087 |
| Oy | 635  | ePrcAla-----AsnGlyLysMetHisSerThrValAspCyAsaGlyValValSe          | 652  |
| Db | 2088 | CCCCAGCGCTCGGGCGAGCGTGAAGCGCAACAGACAGGTGAGTCTCAACAGCGGTAGTGTCT   | 2147 |
| Oy | 652  | rLeuValGlyGlyProSerValProThrSerProValGlyGlnLeuLeuProGluValII     | 672  |
| Db | 2148 | ACTCATGGGG-----CCGCGCTCACAAACAGCGGCGGGCTCTCGCTCGAG----           | 2190 |
| Oy | 672  | eLlAspLysProAlaThrAaRpsAsnGlyThrThrThrGluThrGluMetAaArgLysAr     | 692  |
| Db | 2191 | -----GCACAGACTGAGGTGGAAATTAACAAATA                               | 2219 |
| Oy | 692  | gArGSeSerSerPheHisValSerMetAsPheLeuGluAaPProSergInAaArgLuar      | 712  |
| Db | 2220 | AGGCGCTGAGATCTCTTTATTTCTATGAGCAACAGCTCGCTCTACGAGCGSAAGACAG       | 2279 |
| Oy | 712  | gAlaMetSerLleAlaSerLleLeuThrAsnThr--ValGluGluLeuGluGluSerAr      | 731  |
| Db | 2280 | AATCAACAGCATATGAGCTGTGTCAACAAACAGCTAGTGAAGAGCTGGAAGACTGTCA       | 2339 |
| Oy | 731  | gGlnLysCyProProCysArgProTyrltyrLysPheSerAsnLlePheLuiLerTPAsCySe  | 751  |
| Db | 2340 | GAGAAAGCGCCACCGCTGCGGTATTAAGTTTGGCAACACTTCTCTCATCTGGAGACTGTCA    | 2399 |
| Oy | 751  | rProTyrltyrLeuLysHisValHisHisValAsnLeuValValMetAsPProPheValAs    | 771  |
| Db | 2400 | CCCCTACTGAGATAAATCGTAGAGAGAGATCGTGAACCTATATCGTCAATGAGACCTTTGTAGA | 2459 |
| Oy | 771  | pLeuAlaLleThrLleCysLleValLeuAsnThrLeuPheMetAlaMetGluHisTyPr      | 791  |
| Db | 2460 | CTTAGCCATCTACCAATCTGACATCGTTCGATATAGCTATTATTATGACAAATGAGACACATCC | 2519 |
| Oy | 791  | oMetThrAspLysPheAsnAsnValLeuThrValGlyAsnLeuValPheThrGlyLLePh     | 811  |
| Db | 2520 | CATGACACACAGTTCGACACACGCTGTGGCCGTAGGAAATCTGGTGTTTACCCGGGATCTT    | 2579 |
| Oy | 811  | eThrAlaGluMetPheLeuLysLleLleAlaMetAsPProTyrltyrPheGlnGluG        | 831  |
| Db | 2580 | CACGGCGGAATGTTTGTGAAGCTCAATGACATGAGACCCCTACTATTATTATTCAGGAAGG    | 2639 |
| Oy | 831  | yTrpAsnLlePheAspGlyPheLleValLThrLeuSerLeuValGluLeuGlyLeuAlaAs    | 851  |
| Db | 2640 | CTGGAACAATTTTGAACGATTATATGTCTCCCTCAACTTTAAAGGAGCTAGCTCGTCAGAG    | 2699 |
| Oy | 851  | nValGluGlyLeuSerValLeuAaRgsrPheAaGluLeuAaArgValPheLysLeuAlaLy    | 871  |
| Db | 2700 | TGTGGAGGGCTCTCACTGTCTGGGCTTTTCCAGTCTCCAGATCTTAACTGTGGCAA         | 2758 |
| Oy | 871  | sSerTrpProThrLeuAsnMetLeuLysLleLleGlyAsnSerValGlyAlaLeuG         | 891  |
| Db | 2760 | GTCCTGGCCCAACCTGAAACATGCTGATCAAGATCATCGGGAATCTCGTGGGTGCCCTGGG    | 2819 |
| Oy | 891  | yAsnLeuThrLeuValLeuAlaLleLleValPheLlePheAlaValValGlyMetClnLe     | 911  |

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|----|------|--|------|
| Db | 2820 | CAACCTGACCCCTGGTGTGGCCATCATTCGTTCACTTCGGCCGTGGGGGATGACGCT        | 2879 |
| Qy | 911  | uPhegILySseTtYILySsPCySvAlCySlySILeAlSasrAspCySgInLeuProAr       | 931  |
| Db | 2880 | GTTTGGAAAGATTACAAGAGATGGCGCTGTAAAGATCAACACAGAGATGCAAGCTCCGCG     | 2939 |
| Qy | 931  | gTPrHISmeCAsnAspPheHISserPheLeuILeValPheAtgValLeuCySgILyGI       | 951  |
| Db | 2940 | CTGCACATATGAAGACTTCTTCCACCTCTCCCAACGCTTCCAGATGCGTGTGGGGA         | 2999 |
| Qy | 951  | uTPrILlGILuThMeTtRPaSPCySMeTgILuValAlaAgILyGInAlMeCySLeuThVa     | 971  |
| Db | 3000 | GTGATGTGAGACATGTGGGACTGCTCATGTGAGGTGGCCGGCCAGGCCATGTGCTCATGTCT   | 3059 |
| Qy | 971  | lPheMeTetValMeTValILleGILySAnLeuValValLeuSAnLeuPheLeuAlaLeuLe    | 991  |
| Db | 3060 | CTTCATGATGGTTATGTGTCATTTGGCAACCGTGGTGGTGTGAATCTATTCTCGGCTTCTCT   | 3119 |
| Qy | 991  | u***SerSerPheSerILaSPaSnLeuAlaAlaThrAspAspAspAsnGLuMeCAsnAs      | 1011 |
| Db | 3120 | TCTAGGCTCTCTACGCCACAACAACCTGGGGGCCACAGCAGCAGCGGGGAAATTAACA       | 3179 |
| Qy | 1011 | nLeuGILlLeAlaValaSPaSPrMetHISLySgILyValAlaTArYrValLySArgLySILeTy | 1031 |
| Db | 3180 | CTTCGACATCTCACTGATTCGGGATCAAGAAGGGCGCTGCGCTGGACCAAAAGTCAAGCTCA   | 3239 |
| Qy | 1031 | rGLuPheILleGILnInSerPheILeArGLySILnLySILeAspSILuILeLySProLe      | 1051 |
| Db | 3240 | CGCCTTCATGAGGCTCACCTTC-----AGCAGCGGGAGGGGAGTGAAGTCAAAACCCCT      | 3299 |
| Qy | 1051 | uAspAspLeuAsnAsnLySlySAspSerCySMeTSerAsnHISThr-----GILlLeGIL     | 1070 |
| Db | 3294 | CGAGACAGCTGTATGAGAAGAGGACCACTCATCGCCCAACACACAGCGGCTGTGAATCCA     | 3353 |
| Qy | 1070 | YLyAspAspLeuAspYrILeUaLySAPrValAnGLYThrTrSerGILlLeGILYThnGLySe   | 1090 |
| Db | 3354 | CCGGACGCGCACCTTCCAGAAGAACGGGAACGGAAACCCACCGCGGATC-----GGCAG      | 3407 |
| Qy | 1090 | rSerArILuLySyrILleILeAspGILuSerAspTYrMeTserPheILeAsnAsnProSe     | 1110 |
| Db | 3408 | CAGCTGTGAGAAAGTACATCATCATCAGCAGG---GACCAACATGTCTTCATTTAACACCCAA  | 3466 |
| Qy | 1110 | rLeuThrValThrValProILleAlaValaGLyGILuSerAspPheGILuAsnLeuAsnThnGI | 1130 |
| Db | 3465 | CCTGACCCCTCGGGGTGCCATTTGCTGTGGCGCAGTGTGACTTCGAGAACCTCAACAACAGA   | 3524 |
| Qy | 1130 | uAspPheSerILuSerILuSerAspLeuGILuSILuSerLySGLyLySLeuAsnGILuSerSe  | 1150 |
| Db | 3525 | GGATGTTCAGCGCAATTCAGACCTCGTAGGCGACCAAAAGTAAATCTGGAGAT---ACCG     | 3583 |
| Qy | 1150 | rSerSerGILuLySerThrValaSPILleGILyAlaProValaGILuGILnProValaGI     | 1170 |
| Db | 3582 | CTCCCAAGAAGAGTACATCATCAGACATCAAGCCGTGAGGTGGAAGAGTTCCCGTGGAGCA    | 3644 |
| Qy | 1170 | uProGILuThrLeuGILuProGILuAlaCySPhenHnGILuGILyCySValaGILnArPheLy  | 1190 |
| Db | 3642 | ACCTTAGGAATAACTTGGATTCGGAGCGCTCTTTACAGAGGGTGTGGCTCACCGGTTCAA     | 3701 |
| Qy | 1190 | sCySgYrGILnLeAsnAlaGILuGILuGILyArGgILyLySILnTrPTPrAsnLeuArGITh   | 1210 |
| Db | 3702 | GTGGCGCCAGGTGCACATCAAGAGGAAGACTAGCGCAAGTCTGGTGGATCTTCGGGAAAC     | 3761 |
| Qy | 1210 | rCyAspPheArGLlLeValaGILnHISAnTrPheGILuThrPheILeValaPheMeTILeUe   | 1230 |
| Db | 3762 | CTGCTCTCTCATTTGTGGAGCACAATTGGTTGAGACCTTCATCATCTTCATATCTCTCT      | 3821 |
| Qy | 1230 | uSerSerGILyAlaLeuAlaPheGILuAspILleYrILleAspGILnArGLyThrILleLySth | 1250 |
| Db | 3822 | CAGCAGTGTGGCCCTGGCGCTTGGAGCACACTCATATGAGCAGAGGAAGAACCATCCGAC     | 3881 |
| Qy | 1250 | rMeTLeuGILuYrAlaSPlySValaPheThrTYrILlePheILleGILuMeTLeuLeuLy     | 1270 |

Db 3882 CATTCTGGAGTATCGGACAAAGCTTCACCTACATCTTCACTGGAGATGTTGCTCAA 3941  
 QY 1270 STPVALAATyrglythrphethrasnalatrypcystrpleuasphele 1290  
 Db 3942 GTGGAGACGCTAGGCGTTCGCAAGTCTTCACCAATGCCGGTGGTGGACTTCCT 4001  
 QY 1290 uileuaspvalserleuvalserleuvalasnalaleuuglytyrsergluleu 1310  
 Db 4002 CAATGTGGCTGCTCTTACACACCTTAATAGTAACTCCCTGGCTACCTGGAACTAGG 4061  
 QY 1310 yalaleuyseryleuargthrleuargalaleuargproleuarglaleuaseratgph 1330  
 Db 4062 TGGCATTAAGTCCCTTAGAGACCTTAAGAGCTTGAAGACCTTAAGAGCTTAACAGATT 4121  
 QY 1330 egluglymetargvalvalalaleuuglyalaleuoserillemetasnva 1350  
 Db 4122 TGAAGGATGAGGGGTGGTGGATGCTGGTGGGCGCATCCCTCCATCATGATGT 4181  
 QY 1350 lleuvalcysleuilephetrpleuilepheserilemetglyvalasleuapheal 1370  
 Db 4182 GCTGCTGTGTCTCATCTTCTGCTGATTTTCAGATCATGAGGAGTTAACTGTTTGC 4241  
 QY 1370 aglytyrphetrthiascysileasnthrthrthglyaspargphespiileguaspva 1390  
 Db 4242 GGGGAAATACCACTACCTGTTTAATGAGACTTCGAAATCCGGTTCGAAATCGATATGT 4301  
 QY 1390 lasnanihsthraspcysleuileuileguarganglunth---Alaargtrply 1409  
 Db 4302 CAACAATAAAGGACGCTGAGAGCTCATGAGGAGGCAACGACGAGATCGATGGA 4361  
 QY 1409 saasnvallyvalasnpheaspasnvalglypheglytyrleuaserleuenglinal 1429  
 Db 4362 GAATGTCAATACATCTTGTGATGTGGAGAGCTGACCTGCTTCAAGTGGC 4421  
 QY 1429 aThrphelygltyrphmetaspilemettyrAlaAlaValasbertrgasnvalglule 1449  
 Db 4422 AACCTTCAAGGCTGATGAGCATGATATGCGGCTGATGATTCGGAAGCCAGAGA 4481  
 QY 1449 uglinProlystyrclugluserleuTyrmetyrleuTyrrpheValillepelleleph 1469  
 Db 4482 GCAGCGCTAGACGAGGCAACATCATGTACATCTACTGCTCATCTTCATCATCTT 4541  
 QY 1469 eglYserPhepethrleuasnleupheileglyvalilleleaspsnphesangl 1489  
 Db 4542 CGGCTCTTCTTCACTCCTCAACCTGTTCAATCGGTGATCATGACAACTTCAACGAGA 4601  
 QY 1489 nlysltyrlyspheglyglinalaspillepmetthrgluglunlinsystrytyras 1509  
 Db 4602 GAAGAAAAGCTTGGAGGTGAGACATCTTCATGACAGAGAGAACAGAAAGTACTCAA 4661  
 QY 1509 nalameltyrlyslenglyserlyslsProglinsProleirgProglinsly 1529  
 Db 4662 TGGCATTAAGGCTGGGCTCCAGAAAGCCAGAAAGCCATCCCGGACCTTGAACAA 4721  
 QY 1529 spheglylmetvalpheasphevalthrarglinalpheaspilleserilemet 1549  
 Db 4722 AATCCAAAGGATGCTCTTATCTTGCACCAACAGCCTTGAATGATGATGAT 4781  
 QY 1549 eleuilecysleuasnmetvalthrmetmetvalgluThraspaspilinserytyrva 1569  
 Db 4782 GCTCATTCGCTTAACATGAGGACAAATGATGAGAGACAGACACTGAGAGCAAGCAT 4841  
 QY 1569 lThrThrilleuSerargilleasnleuValpheilleValleuPhepethrthglucysva 1589  
 Db 4842 GGAGAAATCTTACAGGATTAATCGCTTGTGTCATCTCTTCACTCCGAGGTGTGT 4901  
 QY 1589 lleuylsleuileserleuarghistryrtyrphetrilleglytyrtrpansilepasp 1609  
 Db 4902 GCTCAAAATCTTGGCTGAGACACTACTTTCACCATTTGGCGGAAACATCTTGAATT 4961  
 QY 1609 eValValValilleuSerilleValgluMetPheleuValgluileuileguistyrph 1629  
 Db 4962 TGTGTGTGTATCTTCATTTGTGGAAATGTCTGCTGATATATCATGTGAAGATGACTT 5021

QY 1629 eValSerProthrleuphearvalilleargleualarglileglyarglileuargle 1649  
 Db 5022 CGTCTCCCAACCTTATTCGAGTATTCGATTCGATTCGATTCGATTCGATTCGATTC 5081  
 QY 1649 uileuglylvalalysglylileargthrleuPhealeuemetserleuproal 1669  
 Db 5082 GATCAAGGGGCGCAAGAGGATCCGACCTGCTCTTGTGCTTAATGATGTGCGCGCCG 5141  
 QY 1669 aleuPheasnilleglyleuileuPheleuValMetPheleThrAlailepheglyme 1689  
 Db 5142 CTTGTCAACATCGGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5201  
 QY 1689 tSerAsnPhenalatyrVallylsarggluValglylileaspasmetPheasphegluth 1709  
 Db 5202 GTCCAACTTGCATACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5261  
 QY 1709 rPheglyAsnsermetilecysleupheglinlethrThrSerAlaaglytyrtrpasp 1729  
 Db 5262 ATTTGGCAACAGCATGATCTGTGTTGCCAGATCACAACGCTGCTGGCTGGATGGCT 5321  
 QY 1729 uleuAlaProilleuasnserlyspProAspCysAspProasnlyValasProgl 1749  
 Db 5322 GCTGCTCCCAATCTGAAAC---CGCCCTGCTGATGAGCTTGGAGCAAGAGCACCGAG 5378  
 QY 1749 ySerSerVallysglyaspCysglyAspProSerValglylilepPhePheValSerty 1769  
 Db 5379 GAGTGGCTTCAAGAGGAGCTGTGGAAACCTCGGTGGATCTTCTTCTTGTGAGCTA 5438  
 QY 1769 rleileleaserPheleuValValAlasmettyrilleAlaValilleuengluasnp 1789  
 Db 5439 CATCATCATCT 5498  
 QY 1789 eSerValAlaThrclugluserAlaagluProleuSerGlunaspspPheglumetPheTy 1809  
 Db 5499 CAGCTGGCCACGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5558  
 QY 1809 rgluValtyrpoluysPheaspProaspAlaThrGlPheMetgluPhegluysleuse 1829  
 Db 5559 TGAATGTGGAGAGAGTGTGACCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5618  
 QY 1829 rgluPheAlaAlaaleuugluProleuasnleuproglindroasnlyleu 1849  
 Db 5619 AGACTTTCGCGACCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5678  
 QY 1849 uileAlaMetaspheuprometValserglyAspArgillehiscysleuaspilleu 1869  
 Db 5679 CATGCCATGAGCTGCTCCATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5738  
 QY 1869 eAlaPheThrlysarArgValleuuglyluserglylmetaspAlaaleuarglilegime 1889  
 Db 5739 CGCTTTCACCAAGGAGATCTCGGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5798  
 QY 1889 tgluuglurghemetalserasnProserlyslsValSertyglindroilthrthrth 1909  
 Db 5799 GAGAGAGCGGTGCTGAGCATCATCTTCAAGGTGTCTTACAGAGCTTACCAACACAC 5858  
 QY 1909 rleuylsArglyslenglunlinalserAlaValilleleuarglinaltyrargh 1929  
 Db 5859 TCTGCGGCGCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5918  
 QY 1929 sleuileuylsargthrval-----LysglinalSerPheThrlyrinslysls 1946  
 Db 5919 CTTCGCTAGGCGGGCTTCACTTCGCAAAAGATGCTCC-----AACAA 5963  
 QY 1946 sllelysglylvalaasnleuileuileuglylaspmetilleleasparglileangl 1966  
 Db 5964 GCTGAGAAATGA----- 5976  
 QY 1966 uasnSerillethrgluylsThraspheupThrmetSerThrAlaAlaCysProProserTy 1986  
 Db 5977 -GGCACACACAGAGCAAG 6032





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|----|------|--|------|
| OY | 401  | IIePhePheValLeuValIIIPheLeuGlySerPheTyrLeuLeuLeuLeuVala        | 420  |
| OY | 401  | IIePhePheValLeuValIIIPheLeuGlySerPheTyrLeuLeuLeuLeuVala        | 420  |
| Db | 1168 | ATCTCTTTTGCTTGCTGATCATCTCGTGGGTTCTTCTATCCGGTAACTTGATTTGGCT     | 1227 |
| OY | 421  | ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaLeuGlnLys   | 440  |
| Db | 1228 | GTGGTGGCCAAAGCGCTTATGAGAAACAACAACAGGCAACACTGGAGAGGCAAGCAAAAAA  | 1287 |
| OY | 441  | GluAlaGluPheGlnGlnMetIIeGluGlnLeuTyrGlnGlnGlnGlnGluAlaGlnGln   | 460  |
| Db | 1288 | GAGGCCAGATTCAAGGCAACATGCTGGACAACTAAAGACAGACAGAGGAGGCACACAGCT   | 1347 |
| OY | 461  | AlaAlaThrAlaThrAlaSerGlnHisSer-----ArgGluProSer                | 474  |
| Db | 1348 | GCTGCATAGGCCACCTC-AGCGGGCACTGCTCTCGAAGACGCATTAAGAAAGAGGGA      | 1408 |
| OY | 475  | AlaAlaGlyTyrGluSerAsp-SerSerSerGluAlaSerLysLeuSerSerLysSerAl   | 494  |
| Db | 1407 | AGATGGGGTAGCCCTCCGAGGAGCTCTTGTAACTGTAAACTCAGTTCCAAAGACGC       | 1466 |
| OY | 494  | AlysGluTyrGlnAsnTyrGlnLysLysArgLysGlnLysGlnGlnSerGlyGluGlnI    | 514  |
| Db | 1467 | GAAAGACGGCGGAAACCGAGGAAGAAAGAAAGCAAGAAAGGCTCTCGAAGGCGAGA       | 1528 |
| OY | 514  | uLys---AspGluAspGluPheGlnLysSerGluSerGluAspSerIIeArgArgLysG1   | 533  |
| Db | 1527 | GAAAGGGGACCCGGAAGAAAGGTATTAAAGTCAAGAGTGGAAATACGATATGAAAGGAAGGC | 1586 |
| OY | 533  | YpHeArgPheSerIIeGluGlnAsnArgLeuThrTyrGluLysArgTyrSerProH1      | 553  |
| Db | 1587 | CTTCCGG-----CTGCCAACAACAAGATA-----GGAGAGAAAGTTTTCATCATGAA      | 1634 |
| OY | 553  | sgLSerLeuLeuSerIIeArgLysSerLeuPheSerProArgAsnSerArgThrSe       | 573  |
| Db | 1635 | TCACTCGCTGTACAGCAATCCAGGCTCGCCCTCTCTCCGACATTAACGAAAAAGAG       | 1694 |
| OY | 573  | IleuPheSerPheArgLysI--ArgAlaLysAspValGlySerGluAsnAspPheAlaas   | 592  |
| Db | 1695 | CATCTCAGCTTCGGGGACCCGTCGGTGGGACCCCGGCTCGAAGATGAACTTGCGAGA      | 1758 |
| OY | 592  | PasGluHisSerThrPheGluAspAsnGluSerArgArgAspSerLeuPheValProAr    | 612  |
| Db | 1755 | CGATGAACACAGCCACCTGGAGAGAGACGAGGCGCGGTGACTCGCTTCATCCCAT        | 1814 |
| OY | 612  | gArgHisGlyGluArgLysAsn-----SerAlaLeuSerGlnThrSerAr             | 627  |
| Db | 1815 | CCGGGCCCCGAGGCGCGGACAGCACTACAGTGGCTACACGGCTACACGACAGTACGACCG   | 1874 |
| OY | 627  | gSerSerArgMetLeuAlaValPheProAlaAsnGlyLysMetHisSerThrValAspCy   | 647  |
| Db | 1875 | CTGTCGCGC---ATCTCCCAACCTGCGCGGACAGCTGAAGCCACACGACGCTGGACTG     | 1931 |
| OY | 647  | sAnGlyValValSerLeuValIeGlyProSerValProThrSerProValGlyGlnIe     | 667  |
| Db | 1932 | CAACGGCGTAGTGCATCATCTACGGG-----CCGGCTCACACATCGGGCGGCT          | 1979 |
| OY | 667  | uLeuProGluValIleLeuAspLysProAlaThrAspAsnGlyThrThrThrGluTh      | 687  |
| Db | 1980 | CTTCTCT-GAG-----GCACAGCTAGAGT                                  | 2002 |
| OY | 687  | rGluMetArgLysArgArgSerSerPheHisValSerMetAspPheLeuGluAspR       | 707  |
| Db | 2003 | GGAATTAAGAAAGAGCCCTGGACTTTTA-GTTTGTATGAGCAACACTCGCTCTTA        | 2061 |
| OY | 707  | oSerGlnArgGlnArgAlaMetSerIIeAlaSerIIeLeuThrAsnThrVal--GluGlu   | 726  |
| Db | 2062 | CGGACCGGAAGACAGATCAACAGCATTAATGACGGGTGCACAAACACGATGTAAGAG      | 2121 |
| OY | 727  | LeuGluGluSerArgGlnLysCysProCysTyrTyrLysPheSerAsnIIePheLeu      | 746  |
| Db | 2122 | CTGGAAAGTCTCAGAAAGTCCACCGCTGCTGTATTAATTTTGCCAAACTTCTCTC        | 2191 |
| OY | 747  | IleTyrAspCysSerProTyrTyrLeuLysValLysHisValAlaAsnLeuValaMet     | 766  |

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|----|------|--|------|
| Dd | 2182 | ATCTGGAGGTCTCAACCCCTACTGGAATAAACTGAAAGAGATCGTAACCTTAATTCGATG     | 2241 |
| Qy | 767  | ASPRORPHEVALASPLAEUALIAIIEthrlleCysIIleValleuAsnthrIeuphemeIaIa  | 786  |
| Dd | 2242 | GACCCCTTTTGTAGACTTACAGCATCACCATCTGCATGCTGTGAATACCGTAAATTATGACA   | 2301 |
| Qy | 787  | MetGluHISrYrPrometCthAspPhISpheAsnValleuThrValGlyAsnleuVal       | 806  |
| Dd | 2302 | ATGGAGCACCATCCCATGACACCACTTGAAACAGCTTGCCGTAGAAATCTGGTG           | 2361 |
| Qy | 807  | PheThrIeGlyIlePheThrIaGluMetPheLeuYsIIleIleIleMetAspProTYr       | 826  |
| Dd | 2362 | TTCAACGGGAGCTTCACGGGGAAATGTTCTGAACTCATGAGCCATGGAACCCCTACAT       | 2422 |
| Qy | 827  | TyrPheGlnIugIyTPraSnIIlePhAspGlyPheIleValThrIeuSerIeuValGlu      | 846  |
| Dd | 2422 | TATTTCCAAAGAGCGCTGGAACATTTTTCAGCGATTTATGTCTCCCTCAGTTTAATGGAG     | 2483 |
| Qy | 847  | LeuGlyLeuAlaAsnValGluIyIeuSerValIleuArgSerPheArgIeuIeuArgVal     | 866  |
| Dd | 2482 | CTGAGCTCCGAGAGTGGAGGGAGGCGCTCAGCTCGGTCTTCGACTGCTCGAGAGC          | 2543 |
| Qy | 867  | PheYsIleuAlaYsSerTYrProThrIleuAsnMetIeuIleYsIIleIleGlyAsnSer     | 886  |
| Dd | 2542 | TTCAAGCGGGCAGAGCTCTGGCCCAACCCCTGAACATCTGATCAAGATCATCGGAATCC      | 2602 |
| Qy | 887  | ValGlyIaIeugIyAsnleuThrIeulValleuAlaIleIleValPheIleheAlaVal      | 906  |
| Dd | 2602 | GTGGGTGCCCGGGCAACCTGACCCGTGCTCGCATATGCTTCATCTTCATCTTCCCGTG       | 2662 |
| Qy | 907  | ValGlyMetGlnleuPheGlyYsSerTYrIyAspCysValCysYsIIleAlaSerAsp       | 926  |
| Dd | 2662 | GTGGGATGACAGCTGTTGGAAAGACTTCAACGAGATGCGTGTGAAGATCAACAGAGAG       | 2722 |
| Qy | 927  | CysGlnleuProAqTYrPhISmetAsnAspPhePhnISerPheIeuIleValPheArg       | 946  |
| Dd | 2722 | TGCAAGCGCCGGCGCTGGCAATGAAGAGATTTCTTCATCTCTCTCATCTGCTTCCGA        | 2782 |
| Qy | 947  | ValIeuCysGlyIuTPrlIeGluThrMetTPraPcYsMetGluValAlaGlyIaIa         | 966  |
| Dd | 2782 | GTGCTGTGTGGGGATGAGATCGAGACCATGTGGGACTGCATGAGAGGTGGCGGACAGCC      | 2842 |
| Qy | 967  | MetCysIeuThrValPheMetMetValMetValIleGlyAsnleuValValleuAsnleu     | 986  |
| Dd | 2842 | ATGTGCTCATGTGCTTCAAGATGAGGTATGAGCTAATGGAACTGGTGTGTGAATCTA        | 2902 |
| Qy | 987  | PheIeuAlaIeuIeu***SerSerPheSerAlaAspIleuAlaAlaThrAspAspAsp       | 1006 |
| Dd | 2902 | TTCTCGGCGCTTGCTTGTGACCTCTTCACGGCAGACAACTGGCGGCCACACACAGAC        | 2962 |
| Qy | 1007 | AsnGluMetAsnAsnleuGlnIleAlaValaIaAspArgMetHISlyGlyValAlaIaTYrVal | 1026 |
| Dd | 2962 | GGGGAATGTAACAACCTGCGATCTGAGATGCCGATCAAGAAAGGCGCTGGCTGGACC        | 3022 |
| Qy | 1027 | LysArgIySIIeTYrGluPheIleGlnIeGlnIeSerPheIleArgIyGlnIySIIeIeuAsp  | 1046 |
| Dd | 3022 | AAAGTGAAGGTGACAGCTTCATGCAAGGCTCACTTC-----AACCAAGGGAGAGCGGAT      | 3077 |
| Qy | 1047 | GluIleIySProIeuAspPheIeuAsnAsnIySAspSerCysMetSerAsnIsthr         | 1066 |
| Dd | 3076 | GAAGTGAACACCCCTCGACGAGCGTGTATGAAGAAGAACGCCAATGTCATGCGCAACACAG    | 3135 |
| Qy | 1067 | ***GluIleGlyIyAspIeuAspTYrIleuYsAspValaIaSnGlyIthrIthSerGly      | 1085 |
| Dd | 3136 | GCGCTGTGATTCACACCGCGAACCGCGCTTCAGAAAGAACGGGAACGGAACACCGAGCGC     | 3195 |
| Qy | 1086 | IleGlyIyArgIySerIeValGlyIySyrIleIleAspGluSerAspTYrMetSerPhe      | 1105 |
| Dd | 3196 | ATC-----GCGACAGCGGGGAGAAATCATCATCGAGAG--GACACACATGCTCTTC         | 3246 |
| Qy | 1106 | IleAsnAsnProSerIeuThrValThrValProIleAlaValGlyIuSerAspPheGlu      | 1125 |





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Db 739 ATCCAGTCCGTAAGAGCTGCGAGCTGATGATCTCGACAGTCTTCTCGTAGTGT 798
Oy 261 PheAlaLeuIleGlyLeuGlnLeuPheMetIAsnLeuArgAsnLysCysIleGlnTrp 280
Db 799 TTCGCCGATGATGCTGACAGCTCTTCATGAGAACCTTTGAAACACATGTCCTGCTG 858
Oy 281 ProProthrAsnAlaSerLeuGlnLysSerIleGlyAsnIleThrValAsnTrp 300
Db 859 CCC-----ATAACCTTC 870
Oy 301 AsnGlyThrLeuIleAsnGlnTrpValPheGlnPheAspTrpLysSerTrpIleGlnAsp 320
Db 871 AACAGAGCTACCTCGAGAGACGACGACGAGCTTTGACTGGAGAGATATATCAACAT 930
Oy 321 SerArgTrpHisTrpPheLeuGlnGlyPheLeuAspAlaLeuLeuCysGlyAsnSer 340
Db 931 AAAACAACCTTTACATGCTTCGTCGCAATGCTAGAACCTTCGCTGCGGGAACGTTCT 990
Oy 341 AspAlaGlyGlnCysProGlnGlyTrpMetCysValLysAlaGlyArgAspProAsnTrp 360
Db 991 GATCTGCGCAATGC--GAAGGATTCAGTCAGTCAAGGAGGAGGAGGAGGAGGAGGAG 1047
Oy 361 GlyTrpTrpSerPheAspTrpPheSerTrpAlaPheLeuSerLeuPheArgLeuMetTrp 380
Db 1048 GGTACACCACTTGTACACCTTACAGCTGGGCTTCTTGGCATTTTCGGCTTATGACC 1107
Oy 381 GlnAspPheTrpGlnAsnLeuTrpGlnLeuThrLeuArgAlaAlaGlyLysTrpMet 400
Db 1108 CAGAGCTATGCGAAGCTTATACAGCTGACCTTACGAGCGCGGGAACGTCACAG 1167
Oy 401 IlePhePheValLeuValIlePheLeuGlnLysPheTrpLeuIleAsnLeuIleAla 420
Db 1168 ATCTCTTGTCTGCTGCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1227
Oy 421 ValValAlaMetAlaTrpGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 440
Db 1228 GTGGTGGCATGGCTTATGAGAGACAGACAGGACGACGACGACGACGACGACGACGAC 1287
Oy 441 GlnAlaGlnPheGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 460
Db 1288 GAGGCGGATTCAGAGCAATGCTGAGCACTCAAGAGCAGAGGAGGAGGAGGAGGAGG 1347
Oy 461 AlaAlaTrpAlaThrAlaSerGlnLysSer-----ArgLysProSer 474
Db 1348 GCTGCAATGCGCACCTC-AGCGGCACTGCTCGGAGAGGAGGAGGAGGAGGAGGAGG 1406
Oy 475 AlaAlaGlyArgLeuSerAsp-SerSerSerGlnAlaSerLysLeuSerSerLysSerAl 494
Db 1407 AGATGGGATAGGCTCTCCGAGAGAGCTTTCTGAACGTCTAAACTGATCCCAAGAGCC 1466
Oy 494 AlAspGlnArgArgAsnArgArgLysArgLysGlnLysGlnLysGlnLysGlnLysGln 514
Db 1467 GAAGAGGCGGCGGAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1526
Oy 514 uLys--AspLysAspGlnPheGlnLysSerLysSerLysSerLysSerLysSerLys 533
Db 1527 GAAGAGGAGACCGGAGAGGCTTTTAAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 1586
Oy 533 yPheArgPheSerIleGlnGlyAsnArgLeuThrTrpGlnLysArgTrpSerProHis 553
Db 1587 CTTCGG-----CTGCCAGACACAGGATA-----GGAGAGAGATTTTCCATCATGA 1634
Oy 553 sGlnSerLeuLeuSerIleArgGlySerLeuPheSerProArgArgSerArgTrpHis 573
Db 1635 TCAGTCGCTGCTCAGCATTCGAGGCTCGCTTCCTCCGACATACAGCAAGAGAGAG 1694
Oy 573 rLeuPheSerPheArgGly--ArgAlaLysAspValGlySerGlnAsnAspPheAlaAs 592
Db 1695 CATCTTCAGCTTCGGGAGACCGCTCGCTTCGAGAGAGAGAGAGAGAGAGAGAGAG 1754
Oy 592 AspGlnLysSerTrpPheGlnLysAspAsnLysSerArgArgAspSerLeuPheValPro 612
Db 1755 CGATGACACGACCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1814
Oy 612 gArgHisGlyLysArgArgAsn-----SerAsnLeuSerGlnTrpSerArg 627
Db 1815 CCGCCCGCCGAGGCGCCGAGAGAGCTACAGCTGCTACAGCGGCTACAGCGATGACGCG 1874
Oy 627 gSerSerArgMetLeuAlaValPheProAlaAsnGlyLysMetHisSerThrValAspCy 647
Db 1875 CTGCTGCGCC--ATCTCCCAAGCCTGCGCGAGAGGTAGAGCAAGAGAGAGAGAGAG 1931
Oy 647 sAsnGlyValValSerLeuValGlyLysProSerValProThrSerProValGlyLeu 667
Db 1932 CAACGCGGTAGGTACATCATCGGG-----CCCGGCTACACATCGCGCGGCT 1979
Oy 667 uLeuProGlnValIleIleAspLysProAlaThrAspAspAsnGlyThrThrGlnThr 687
Db 1980 CCTGCT-GAG-----+-----GCACGACGTCAGCT 2002
Oy 687 rGlnMetArgLysArgArgSerSerPheHisValSerMetAspPheLeuGlnAspPr 707
Db 2003 GGAATATTAAGAAAGAGGCGCTGAGCTCTTTA--GTTCTATGAGCAACACTGCGCTCT 2061
Oy 707 oSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeuThrAsnThrVal--GlnGln 726
Db 2062 CGAGAGGAGAGAGAGAGATACAGACGATATGAGCGTGGTACACAAACAGCTAGTGAAG 2121
Oy 727 LeuGlnLysSerArgGlnLysCysProProCysTrpTrpLysPheSerAsnIlePheLeu 746
Db 2122 CTGGAAGATCTCAGAGAAAGTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2181
Oy 747 IleTrpAspCysSerProTrpTrpLeuLysValLysHisValValAsnLeuValMet 766
Db 2182 ATCTGGAGATGTCACCCCTGATGATATACAGAGAGAGAGAGAGAGAGAGAGAGAG 2241
Oy 767 AspProPheValAspLeuAlaIleThrIleCysIleValLeuAsnThrLeuPheMetAla 786
Db 2242 GACCTTTGTAGACTTACATCAGCATGATGATGATGATGATGATGATGATGATGATGAT 2301
Oy 787 MetGlnHisTrpProMetLeuThrAspHisPheAsnAsnValLeuThrValGlnLysLeuVal 806
Db 2302 ATGGACACCATCCCATGACACCATGACACCATGACACCATGACACCATGACACCATG 2361
Oy 807 PheThrGlyIlePheThrAlaGlnMetPheLeuLysIleIleAlaMetAspProTrpTrp 826
Db 2362 TTCACCGGATCTTCACGCGGAGAAATGTTTCAAGCTCATAGCCATGAGACCCCTACT 2421
Oy 827 TyrPheGlnGlnLysTrpAsnIlePheAspGlyPheIleValThrLeuSerLeuValGln 846
Db 2422 TATTTCCAAAGAGGCTGGAACATTTTGAAGATTTATTTGCTCCCTCAGTTAATGAG 2481
Oy 847 LeuGlyLeuAlaAsnValGlnGlyLeuSerValLeuArgSerPheArgLeuLeuArgVal 866
Db 2482 CTGAGCTGCGACATGATGAGAGGCGCTCAAGCTCGGCTCGGCTCGGCTCGGCTCG 2541
Oy 867 PheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIleLysIleIleGlyAsnSer 886
Db 2542 TTCAAGCTGCGCAAGTCTGCGCCACCTGACATGCTGATCANAGTCAATCGGAGCTCC 2601
Oy 887 ValGlyAlaLeuGlnLysLeuThrLeuValLeuAlaIleIleValPheIlePheAlaVal 906
Db 2602 GTGGGTCCTGCGGCAACCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2661
Oy 907 ValGlyMetGlnLeuPheGlnLysSerTrpLysAspCysValCysLysIleAlaSerAsp 926
Db 2662 GTGGGATCGACGCTTTGGAAGATTTCAAGAGAGTGGCTGTGAAGTCAACAGAGAG 2721
Oy 927 CysGlnLeuProArgTrpHisMetAsnAspPheHisSerPheLeuIleValPheArg 946
Db 2722 TGCAGCTCCCGCGTGGACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2781
Oy 947 ValLeuCysGlyLysTrpIleGlnThrMetTrpAspCysMetAluValAlaGlyAla 966
Db 2782 GTCTCTGTGGGAGTGGATGAGACATGTTGAGAGAGAGAGAGAGAGAGAGAGAGAG 2841
```

|    |      |   |      |
|----|------|---|------|
| QY | 967  | MetCysLeuThrValIPheMetMetValMetValIleGlyAsnLeuValValLeuAsnLeu   | 986  |
| Db | 2842 | ANGTCCCATTCGTCCTCATGATGGTATTGTCATTGGCAACCTGGTGTCTGTCATCTA       | 2901 |
| QY | 987  | PheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeuAlaAlaThrAspAsp       | 1006 |
| Db | 2902 | TTCCTGGCCTTGTCTTCGAGCTCTCTTCAGGCGACAACTGGCGCCACAGACAGAC         | 2966 |
| QY | 1007 | AsnGluMetAsnAsnLeuGlnIleAlaValaAspArgMetHisGlyGlyValaAlaTyrVal  | 1026 |
| Db | 2962 | GGGGAAATGAACAACCTGCAGATCTCATGATCTCGGATCAAGAAGGCGCTGGCTGGACC     | 3021 |
| QY | 1027 | LysArgLysIleIleTyrGluPheIleGlnGlnSerPheIleArgLysGlnLysIleLeuAsp | 1046 |
| Db | 3022 | AAAGTAAGGTGCACGGCTCTCATGACGGTCACATTC-----AAGCAGCGGAGGCGGAT      | 3075 |
| QY | 1047 | GluIleLysProLeuAspAspPheAsnAsnLysIleAspSerCysMetSerAsnHisThr    | 1066 |
| Db | 3076 | GAAGGAAACCCCTGCAGACGCTGTATGAGAAAGAACGCCAACGTCACCCAAACACAG       | 3135 |
| QY | 1067 | ---**GluIleGlyLysAspLeuAspTyrLysLeuAspValAsnGlyThrThrSergly     | 1088 |
| Db | 3136 | GGCGGTATATCCACCGGAACGGGAGATTCTCACAAGAAGGAGACGAACCAACGACGGC      | 3199 |
| QY | 1086 | IleGlyThrGlySerSerValGluLysTyrIleIleAspGluSerAspTyrMetSerPhe    | 1105 |
| Db | 3196 | ATC-----GGCACACACGCTGGAGAGATCATCATCGACGAG---GACCACATGTCTTC      | 3246 |
| QY | 1106 | IleAsnAsnProSerLeuThrValThrValProIleAlaValGlyGlnSerAspGlu       | 1122 |
| Db | 3247 | ATTAAACAACCCAAACCTGCACCGTCCGGTCCCATTCGCTGGGAGATCTGACTTCGAG      | 3306 |
| QY | 1126 | AsnLeuAsnThrGluAspPheSerSergLysSerAspLysGlnLysIleSergLysLeu     | 1145 |
| Db | 3307 | AAACCAACAACAGAGATGTATTAGCAGGAAATCAGACCTCGAAGGACGAACAGATTAAC     | 3366 |
| QY | 1146 | AsnGluSerSerSerSergGlySerrThrValAspIleGlyAlaProValGluGln        | 1165 |
| Db | 3367 | GACACT---ACCAGCTCTCTCAGAAAGAGATACATGCATGACATGACGCTGAGTGGAGA     | 3422 |
| QY | 1166 | GlnProValValGluProGluGlnThrLeuGlnProGluAlaCysPheThrGluGlyCys    | 1188 |
| Db | 3424 | GTTCCTGGGAGCAACTGTAGGAATATCTTGGAATCCGGACGCTGCTTAACAAGAGGTTC     | 3483 |
| QY | 1186 | ValGlnArgPheLysCysCysGlnIleAsnValGlnGlnGlyArgGlyLysGlnThrP      | 1205 |
| Db | 3484 | GTCCAGCGGTTCAAGTCTCTCCAGGTACATGTAGAGAAAGACTAGGCAAGCTGTGGTGG     | 3543 |
| QY | 1206 | AsnLeuArgArgThrCysPheArgIleValGlnHisAsnTrpPheGluThrPheIleVal    | 1225 |
| Db | 3544 | ATCTTGGGGAATAACCTGCTTCCATGTGTGACACACAATTGGTTGAGACCTTCATCATC     | 3603 |
| QY | 1226 | PheMetIleLeuLeuSerSergIlyAlaLeuAlaPheGluAspIleTyrIleAspGlnArg   | 1245 |
| Db | 3604 | TTCATGATTCGTCACACAGTGGGCGCTGGCTTTGAGAGACATCTACATTAGACAGAG       | 3663 |
| QY | 1246 | LysThrIleLysThrMetLeuGlnTyrAlaAspLysValPheThrTyrIlePheIleLeu    | 1265 |
| Db | 3664 | AAAGCAATCCGACACATCTCGAGATAGCGGACAGAGCTTCACTCAATCTTCAATCTCG      | 3722 |
| QY | 1266 | GluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPheThrAsnAlaTrpCys    | 1285 |
| Db | 3724 | GAGATGTTCACAGTGCAGCACGATACGATGCGCTTCGTAAGTCTTCAACCAATGCCG       | 3783 |
| QY | 1286 | TrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThrAlaAsnAlaLeuGly    | 1305 |
| Db | 3784 | TGGTGGACTTCCTCATGTGGCTGTCTCTTAAGTCAGCTTAATGCTTAATGCCCTCGGC      | 3843 |
| QY | 1306 | TyrSergLysLeuGlyAlaIleLysSerLeuArgThrLeuArgAlaLeuAspProLeuArg   | 1325 |
| Db | 3844 | TACTCGCAACAGTGGCCATTAAGTCCCTTAGGACCCCTTAAGAGCTTTTGAGACCCCTTA    | 3903 |
| QY | 1326 | AlaLeuSerArgPheGluGlnGlyMetArgValValaAsnAlaLeuGlnGlyAlaIlePro   | 1345 |

|    |      |   |      |
|----|------|---|------|
| Dd | 3904 | GCCTTATACACATTGGAAGGATGAGGGTGTGGTAAATGCTTGGTGGTCCATCC           | 3963 |
| Oy | 1346 | SerIleMetAsnValIleuLeuValCysIleIlePheTrpIleIlePheSerIleMetIy    | 1365 |
| Dd | 3964 | TCACATCATGAAATGTGCTGCTGGTGTGTCTTATCTTTGGCTGATTTTTCAGCATATGGGA   | 4023 |
| Oy | 1366 | ValAsnLeuPheAlaGlyLysPheTyHIsCysIleAsnThrThrTrpGlyAspArgPhe     | 1385 |
| Dd | 4024 | GTTAAACGCTTTGGGGGAAATACCACTACTGCTTAAAGAGACCTTCGAATCCGGTTC       | 4083 |
| Oy | 1386 | AspIleGlyAspValAsnAsnHISThrAspCysLeuLysLeuIleGluArgAsnGluThr    | 1405 |
| Dd | 4084 | GAAATCGATTTATGTCAACAAATAAACGAGACTGTGAGAACCTATGAGAGGGCAACAGACAG  | 4143 |
| Oy | 1406 | ---AlaArgTrpLysAsnValLysValAsnPhaAspAsnValGlyPheGlyTrpLeuSer    | 1424 |
| Dd | 4144 | GAGATCGGATGGAAGAAATGTCAAGATCACTTTGACAAATGTGGACAGGATTCCTGGCC     | 4203 |
| Oy | 1425 | LeuLeuGlnValAlaIleThrPheLysGlyTrpMetAspIleMetCysAlaIleValAspSer | 1444 |
| Dd | 4204 | CTTCTTCAAGTGGCAGACCTTCAAAAGGTGGATGAGATCATGTATAGCGGCTTACATTC     | 4263 |
| Oy | 1445 | ArgAsnValGluLeuGlnProLysTyrgluGluSerLeuTyMetLysIleuTyPheVal     | 1464 |
| Dd | 4264 | CGAAAGCCAGACAGACAGACCTGACTACGAGGGCAACATCATATGATCATCTTCTGTC      | 4323 |
| Oy | 1465 | IlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIleGlyAlaIleLeasp     | 1484 |
| Dd | 4324 | ATCTTCATCATCTTCGGCTCTCTTCACCCCTCAACCTTTCATCGGTCTCATTCATTCAC     | 4383 |
| Oy | 1485 | AsnPhaAsnGlnGlnLysLysPheGlyGlyGlnAspIlePheMetThrGluGlnGln       | 1504 |
| Dd | 4384 | AAC TTCACACGCAAGAAAGAAAGTTGGAGGTCAAGACATCTTCAITGACAGAGGAAG      | 4443 |
| Oy | 1505 | LysLysTyTyTyrAsnAlaMetLysLysLeuGlySerLysLysProGlnLysProIlePro   | 1524 |
| Dd | 4444 | AAGAAGTCACTAATGCGCATGAAGAAAGCTGGGCTCCAGAGCAACAGAGCCATCC         | 4503 |
| Oy | 1525 | ArgProGlyAsnLysPheGlnGlyMetValPheAspPheValThrArgGlnValPheAsp    | 1544 |
| Dd | 4504 | CGACCCCTGGAACAAACCAAGGATGTGCTTGTGATTTGCTACATCAACACCTTGTAC       | 4563 |
| Oy | 1545 | IleSerIleMetIleLeuIleCysIleAsnMetValThrMetMetValGluThrAspSp     | 1564 |
| Dd | 4564 | ATTGTGATCATGATGCTCATCTGCTTAACTGATGTACATGATGGTGGACAGACACT        | 4623 |
| Oy | 1565 | GlnSerLeuTyValThrThrIleLeuSerArgIleAsnLeuValPheIleLeuPhe        | 1584 |
| Dd | 4624 | CAGAGCAAGCAGATGGAGAACATCTTACTGATTAATCTGGTCTTGTATCTTCTTC         | 4683 |
| Oy | 1585 | ThrGlyGlyCysValIleuLysLeuIleSerLeuArgHisTyTyTrpPheThrIleGlyTrp  | 1604 |
| Dd | 4684 | ACCTCGCGAGTGTGGCTCAAAAGATTTGGCTTGAGACACTACTACTTCAACCTTGGCTGG    | 4743 |
| Oy | 1605 | AsnIlePheAspPheValIleValIleLeuSerIleValGlyMetPheLeuAlaGluLeu    | 1624 |
| Dd | 4744 | AACATCTTGACTTTGGTGGTGGTCAATCTCTCATTTGTGGAAATGTTCTTGCTGATATC     | 4803 |
| Oy | 1625 | IleGluLysTyPheValSerProThrLeuPheArgValIleArgLeuAlaArgIleGly     | 1644 |
| Dd | 4804 | ATTGGAAGTACCTTCGCTCCCAACACCTATTCGAGTTATCGAATTTGGCCGATTTGG       | 4863 |
| Oy | 1645 | ArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLeuLeuPheAlaLeuMet    | 1664 |
| Dd | 4864 | CGCATCTTGGCTGTGATCAAGGGCGCCAAAGGATCCGACACTCTCTTGGCTCTGATG       | 4923 |
| Oy | 1665 | MetSerLeuProIleLeuPheAsnIleGlyLeuLeuLeuPheLeuValMetPheIleTy     | 1684 |
| Dd | 4924 | ATGTGCTGGCCGCGCTTTCACATCGGCTCTGCTCTCTCTGCTATGTATCTTC            | 4983 |
| Oy | 1685 | AlaIlePheGlyMetSerAsnPheAlaIleValLysArgGluValGlyIleAspAspMet    | 1704 |



Db 4984 TCCATTTTGGCATGTCACACTTCGATACGTGAGACAGAGCGCGCATTCAGCATG 5043  
 QY 1705 PheasnPhcgluThrPhegluysnserMetlleCysaleuPhegluThrThrSerAla 1724  
 Db 5044 TTCACCTTCGACATTTGGCAACAGCATGATCTGTTTCTTCAGATCAACAGCTGCT 5103  
 QY 1725 GLYTPASGLVleuenuAlaProIleleuasnSerlyProProaspCysaspProdan 1744  
 Db 5104 GGCCTGGAGGCGCTGCTGCTGCAATCCTGANC--CGCCCTCTGACTGACCTTGAC 5160  
 QY 1745 LysValasnProgluSerSerVallysglyAspCysgluYasnProserValglyIlePhe 1764  
 Db 5161 AAAGACACCCAGGAGGAGCTGCTTCAAGGAGACTGTGGAGACCCCGGTGGGCATCTTC 5220  
 QY 1765 PhepheValSerlyIlelleIleSerPheleuValValValasnMetlyrIleAlaVal 1784  
 Db 5221 TTCCTGTAGCTACATCATCATCTCTCTGATGTGTGTGAMCATGTGCATCGCCATC 5280  
 QY 1785 IleleuGlunasnPheSerValAlaThrGlunGlunSerAlaGlunProleuSerGlunAsp 1804  
 Db 5281 ATCTGAGAGAACTTCAGCTGGCCAGCAGAGAGAGAGCGCCGCTCTGAGTGAGATGAC 5340  
 QY 1805 PhegluMetPheThrlygluValTTPgluLysPheaspProaspAlaThrgluPheMetglu 1824  
 Db 5341 TTCGAGACCTTCTATGATGATGAGAGAACTTTCAGCCAGCCACCCAGTTCATCGAG 5400  
 QY 1825 PhegluLysLeuSerGlunPheAlaAlaIleuGlunProProleuasnleuProgluPro 1844  
 Db 5401 TACTGTAAGCTGGCAGACTTTCGCGAGCCCTGGAGACACCCGCTCGAGTACCAAGCC 5460  
 QY 1845 AsnLysLeuGlunleuIleAlaMetaspLeuProMetValSerIlyaspArgIleHisCys 1864  
 Db 5461 AACACATCGAGGTCTATGATGATGAGAGACCTCCATGATGAGAGAGATCCATCCATCG 5520  
 QY 1865 LeuaspIleleuPheAlaPheThrlyArgValIleuGlunSerlygluMetaspAla 1884  
 Db 5521 TTGGATATCTTTCCTTCCTTCACCAAGCGATCTCGGAGACAGTGGAGGTGGAGATC 5580  
 QY 1885 IleuArgIleleuGlunGlunArgPheMetAlaSerAsnProSerlyValSerlyrGln 1904  
 Db 5581 CTCGCGAGCAGATGAGAGAGCGGTTCGTGCATCCATCTTCCAAAGTCTTACGAA 5640  
 QY 1905 ProIleThrThrleuLysArglysglnGlunGlunValSerAlaValIlelleGlnArg 1924  
 Db 5641 GCCTATCACACCTCTGCGCGCAACGAGAGAGGTGTCTGACAGTGTCTCGACCGT 5700  
 QY 1925 AlaTyrArgThrIleuLysleuLysArgThrVal-----LysGlnAlaSerPheThr 1941  
 Db 5701 GCCTACAGGGAGACACTTGGTAGCGGGGCTTTCATCTGCAAAAGATGGCTCTC----- 5754  
 QY 1942 TyrAsnLysAsnLysIleLysgllyAlaAsnleuIleLysgluAspMetIleIle 1961  
 Db 5755 -----AACAGCTGAGAAATGAG----- 5772  
 QY 1962 AspArgIleasnLysnSerIleThrGlunLysThrAspLeuThrMetSerThrAlaAla 1981  
 Db 5773 -----GGCACAACAGACAGACAAAGAGAGAGACCCCGCTCACAGCTCC 5817  
 QY 1982 CysProProSerTyrAspArgValThrLysProIleValGluLysHisGlu-----Gln 1999  
 Db 5818 CTC-----CCCTCTTACGACAGCTCACAAAGCCAGACAGAGAGAGAGAGCGGTGGAG 5874  
 QY 2000 GluGlyLysAspGluLysAlaLys 2007  
 Db 5875 GAGGGCAGAGGAGAAAGCCAG 5898

## RESULT 14

US-09-634-920-3  
 ; Sequence 3, Application US/09634920  
 ; Patent No. 6342357

## GENERAL INFORMATION:

; APPLICANT: Splawski, Igor  
 ; APPLICANT: Keating, Mark T.

TITLE OF INVENTION: ALTERATIONS IN THE LONG QT SYNDROME GENES KVLQ1 AND  
 TITLE OF INVENTION: SCNSA AND METHODS FOR DETECTING SAME  
 FILE REFERENCE: 2323-155  
 CURRENT APPLICATION NUMBER: US/09/634,920  
 PRIOR FILING DATE: 2000-08-09  
 PRIOR APPLICATION NUMBER: 60/190,057  
 PRIOR FILING DATE: 2000-03-17  
 PRIOR APPLICATION NUMBER: 60/147,488  
 PRIOR FILING DATE: 1999-08-09  
 NUMBER OF SEQ ID NOS: 4  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 3  
 LENGTH: 6048  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (1)..(6048)  
 US-09-634-920-3  
 Alignment Scores:  
 Pred. No.: 0 Length: 6048  
 Score: 6312.00 Matches: 1287  
 Percent Similarity: 72.72% Conservative: 230  
 Best Local Similarity: 61.70% Mismatches: 386  
 Query Match: 60.71% Indels: 184  
 Gaps: 30  
 US-09-930-871-12 (1-2009) x US-09-634-920-3 (1-6048)  
 QY 6 LeuValProProgluYProaspSerPheasnPheThrArggluSerleuAlaIle 25  
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 QY 26 GluArgArgIleAlaGluGluValAlaLysasnProLysProaspLysAsp----- 43  
 Db 73 GAGAGGCGCATGGCGGAGAGAAAGCAAGCCCGCGCTCAACACCTTCAGAGAGAGAG 132  
 QY 44 -----AspAspGluasnGlyProLysProasnSerAspLeuAlaGlyLysasnleu 61  
 Db 133 GGGCTGCCCGAGGAGAGAGCTCCCGGCCAGCTGACCTGCAGAGCGCTCCAAAAAGCTG 192  
 QY 62 ProheleThrlygluAspIleProProgluMetAlaSergluProleuGlunAsp 81  
 Db 193 CCAATATCTTATGCAATCCACCCAGAGCTCATCGAGAGCCCTGGAGAGCTTGAC 252  
 QY 82 ProTyrTrIleAsnLysLysThrPheIleValLeuasnLysGlyLysAlaIlePheArg 101  
 Db 253 CCTTCTATAGCACCCAAAGACTTTCATCTGATGATTAAGGCAAGACCATCTTCGG 312  
 QY 102 PheSerAlaThrSerAlaLeuTyrIleleuThrProPheasnProleuArgLysIleAla 121  
 Db 313 TTCAGTGCACCAAGCGCTTGTATGCTCCTGAGTCCCTCCACCAAGTTCGAGAGCGCT 372  
 QY 122 IleLysIleuValHisSerleuPheSerMetleuIleMetCysThrIleleuThrAsn 141  
 Db 373 GTGAGATTCGTGGTCACTGCTCTTCAACAGTCTCATCATGAGTGCATCATCCAGC 432  
 QY 142 CysValPheMetThrMetSerAsnProProaspTrpThrLysAsnValGluTyrThrPhe 161  
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 QY 162 ThrGlyIleTyrThrPhegluSerleuIleLysIleIleAlaArgGlyPheCysleuGlu 181  
 Db 493 ACCGCCATTATACCTTGTAGTCTGTGATCAAGATTGTGCTGAGCTTCTGCTGCAC 552  
 QY 182 AspPheThrPheleuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPheAla 201  
 Db 553 GCGTTCACTTTCCTCGGAGCCATGGAAGCTGGAGCTTGTAGTATTATCATGAGCA 612  
 QY 202 TyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgValleu 221  
 Db 613 TACACAACTGAATTGTGGACCTGGGCAATGTCTCAGCTTACCGCCTTCGAGTCTC 672





QY 1607 easphevalvalalleleuSerllevalglyMetpheleuallagluenuillegly 1627  
 DB 4782 CGACTGTGGTGTCAATCTTCATCGTGAGCACTGTGCGCATCATCAATCAACAA 4841  
 QY 1627 styPheValSerProthLeuPheArGValIleArGLeuAlaArgIleGlyArGIIe 1647  
 DB 4842 GTACTTCTTCCCGAGCGCTTCCAGATCATCCGCTGGCCGGAATAGCGCGCATCT 4901  
 QY 1647 uArgLeuIleArgIleValArgIleArgIleuPheAlaMetSerle 1667  
 DB 4902 CAGACTATCCGAGGCGCAAGGAGATCCGACGCTCTTTCCTTCATCATGATCTCCT 4961  
 QY 1667 uProAlaLeuPheAsnIleGlyLeuLeuPheValMetPheIleTyAlaIlePh 1687  
 DB 4962 GCGTGCCTCTTCAACATCGGCGTGTCTCTCTCTCATGTTCATCTCACTCATCTT 5021  
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 DB 5022 TGGCATGGCAACTTCCTTATGTCAAGTGGAGGCTGGCAATCGACATGTTCAACT 5081  
 QY 1707 eGluThrPheGlyAsnSerMetIleCysLeuPheGlnIleThrSerAlaGlyTPas 1727  
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 DB 5142 TGGCTCTCTCAGCCCTCAACACTGGGCGCGCTCTACTGAGCAACCCACTGCGCAA 5201  
 QY 1747 nProGlySerSerValLysGlyAspCysGlyAsnProSerValGlyIlePhePheVa 1767  
 DB 5202 CACCAATGCTCT---CGGGGGGAGCTGCGGAGCCGCGTGGGCACTCTTCTTCTCAC 5258  
 QY 1767 lSerTyIleIleIleSerPheLeuValValAsnMetTyIleAlaValIleuG 1787  
 DB 5259 CACCTACATCATCT 5318  
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 US-08-843-417-9  
 : Sequence 9, Application US/08843417  
 : Patent No. 6184349  
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 : GENERAL INFORMATION:  
 : APPLICANT: Herman, Ronald C  
 : APPLICANT: Delgado, Stephen G  
 : APPLICANT: Fish, Linda M  
 : APPLICANT: Sangameswaran, Lakshmi  
 : APPLICANT: Rabert, Douglas K  
 : TITLE OF INVENTION: CLONED PERIPHERAL NERVE  
 : TITLE OF INVENTION: TETRODOXIN-RESISTANT SODIUM CHANNEL alpha-SUBUNIT  
 : NUMBER OF SEQUENCES: 10  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Heller Eberman White & McAniff  
 : STREET: 525 University Ave  
 : CITY: Palo Alto  
 : STATE: CA  
 : COUNTRY: U.S.A.  
 : ZIP: 94301  
 :  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PatentIn Release #1.0, Version #1.30  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/843,417  
 : FILING DATE: April 15, 1997  
 : CLASSIFICATION: 536  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Schmonsees, William  
 : REGISTRATION NUMBER: 31,796  
 : REFERENCE/DOCKET NUMBER: 28340-P1  
 : TELEPHONE: (415)-324-7041  
 : TELEFAX: (415)-324-0638  
 : INFORMATION FOR SEQ ID NO: 9:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 5874 base pairs  
 : TYPE: nucleic acid  
 : STRANDEDNESS: unknown  
 : TOPOLOGY: unknown  
 : MOLECULE TYPE: CDNA  
 : HYPOHETICAL: NO  
 : ANTI-SENSE: NO  
 : US-08-843-417-9  
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 : Alignment Scores:  
 : Pred. No.: 0  
 : Score: 5555.00  
 : Percent Similarity: 68.128  
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 : Query Match: 53.438  
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QY 208 AspLeuGlyLysAlaSerIleLeuArgThrPheArgValLeuArgAlaLeuLysThrIle 227
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Db 679 TCTGTGATCCAGGCTGAGAGCTGATGTTGGGGCCCTGATTCACCTGAGAGAACTG 738
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QY 548 ArgTyrSerSerProHisGlnSerLeuLeuSerIleArgGlySerLeuPheSerProArg 567
Db 1447 -----AACACGCGCAGAGATGCTTTCTAGCGCTCCCTCTGGAAGAAC 1491
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GenCore version 5.1.4\_p5\_4578  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 23, 2003, 01:44:31 ; Search time 287 Seconds  
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Title: US-09-930-871-12

Perfect score: 10397

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Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 709820 seqs, 544064369 residues

Total number of hits satisfying chosen parameters: 1419640

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Command line parameters: -DEV-xlh  
-MODEL-frame+ p2n.model -DEV-xlh  
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Database: Published Applications\_NA:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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|------------|---------|-------------|--------|-------|------------------|
| 1          | 10393   | 100.0       | 6030   | 10    | US-09-930-871-11 |
| 2          | 10320.5 | 99.3        | 5997   | 10    | US-09-930-871-11 |
| 3          | 10197   | 98.1        | 5922   | 10    | US-09-930-871-13 |
| 4          | 10124.5 | 97.4        | 5889   | 10    | US-09-930-871-3  |

|    |        |      |      |    |                     |
|----|--------|------|------|----|---------------------|
| 5  | 8448.5 | 81.3 | 6822 | 10 | US-09-917-800A-1604 |
| 6  | 7511   | 72.2 | 4362 | 10 | US-09-930-871-15    |
| 7  | 7438.5 | 71.5 | 4329 | 10 | US-09-930-871-5     |
| 8  | 7181   | 69.1 | 4179 | 10 | US-09-930-871-17    |
| 9  | 7108.5 | 68.4 | 4146 | 10 | US-09-930-871-7     |
| 10 | 7105.5 | 68.3 | 4197 | 10 | US-09-930-871-19    |
| 11 | 7033   | 67.6 | 4164 | 10 | US-09-930-871-9     |
| 12 | 6312   | 60.7 | 6048 | 10 | US-09-840-125-3     |
| 13 | 6310   | 60.7 | 6048 | 9  | US-09-896-994-1     |
| 14 | 2037   | 19.6 | 1192 | 10 | US-09-864-761-10189 |
| 15 | 1967.5 | 18.9 | 1194 | 10 | US-09-864-761-18334 |
| 16 | 1933.5 | 18.6 | 1178 | 10 | US-09-864-761-26829 |
| 17 | 1655   | 15.9 | 969  | 10 | US-09-864-761-1576  |
| 18 | 1562.5 | 15.0 | 6501 | 9  | US-10-029-413A-3    |
| 19 | 1555   | 15.0 | 7193 | 9  | US-10-029-413A-17   |
| 20 | 1555   | 15.0 | 7193 | 9  | US-10-029-413A-19   |
| 21 | 1526.5 | 14.7 | 5565 | 9  | US-10-029-413A-1    |
| 22 | 1520.5 | 14.6 | 6816 | 10 | US-09-935-541-1     |
| 23 | 1520.5 | 14.6 | 6855 | 10 | US-09-935-541-3     |
| 24 | 1517   | 14.6 | 6160 | 9  | US-10-029-413A-11   |
| 25 | 1517   | 14.6 | 6160 | 9  | US-10-029-413A-13   |
| 26 | 1510.5 | 14.5 | 6503 | 10 | US-09-935-541-12    |
| 27 | 1502.5 | 14.5 | 6083 | 9  | US-10-029-413A-21   |
| 28 | 1484.5 | 14.3 | 6639 | 10 | US-09-917-800A-1586 |
| 29 | 1453.5 | 14.0 | 7362 | 9  | US-10-029-413A-15   |
| 30 | 1422.5 | 13.7 | 7011 | 12 | US-10-033-026-9     |
| 31 | 1408.5 | 13.5 | 7177 | 12 | US-10-033-026-7     |
| 32 | 1408.5 | 13.5 | 7364 | 10 | US-09-954-456-1179  |
| 33 | 1408.5 | 13.5 | 7364 | 12 | US-10-033-026-5     |
| 34 | 1402.5 | 13.5 | 7376 | 12 | US-10-033-026-3     |
| 35 | 1364.5 | 13.1 | 6615 | 9  | US-10-029-413A-9    |
| 36 | 992.5  | 9.5  | 5562 | 10 | US-09-030-482B-18   |
| 37 | 572    | 5.5  | 347  | 10 | US-09-864-761-31970 |
| 38 | 552    | 5.3  | 467  | 10 | US-09-864-761-15456 |
| 39 | 533    | 5.1  | 343  | 10 | US-09-030-482B-17   |
| 40 | 464    | 4.5  | 487  | 10 | US-09-864-761-15573 |
| 41 | 464    | 4.3  | 249  | 10 | US-09-864-761-32083 |
| 42 | 447    | 4.3  | 480  | 10 | US-09-864-761-10615 |
| 43 | 433    | 4.2  | 249  | 10 | US-09-864-761-27066 |
| 44 | 418    | 4.0  | 264  | 10 | US-09-864-761-27235 |
| 45 | 409    | 3.9  | 465  | 10 | US-09-864-761-10437 |

## ALIGNMENTS

RESULT 1  
US-09-930-871-11  
Sequence 11, Application US/09930871  
Patient No. US20020076780A1  
GENERAL INFORMATION:  
APPLICANT: Turner, C. Alexander Jr.  
APPLICANT: Mathur, Brian  
TITLE OF INVENTION: No. US20020076780A1 Human Ion Channel Proteins and Poly  
FILE REFERENCE: LEX-0216-USA  
CURRENT FILING DATE: 2001-08-14  
PRIORITY FILING DATE: 2000-08-16  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 11  
LENGTH: 6030  
TYPE: DNA  
ORGANISM: homo sapiens  
US-09-930-871-11

Alignment Scores:  
Pred. No.: 0  
Score: 10393.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Length: 6030  
Matches: 2009  
Conservative: 0  
Mismatch: 0

Query Match: 99.96% Indels: 0  
DB: 10 Gaps: 0  
US-09-930-871-12 (1-2009) x US-09-930-871-11 (1-6030)

QY 1 MetGluGlnThrValIleuValProGluProAspSerPheAsnPhePheThrArgGlu 20  
DB 1 ATGGAGCAACAGCTGCTTACACACAGACCTGACACCTTCACCTTCACACAGAGA 60  
QY 21 SerLeuAlaIleGluArgGileAlaGluGluValAlaLysAsnProLysProAsp 40  
DB 61 TCTCTGGGGCTATTGAAAGACGATTCACAGAAAGGCAAGAAATCCCAACACAG 120  
QY 41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60  
DB 121 AAAAAAGATGACGAGCAAAATGGCCCAAGCAAAATAGTGAAGCTGGAAGCTGAAAGAAC 180  
QY 61 LeuProPheIleTyrrGlyAspIleProGluMetValSerGluProLeuGluAspLeu 80  
DB 181 CTTCATTATTATGAGACATTCCTCCAGAGATGGTGACAGACCCCTGAGAGACCTG 240  
QY 81 AspProTyrrIleAsnLysLysThrPheIleValIleAsnLysGlyLysAlaIlePhe 100  
DB 241 GACCCCTACTATCAAAAGAAAATTTTATGATTAAGATTAAGAGAGGACCTATTC 300  
QY 101 ArgPheSerAlaThrSerAlaLeuTyrrIleLeuThrProPheAsnProLeuArgLysIle 120  
DB 301 CGGTTCAGTGGCCCTGCTGCTGATCAATTTAACTCCCTCAATCCTTAGAGAAATA 360  
QY 121 AlaIleLysIleLeuValHisSerLeuPheSerMetIleMetCysThrIleLeuThr 140  
DB 361 GCTATTAAAGATTGGTACATTCATTATTCAGACATGATTAATGATGACATATTTGACA 420  
QY 141 AsnGlyValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrrThr 160  
DB 421 AACGTGCTGTTATGACATATGATGACCTCTCTGATTTGGACAAAGATGTAATACACC 480  
QY 161 PheThrIleTyrrThrPheGluSerLeuIleLysIleAlaArgGlyPheCysLeu 180  
DB 481 TTCACAGAAATATATACTTTTGAATCACTTATAAATTAATATGCAAGGGAGTCTGTTTA 540  
QY 181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200  
DB 541 GAAATATTTACTTCTCCCTGGGATCCAGTCAAGTGGCTGCTGATTCATTCATTTT 600  
QY 201 AlaTyrrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220  
DB 601 GCGTACGTCACAGACTTTGTGACCTGGGCAATGCTCGGCAATGAGACATTCAGAGTT 660  
QY 221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240  
DB 661 CTCGAGACATGGAAGACATTTCAAGTCATTCAGGCTGAAACCATTTGTGGAGCCCTG 720  
QY 241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260  
DB 721 ATCCAGCTGTGAAGAACCTCTGAGATGATGATCCGACTGTGCTGTGCTGAGCTTA 780  
QY 261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280  
DB 781 TTTGCTCTAATATGGGCTGACACTGTCTCATGGGCAACCTGAGGAATTAATATACAAAG 840  
QY 281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyrr 300  
DB 841 CCTCCCAACCAATGCTCTCTGAGAGAACATAGTATAGAAAGATATATACCTGAAATAT 900  
QY 301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrrIleGlnAsp 320  
DB 901 AATGTCACACTTAATAAGAAAGCTCTTGAAGTTGACTGGAAGTCAATATATCAAAAT 960  
QY 321 SerArgTyrrHisTyrrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340  
DB 961 TCAGATATATCTATTTCTCTGAGGGTTTTTTATGATGACACTATATGGAATATAGCTCT 1020

QY 341 AspAlaGlyGlnCysProGluGlyTyrrMetCysValLysAlaGlyArgAsnProAsnTyrr 360  
DB 1021 GATGAGGCCCAATGTCACAGAGGATATATGCTGTGAAGAGCTGTGTGAATATCCCAATAT 1080  
QY 361 GlyTyrrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380  
DB 1081 GGCTACACAAAGCTTGTATACCTTCAGTTGGGCTTTTGTGCTGCTGCTGCTGCTGCTGCT 1140  
QY 381 GluAspPheTrpGluAsnLeuTyrrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrrMet 400  
DB 1141 CAGGACTTGGGAAATCTTTATACACTGACATTAACGTGCTGGGAAACGTRACATG 1200  
QY 401 IlePhePheValIleuValIlePheLeuGlySerPheTyrrLeuIleAsnLeuIleAla 420  
DB 1201 ATATTTTGTGTGTGTATTTCTTGGGCTCATTTCTACCTAATATTAATTTGATTCGGGCT 1260  
QY 421 ValValAlaMetAlaTyrrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440  
DB 1261 GTGGTGGCCATGGCTACAGAGGACAGAAATTCAGGCCACCTTGGAAAGAACCAACAGAAA 1320  
QY 441 GluAlaGluPheGlnGluMetIleGluGlnLeuLysLysGlnGlnGluAlaIleGlnGln 460  
DB 1321 GAGGCCGAATTTACAGACAGATGATTAACAGCTTAATAAACCAACAGAGGACCTCAGCAG 1380  
QY 461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480  
DB 1381 GCAGCAAGCGCAACCTGCTCAGACATTCACAGAGCCAGTGCAGCAGGCGCTCTA 1440  
QY 481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500  
DB 1441 GACAGCTCATCTGAAAGCCCTTAAGTTGACTTCAAGAGTGTCAAGAAAGAAATACCG 1500  
QY 501 ArgLysLysArgLysGlnLysGlnLysGlnSerGlyGlyGluLysAspGluAspGluPhe 520  
DB 1501 AGGAAGAAAGAAAGAAACAGAAAGACAGTCTGTGGGGAAGAAAGATGAGATGATATTC 1560  
QY 521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540  
DB 1561 CAAAATATGATCTGAGAGACAGATCAGAGAGAAAGTTTCCTTCCTCAATGAGAGG 1620  
QY 541 AsnArgLeuThrTyrrGluLysArgTyrrSerSerProHisGlnSerLeuLeuSerIleArg 560  
DB 1621 AACCATTTGACATATGAAGAAAGAGTACCTCCACACACCAATCTTGTGTGAGACATCT 1680  
QY 561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580  
DB 1681 GGCTCCCTATTTTACCAAGGCGAAATAGCAACAAAGCCTTTTACGCTTTAGAGGGCGA 1740  
QY 581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600  
DB 1741 GCAAGAGATGTGGATCTGAGAGACATTCGCAAGATGATGACACAGACCTTTAGAGAT 1800  
QY 601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620  
DB 1801 AACGAGAGCGGTAGAGATCTTGTGTGCCCCACAGCACAGAGAGAGAGCAACAGC 1860  
QY 621 AsnLeuSerGlnThrSerArgSerSerArgMetIleAlaValPheProAlaAsnGlyLys 640  
DB 1861 AACCTGATGACAGACAGTATGATATCCGAGATGCTGGGCAAGTGTTCACCGCAATGGAGAG 1920  
QY 641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyLysProSerValPro 660  
DB 1921 ATGCACAGACACTGTGATTCGAATGTGTGGTTCCTGCTGCTGCTGCTGCTGCTGCTGCT 1980  
QY 661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680  
DB 1981 ACATGCGCTGTGGACAGCTTCTCCAGAGGGGATGAATAAGATTAACCAAGCTACTGATGAC 2040  
QY 681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerPheHisValSer 700  
DB 2041 AATGGAACACCACTGAACACTGAATGAGAAAGAGAGAGGTCAAGTTCTTCCACGCTTCC 2100  
QY 701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAsnSerIleLeu 720

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Db 2101 ATGGACCTTCTAGAGATCCCTCCAAAGCAGCAGCAATGATATGCGCATTTCTA 2160  
Qy 721 ThrAsnThrValGluGluLeuGluGluSerArgGlnTyrScyProProCysTrpTyrLys 740  
Db 2161 ACAATATACAGTAAAGAACTTGAAGAAATCCAGCGCAAAATGGCCACTGGTGGATATAA 2220  
Qy 741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysIleVal 760  
Db 2221 TTTTCCAAATATCTTATCTATGCGAGCTGTCATATGTTGTTAAAGTAAACATGTT 2280  
Qy 761 ValAsnLeuValIleMetAspProPheValAspLeuValIleThrIleCysIleValLeu 780  
Db 2281 GTCAACCTGGTGTGATGAGCCATTGTGTGACCTGGCCATCCACATCTGATGTCTTA 2340  
Qy 781 AsnThrLeuPheMetAlaMetGluHisTyrProMetLysPheAspIlePheAsnValLeu 800  
Db 2341 AATACCTTTTCATGCGCATGAGCAGCATATCCAAATGAGGACCATTTCAATATGCTT 2400  
Qy 801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820  
Db 2401 ACAGTAGAGAACTTGTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAATATAT 2460  
Qy 821 AlaMetAspProTyrTrpTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840  
Db 2461 GCCATGGATCCCTTACTATATATTTCCAAAGAGCGTGAATATCTTGTACCGTTTATGTG 2520  
Qy 841 ThrLeuSerLeuValGluLeuGlyLeuValAsnValGluGlyLeuSerValLeuArgSer 860  
Db 2521 ACGCTTACCTGGTGAACCTTGAGACTCGCCAAATGAGCAAGATTTATCTTCTCCGTTC 2580  
Qy 861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880  
Db 2581 TTTGCATGCTGCGAGTTTTCAGATTGGCAAAATCTTGCCCAACGTTAAATGTCAATA 2640  
Qy 881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900  
Db 2641 AAGATCAGTCGGCAATTCCTGGGCGTCGGAATTTAAACCTGCTGTCGCCATCAGTC 2700  
Qy 901 ValPheIlePheAlaValAlaIleValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920  
Db 2701 GTCTTCATTTTGGCGTGGTGGCATGCAAGCTTTTGTGTAATAAGCTACAAAGATTGTGTC 2760  
Qy 921 CysLysIleAlaSerAspGlyLeuProArgTrpHisMetAsnAspPheHisSer 940  
Db 2761 TGCAGATGCGCAGATGATGTCACCTCCACGCTGGCACATGATACCTTCTCCACTCC 2820  
Qy 941 PheLeuIleValPheArgValLeuGlyGlyIleTrpIleGluThrMetTrpAspCysMet 960  
Db 2821 TTCCGATTTGTTCCGCTGCTGCTGGTGGAGTGGATGAGACCCATGCGGAGCTGTATG 2880  
Qy 961 GluValAlaGlyAlaIleMetCysLeuThrValPheMetMetValMetAlaIleGlyAsn 980  
Db 2881 GAGGTTGCTGGTCAAGCCATGTGCTTACTGCTTCATGATGCTCATGATTTGGAAC 2940  
Qy 981 LeuValIleLeuAsnLeuPheLeuAlaLeuLeu\*\*\*SerSerPheSerAlaAspAsnLeu 1000  
Db 2941 CTAGTGGTCCGTAATCTCTTCTGGCCCTGCTTGTGAGCTCATTTAGTCAGACACCT 3000  
Qy 1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020  
Db 3001 CGAGCCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3060  
Qy 1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnIleSerPheIleArg 1040  
Db 3061 AAGAGTAGTCTTATGTGAAAGAAATATATGATTTATTCACAGTCCCTTCATTAGG 3120  
Qy 1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnLysLysAspSer 1060  
Db 3121 AAACAAGAAATTTAGATGAATTAACAACCTGATGATCTAACAACAAGAAAGACAGT 3180  
Qy 1061 CysMetSerAsnHisThr\*\*GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080  
|||||

Db 3181 TGTATGTCATCATCAGACAGAAATGGGAAGATCTTGACTATCTTAAGATGTAAAT 3240  
Qy 1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100  
Db 3241 GGAACTACAAAGGTGTATGAGAACCTGGCAGCAGGTGTGAAAAAATCATTTATGTGAAGT 3300  
Qy 1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120  
Db 3301 GATTACATGTCATTCATTAACAACCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3360  
Qy 1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140  
Db 3361 GAATCGACTTGAATAATTTAAACAGCAAGACCTTATGATGATGATGATGATGATGATG 3420  
Qy 1141 SerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGly 1160  
Db 3421 AGCAAGACAAACTGATGATGAACAGCATAGCTCATCAGAAAGTACGTGCGCATCCGCC 3480  
Qy 1161 AlaProValGluGluGlnProValIleGluProGluGluThrLeuGluProGluAlaCys 1180  
Db 3481 GCACCTGTAGAAAGACAGCCGTAAGAGAACTGAGAAACCTTGAAACCAAGAGCTTGT 3540  
Qy 1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleLeuValGluGluArg 1200  
Db 3541 TTCACGTGAAGCTGTGTACAAATTCATCACTGTTGCAATTCATTCATTCATTCATTCAT 3600  
Qy 1201 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe 1220  
Db 3601 GGAAACAAATGGTGAAGACCTGAGAAAGACGTTGTTCCGATGATGTAACATTAATCGT 3660  
Qy 1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240  
Db 3661 GAAACCTCATTTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3720  
Qy 1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGlnTyrAlaAspLysValPheThr 1260  
Db 3721 TATATGATCAGCGAAAGACGATTAAGACCATGTGTGAATATGCTGACAAAGTTTCACT 3780  
Qy 1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrPhe 1280  
Db 3781 TACATTTTCATCTCGAAAGCTTCTTAAATGGGTGCAATATGCTTCAACATATATTC 3840  
Qy 1281 ThrAsnAlaTrpProSerTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300  
Db 3841 ACCAATGCTCGGTGGTGGGCTGCTTATATGTTATGTTATGTTATGTTATGTTATG 3900  
Qy 1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320  
Db 3901 GCAATGCTTGGGTTACTGAGAACTTGAGCCATCAATCTTCAGACACTAAGAGCT 3960  
Qy 1321 LeuArgProLeuArgAlaLeuSerArgPheGluGluIleMetArgValValAlaAsnAlaLeu 1340  
Db 3961 CTGAGACCTTAAGAGCTTATCTCGATTTGAAGAGTGAAGGGTGTGTAATGCCCTT 4020  
Qy 1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIle 1360  
Db 4021 TTAGAGCAATTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 4080  
Qy 1361 PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThr 1380  
Db 4081 TTCAAGCATCATGGCGTAATTTGTTGCTGGCAAAATTCATCACTGATATTAACACACA 4140  
Qy 1381 ThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIle 1400  
Db 4141 ACTGCTAGACAGGTTTGACATCGAAAGACGTGATATATCATCTGATGCTTAAACTATA 4200  
Qy 1401 GluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyPhe 1420  
Db 4201 GAAAGAAATAGACTGCTCATGAGAAAAAGTGAATAAATCTTGATATGTGAGATT 4260  
Qy 1421 GlyTyrLeuSerLeuGluGlnValAlaThrPheLysGlyTrpMetAspIleMetTyrAla 1440  
Db 4261 GGGATCTCTCTTCTTCAAGTTGCCACATTCAAAGATGATGATATATATATGCA 4320  
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QY 1441 AlaValAspSerArgAsnValGluLeuGlnProLysTyrGluGlnSerLeuTyrMetTyr 1460  
 DB 4321 GCGATGATTCAGAAATGGAGAACCTCAGATGATGAAAGAACTGTCATCTAT 4380  
 QY 1461 LeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIleGly 1480  
 DB 4381 CTTTACTTGTATTTTCATCATCTTTGGGTCTTCTTCACTTGAACCTGTTATTTGGT 4440  
 QY 1481 ValIleIleAspAsnPheAsnGlnGlnIleLysLysPheGlyGlnAspIlePheMet 1500  
 DB 4441 GTCATCATGATTAATTTCAACAGAGAAAGAGTTGGAGGTCAAGCATCTTATG 4500  
 QY 1501 ThrGluGluGlnLysLysTyrTyrAsnAlaMetLysLysLeuGlnSerLysLysProGln 1520  
 DB 4501 ACAGAGAAACAGAGAAATACATTAATGCAATGAAAAATAGATCGAAAAACCGCAA 4560  
 QY 1521 LysProIleProArgProGlnArgLysAsnLysPheGlnGlyMetValPheAspPheValThrArg 1540  
 DB 4561 AACCTATACCTCGACAGAGAAACAAATTTCAAGAAATGCTTTGACTTCGTACACAGA 4620  
 QY 1541 GlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMetMetVal 1560  
 DB 4621 CAAGTTTTCAGACATAGCATCATGATTCATCTGCTTACATGGTCACAAATGATGCTG 4680  
 QY 1561 GluThrAspAspGlnSerGluTyrValThrThrIleLeuSerArgIleAsnLeuValPhe 1580  
 DB 4681 GAACAGAGAGACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4740  
 QY 1581 IleValIlePheThrGluGlyLysValIleLysLeuIleSerLeuArgHisTyrTyrPhe 1600  
 DB 4741 ATTTGGCTATTTACTGGAGAGGTGTACTGAACCTCATCTCTACGCCATTTATTTT 4800  
 QY 1601 ThrIleGlyTyrAsnIlePheAspPheValValIleLeuSerIleValIleGlyMetPhe 1620  
 DB 4801 ACCATTTGATGGAATTTTGTGATTTGTGTTGTGTTGTGTTGTGTTGTGTTGTGTTGT 4860  
 QY 1621 LeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPheArgValIleArgLeu 1640  
 DB 4861 CTTGGCCGAGCTGATAGAAAAAGTATTCGTGCTCCCTACCTGTCGAGATGCCCTT 4920  
 QY 1641 AlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLeuLeu 1660  
 DB 4921 GCTTAGGATGGCGGAATCTTACGTCGTGATCAAGAGCAAGGGGATCCGACGTCGTC 4980  
 QY 1661 PheAlaLeuMetMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuPheLeuVal 1680  
 DB 4981 TTTGCTTTGATGATGATGCCCTTCTGCGTTGCTTAAACATGGCCCTTACTCTTCTAGTC 5040  
 QY 1681 MetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgGluValGly 1700  
 DB 5041 ATGTCATCATTCAGCATCTTTGGGATGTCCAACTTGTCTATTAAGAGGAAGTTGGG 5100  
 QY 1701 IleAspAspMetPheAsnGlnGluThrPheGlyAsnSerMetIleCysLeuPheGlnIle 1720  
 DB 5101 ATCGATGATGATTCACATTTGAGACCTTTGGCAACAGATGATGATGATGATGATGATG 5160  
 QY 1721 ThrThrSerAlaGlyTyrPheGlyLeuLeuAlaProIleLeuAsnSerLysProAsp 1740  
 DB 5161 ACAACCTCGCGCGGTGGGATGATGATGATGATGATGATGATGATGATGATGATGATG 5220  
 QY 1741 CysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsnProSer 1760  
 DB 5221 TGTGACCTTAATTAAGTTAACCTGAGAGCTGATTAAGAGGAGACTGTGGAAACCATCT 5280  
 QY 1761 ValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValValAsnMet 1780  
 DB 5281 GTTGAATTTTCTTTTGTCTGATTCATCATCATCATCATCATCATCATCATCATCATCAT 5340  
 QY 1781 TyrIleAlaValIleLeuGlnAsnPheSerValAlaThrGluGlnSerAlaGluProLeu 1800  
 DB 5341 TACATCGCGGTGATCCTGGAGAACTTCACTGTGTGATGAGAAAGTGCACAGACCTCTG 5400

QY 1801 SerGluAspAspPheGluMetPheTyrGluValIleProLysPheAspProAspAlaThr 1820  
 DB 5401 AGTGAGATGATCACTTTGAGATGTTCTATGAGTTGGAGAAATTTGATCCGATGCAACT 5460  
 QY 1821 GlnPheMetGluPheGluLysLeuSerGlnPheAlaIleAlaLeuGluProProLeuAsn 1840  
 DB 5461 CAGTTTCAGAAATTTGAAAAATTAATTCAGTTTGCACCTGGCTTGAACCGCTTCAT 5520  
 QY 1841 LeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSerGlyAsp 1860  
 DB 5521 CTGGCAACAAACAAACCAACCTCAGCTCATTTGCCATGATTTGCCATGGTAGTGAGAC 5580  
 QY 1861 ArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlnGluSerGly 1880  
 DB 5581 CGGATCCAGCTGCTGATATCTTATTTGCTTTTACAAAGCGGGTTCAGAGAGAGTGA 5640  
 QY 1881 GluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsnProSerLys 1900  
 DB 5641 GAGATGATGCTCTTACAGAAATGAGATGAGAGAGAGATTCATGCTCCATCTCCAG 5700  
 QY 1901 ValSerTyrGlnProIleThrThrThrLeuLysArgGlyGlnGluValSerAlaVal 1920  
 DB 5701 GTCTCCATAGCCCATCATCATCTTAAACGAAACAGAGAGAGATGCTGCTGTC 5760  
 QY 1921 IleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGlnAlaSerPhe 1940  
 DB 5761 ATATTCAGAGCTGCTTACAGACGCACTTTAAAGGAACTGTAAACAAAGCTCTCTT 5820  
 QY 1941 ThrTyrAsnLysAsnLysIleLysGlyAlaAsnLeuLeuIleLysGluAspMetIle 1960  
 DB 5821 ACCTACAAATTAACAAACAAACAAAGGTGGGCTTAACTCTTATTAACAAAGCATGATA 5880  
 QY 1961 IleAspArgIleAsnGlnAsnSerIleThrGlnLysThrAspLeuPheMetSerThrAla 1980  
 DB 5881 ATTAGCAGAAATTAATGAATCTTATTAACGAAAACTATCTGACCATGTCACATGCA 5940  
 QY 1981 AlaCysProProSerTyrAspArgValThrLysProIleValGluLysHisGluGlnGlu 2000  
 DB 5941 GCTTTCACACTTCCTATGACGCGGTGACAAACCAATTTGTGAAAAACTGACAAAGA 6000  
 QY 2001 GlyLysAspGluLysAlaLysGlyLys 2009  
 DB 6001 GGCAAAGATGAAAAACCAAGGAA 6027

RESULT 2  
 US-09-930-871-1  
 : Sequence 1, Application US/09930871  
 : Patent No. US20020076780A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Turner, C. Alexander Jr.  
 : APPLICANT: Mathur, Daniel  
 : APPLICANT: Mathur, Brian  
 : TITLE OF INVENTION: No. US20020076780A1 Human Ion Channel Proteins and Polynuc.  
 : FILE OF INVENTION: Same  
 : FILE REFERENCE: LEX-0216-USA  
 : CURRENT APPLICATION NUMBER: US/09/930,871  
 : PRIOR APPLICATION NUMBER: US 60/225,989  
 : NUMBER OF SEQ ID NOS: 20  
 : SOFTWARE: FastSeq for Windows Version 4.0  
 : SEQ ID NO 1  
 : LENGTH: 5997  
 : TYPE: DNA  
 : ORGANISM: homo sapiens  
 : US-09-930-871-1

Alignment Scores:  
 Pred. No.: 0 Length: 5997  
 Score: 10320.50 Matches: 1998  
 Percent Similarity: 99.458 Conservative: 0  
 Best Local Similarity: 99.458 Mismatches: 0  
 Query Match: 99.268 Indels: 11

DB: 10 Gaps: 1  
US-09-930-871-12 (1-2009) x US-09-930-871-1 (1-5997)  
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DB 1 ATGAGCAACAGCTGCTTGTACACAGAGCTGACAGCTTCACTTCACACAGAGA 60  
QY 21 SerLeuAlaAlaIleGIuArgArgIleAlaGIuGIuLysAlaLysAsnProLysProAsp 40  
DB 61 TCTCTGGCGCTATTGAAAGAGCATTTGCAGAAAGCAAGCAATGCCAAACAGAGC 120  
QY 41 LysLysAspAspAspGIuAsnGIuProLysProAsnSerAspLeuGIuAlaGIuLysAsn 60  
DB 121 AAAAAAGATGACGAGAAATGAGCCCAAGCAATAGGACTTGGAGCTGGAAAGAAC 180  
QY 61 LeuProPheIleTyrGIuAspIleProProGIuMetValSerGIuProLeuGIuAspLeu 80  
DB 181 CTTCATTATTATTAGAGACATTCCTCCAGAGATGCTCCAGAGCCCTGGAGAGCTG 240  
QY 81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGIuLysAlaIlePhe 100  
DB 241 GACCCCTACTATATCAATGAAAGAACTTTATGATTAATGAAAGAGAGCCACTTC 300  
QY 101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120  
DB 301 CGGTTACAGGCGACCTGCTCCCTGACATTTAACTCCCTCAATCCTTGAAGAAAAA 360  
QY 121 AlaIleLysIleLeuValHisSerLeuPheSerMetIleIleMetCysThrIleLeuThr 140  
DB 361 GCTATTAAAGATTGGTACATTCATTATTACAGATCTTAATATGCGCTATTGGA 420  
QY 141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGIuTyrThr 160  
DB 421 AACTGTGTATTATGCAATGATGTAACCTCGATTTGAGCAAGAAATGATGATACAC 480  
QY 161 PheThrGIuIleTyrThrPheGIuSerLeuIleLysIleIleAlaArgGIuPheCysLeu 180  
DB 481 TTCACAGGAAATATACCTTTGATATCACTTAAATAATATGCAAGGGGATCTCTTTA 540  
QY 181 GIuAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200  
DB 541 GAAGATTACTTCTCTGCGATTCATGCAAGACTGCTGATTCCTGCTCATTTACATTT 600  
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QY 221 LeuArgAlaLeuLysThrIleSerValIleProGIuLeuLysThrIleValGIuAlaLeu 240  
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QY 241 IleGIuSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260  
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QY 281 ProProThrAsnAlaSerLeuGIuGIuHisSerIleGIuLysAsnIleThrValAsnTyr 300  
DB 841 CCTCCACCAAACTCTCTCTGAGAGCAATGATATGAAAGAAATTAACCTGGAATTAAT 900  
QY 301 AsnGIuThrLeuIleAsnGIuThrValPheGIuPheAspTrpLysSerTyrIleGIuAsp 320  
DB 901 AATGGACACTTAAATATAAACTGTCTTGAAGTTGACTGGAAGCATATATATCAAGAT 960  
QY 321 SerArgTyrHisTyrPheLeuGIuGIuPheLeuAspAlaLeuLeuCysGIuLysSerSer 340  
DB 961 TCAGATATCATATTATCTCTGAGAGGCTTTTATGATGCACTATATGTAATAATACCTCT 1020  
QY 341 AspAlaGIuGIuCysProGIuGIuTyrTyrMetCysValLysAlaGIuArgAsnProAsnTyr 360

DB 1021 GATGACGGCCCAATGCTCAGAGGATATGCTGTGTAAGAGCTGTGAAATCCCATTTAT 1080  
QY 361 GIuTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380  
DB 1081 GCTACACAAAGCTTCAATACCTTCACTGAGTGGCTTTTGTCTCTGTTGCAATTAAGACT 1140  
QY 381 GIuAspPheTrpGIuAsnLeuTyrGIuLeuThrLeuArgAlaAlaLysThrTyrMet 400  
DB 1141 CAGGACTCTGGGAAATTTTATCACTGACATTAAGCTGCTGGGAAAGGTACATG 1200  
QY 401 IlePhePheValIleValIlePheLeuGIuSerPheTyrLeuIleAsnLeuIleAla 420  
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QY 421 ValValAlaMetAlaTyrGIuGIuGIuAsnGIuAlaThrLeuGIuGIuAlaGIuLys 440  
DB 1261 GTGTGCGCATGCGCTACAGAGAACAGAAATCAGCCACTTGGAGACAGAACAGAAA 1320  
QY 441 GIuAlaGIuPheGIuGIuMetIleGIuGIuLeuLysLysGIuGIuAlaGIuGIu 460  
DB 1321 GAGGCGGAATTTTCAGCAGATGATGTAACAGCTTAAACACACAGAGCGCTCAGCAG 1380  
QY 461 AlaAlaThrAlaThrAlaSerGIuHisSerArgGIuProSerAlaAlaGIuArgLeuSer 480  
DB 1381 GCAAGCAAGGCACTGCTCAGACATTCACAGAGCCCAAGTGCAGCAGGCGCTCTCA 1440  
QY 481 AspSerSerSerGIuAlaSerLysLeuSerSerLysSerAlaLysGIuArgArgAsnArg 500  
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QY 561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGIuArg 580  
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DB 1741 GCAAGAGATGTGGATCTGAG 1800  
QY 601 AsnGIuSerArgArgAspSerLeuPheValProArgArgHisGIuGIuArgArgAsnSer 620  
DB 1801 AACGAGAGCGGTGAGATTCCTTGTGTGCTCCCGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860  
QY 621 AsnLeuSerGIuThrSerArgSerSerArgMetLeuAlaValPheProAlaAsnGIuLys 640  
DB 1861 AACCTGAGTCAGACAGTGTGATCCCGAGATGCTGCGAGTGTTCAGAGAGAGAGAGAGAG 1920  
QY 641 MetHisSerThrValAspArgAsnGIuValValSerLeuValGIuGIuProSerValPro 660  
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QY 661 ThrSerProValGIuGIuLeuLeuProGIuValIleIleAspLysProAlaThrAspAsp 680  
DB 1981 ACATGCGCTGTGGAGAGCTTCTGCCAGAG 2040  
QY 681 AsnGIuThrThrThrGIuThrGIuMetArgLysArgArgSerSerPheHisValSer 700  
DB 2011 ---GGAACAACACCTGAATGAAATGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2067  
QY 701 MetAspPheLeuGIuAspProSerGIuArgArgArgAlaMetSerIleAlaSerIleLeu 720



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Db 2188 TTTTCCAAATATCTTATATCTGGAGACTGTTCTCATATGTGTTAAAGTGAACATGTT 2247  
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Oy 781 AsnThrLeuPheMetAlaMetGluHisTyrPrometThrAspHisPheAsnAsnValLeu 800  
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Oy 861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrrProThrLeuAsnMetLeuIle 880  
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Oy 921 CysLysIleLeuSerAspCysGlnLeuProArgTrrPHisMetAsnAspPheHisSer 940  
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 5188 TGTGACCTTAATAAGTAAACCTCGAAGCTGATTAAGAGAGAGCTGGGAACCCCATCT 5247  
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 5308 TACATCCGCGTCACTCGAAGAACTCAAGTTGCTCACTGAAAGAAAGTGAAGAGCCCTG 5367  
 1801 SerGluAspAspPheGluMetPheTyrGluValIleProLysPheAspProAspAlaThr 1820

5368 AGTACAGATGATCTTACAGATGTTCTATGAGGTTTGGAGAAAGTTGATCCGATGCACT 5427  
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 5548 CGGATCCACTGCTTATATCTTATTTGCTTTTACAAAGCGGCTTACGAGAGAGTGA 5607  
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 5668 GTCTCTATCAGCAATCACTACTACTTAAAGCAAAACAGAGAGAGATTTGCTGTC 5727  
 1921 IleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGlnAlaSerPhe 1940  
 5728 ATTATTCAGGCTGCTTACAGACGCCACACTTTTAAAGCAATCTTAAAGCAAGTCTCTT 5787  
 1941 ThrTyrAsnLysAsnLysIleLysGlyAlaAsnLeuLeuIleLysGluAspMetIle 1960  
 5788 ACCTACAAATTAACAAACAAAGAGTGGGCTTAATCTTCTTAAAGAAAGACATGATA 5847  
 1961 IleAspArgIleAsnGluAsnSerIleThrGluLysThrAspLeuThrMetSerThrAla 1980  
 5848 ATGACAGAAATTAATGAAACTTATTAAGAAAACTATCTGACCATGTCACATGCA 5907  
 1981 AlaCysProProSerTyrAspArgValThrLysProIleValGluLysHisGluGlnGlu 2000  
 5908 GCTTGTCCACTTCTTATGACCGGCTGACAAAGCAATTTGTGAAAAACATGACAAAGAA 5967  
 2001 GlyLysAspGluLysAlaLysGlyLys 2009  
 5968 GCGAAAGATGAAAAAGCCAAAGGGA 5994

RESULT 3.  
 US-09-930-871-13  
 ; Sequence 13, Application US/09930871  
 ; Patent No. US20020076780A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Turner, C. Alexander Jr.  
 ; APPLICANT: Mathur, Daniel  
 ; APPLICANT: Mathur, Brian  
 ; TITLE OF INVENTION: NO. US20020076780A1 Human Ion Channel Proteins and Polyr  
 ; FILE REFERENCE: Lex -0216-USA  
 ; CURRENT APPLICATION NUMBER: US/09/930, 871  
 ; CURRENT FILING DATE: 2001-08-14  
 ; PRIOR APPLICATION NUMBER: US 60/225, 389  
 ; PRIOR FILING DATE: 2000-08-16  
 ; NUMBER OF SEQ ID NOS: 20  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 13  
 ; LENGTH: 5922  
 ; TYPE: DNA  
 ; ORGANISM: homo sapiens  
 ; US-09-930-871-13

Alignment Scores:  
 Pired. No.: 0  
 Score: 10197.00  
 Percent Similarity: 100.00%  
 Best Local Similarity: 100.00%  
 Query Match: 98.08%  
 DB: 10  
 Length: 5922  
 Matches: 1972  
 Conservative: 0  
 Mismatches: 0  
 Indels: 0  
 Gaps: 0

US-09-930-871-12 (1-2009) x US-09-930-871-13 (1-5922)

Oy 1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhenThrArgIu 20  
 Db 1 ATGGAGCAAAAGCTCTGTACCCAGAGACCTGACGCTCAACCTCTTCCACGAGAGA 60  
 Oy 21 SerLeuAlaAlaIleGluArgArgIleAgluGluIuLysAlaLysAsnProLysProAsp 40  
 Db 61 TCTCTGGGGCATATGAAGAAGCAGATGAGAGAAAGGAGAAAGATCCCAACAGAGC 120  
 Oy 41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAgluLysAsn 60  
 Db 121 AAAAAAGATGAGAGCAAAATGCCCCCAAGCCAAATAGAGCTTGAGAGCTGAGAAAGAAC 180  
 Oy 61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80  
 Db 181 CTTCCATTTATTTATGAGACATTCCTCCAGAGATGAGTCCAGAGCCCTCGAGAGACCTG 240  
 Oy 81 AspProTyrTyrIleAsnLysLysThrPheIleValIleAsnLysGlyLysAlaIlePhe 100  
 Db 241 GACCCCTACTATATCAATATAGAAAACCTTTATAGATTAATTAAGGAGAGCCATCTTC 300  
 Oy 101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120  
 Db 301 CGGTCAGATGCCACCTGCTGCTGACATTTAACTCCCTCAATCCCTCTTAGAAATA 360  
 Oy 121 AlaIleLysIleLeuValHisSerLeuPheSerMetIleIleMetCysThrIleLeuThr 140  
 Db 361 GCTATTAAGATTTGGTGCATTCATTCATTCACAGATGCTAATATATGACATTTTGGACA 420  
 Oy 141 AsnCysValPheMetThrMetSerAsnProProAspTyrThrLysAsnValGluTyrThr 160  
 Db 421 AACTGTGCTTATATACATATGATGTAACCTCTGATGAGACAAAGATATACAAATACACC 480  
 Oy 161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180  
 Db 481 TTCACAGAAATATATACCTTTGAATCACCATTATATAAAATATATGCAAGGGAGATTCGTTTA 540  
 Oy 181 GluAspPheThrPheLeuArgAspProTyrPheAsnThrPheLysPheThrValIleThrPhe 200  
 Db 541 GAAGATTTTACTCTCTCGGATCCAGATGCAAGAACTGGCTCGATTCATCTCATTCATTT 600  
 Oy 201 AlaTyrValThrGluPheValAspLeuGluAsnValSerAlaLeuArgThrPheArgVal 220  
 Db 601 GCGTACGTCACAGAGATTTGTGACCTGGGCAATGTCTGGCATTTAGAAATCATTCAGAGTT 660  
 Oy 221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240  
 Db 661 CTCCGAGCATTGAAAGACATTTCACTCATTCAGAGCCGTAAGAACCATTTGTGGAGCCCTG 720  
 Oy 241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260  
 Db 721 ATCCAGCTGTGAGAGAGCTTCAGATGTAATGATCTGACGTGTCTGTGAGCGTA 780  
 Oy 261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTyr 280  
 Db 781 TTTGCTCATTTGGGCTGACGCTGTTCATGGCAACCTGAGAAATATATGATACATG 840  
 Oy 281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300  
 Db 841 CCTCCACCAATGCTTCTTGGAGAGACATAGTATAGAAAGAAATATATACCTGAAATAT 900  
 Oy 301 AsnGlyThrIleLeuIleAsnGluThrValPheGluPheAspTyrPlySerTyrIleGlnAsp 320  
 Db 901 AATGATACACTTAATAAGAACTGCTTTGAGTTGAGTTCATGATATATTTCAAGAT 960  
 Oy 321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyLysAsnSer 340  
 Db 961 TCACATATCATATATTTCTCGAGAGGTTTATAGATGCACATCTATATGGAATATAGCTCT 1020  
 Oy 341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360

Db 1021 GATGAGGCCAATGTCAGAGGATATATGCTGTGAAAGCTGTAGAAATCCCAATAT 1080  
 Oy 361 GlyTyrThrSerPheAspThrPheSerThrPalaPheLeuSerLeuPheArgLeuMetThr 380  
 Db 1081 GGCTACACAGAGCTTTGATACCTTCAGATGGCTTTTGTCTCTGTTGAGCAATAGACT 1140  
 Oy 381 GluAspPheThrPgluAsnLeuTyrGlnLeuThrLeuArgAlaIleGlyLysThrTyrMet 400  
 Db 1141 CAGAGCTTCTGGGAAATCTTATACAGCATATACGTGCGTGGGAGAAAGCTACAG 1200  
 Oy 401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420  
 Db 1201 ATATTTTGTGTGTGTCATTTCTTGGGCTCATTCATTCATTAATTAATTTGATCCGCT 1260  
 Oy 421 ValValAlaMetAlaIleTyrGluGluGluAsnGlnAlaIleThrLeuGluGluIleGluLys 440  
 Db 1261 GTGTGGCCATGTGCTTACAGAGAGACAAATACAGGCCCTTGGAGAACAGAGAGAA 1320  
 Oy 441 GluAlaGluPheGlnGluMetIleGluGluLeuLysLysGlnGluIleAlaIleGln 460  
 Db 1321 GAGGCCGAATTTACACAGATATGATTAACAGCTTAATAAGCAACAGAGGACCTCAGAG 1380  
 Oy 461 AlaIleThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaIleArgLeuSer 480  
 Db 1381 GCAGCAAGCGCAACTGCTCAGACATTCACAGAGAGCCAGAGGAGAGGAGGCTCTCA 1440  
 Oy 481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500  
 Db 1441 GACAGCTCATCTGAAGCCCTCTAAGTTGAGTTCCAAAGAGTGTAGGAAAGAAATCCG 1500  
 Oy 501 ArgLysLysArgLysGluLysGluGlnSerGlyGluGluLysAspGluAspGluPhe 520  
 Db 1501 AGAAGAAAGAAAGAAACAGAAAGAGAGCTGTGGTGGAGAGAAAGATAGAGATGATATC 1560  
 Oy 521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540  
 Db 1561 CAAAATCTGAAATCTGAGAGACAGATCAGAGAGAAAGGTTTCGCTTCCATTTGAGAGG 1620  
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 Db 1621 AACCATTGACATATAGAAAGAGGTACCTCCCAACCACTCTTGTGTGAGCATCCCT 1680  
 Oy 561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580  
 Db 1681 GGCTCCCTATTTTCCACAAAGCGAAATAGCAGAAAGAGCTTTTCACTTTAGAGGCGA 1740  
 Oy 581 AlaLysAspValGlySerGluAsnAspPheAlaAspArgLysIleSerThrPheGluAsp 600  
 Db 1741 GCAAGAGATGTGGATCTGAGAAACGACTTCGAGATGATGACACAGACACTTTGAGAT 1800  
 Oy 601 AsnGluSerArgArgAspSerLeuPheValProAlaGlyHisGlyLysArgArgAsnSer 620  
 Db 1801 AACGAGAGCCGTAGAGATTTCTTGTGTGCTCCCAACAGACAGAGAGAGAGCAACAC 1860  
 Oy 621 AsnLeuSerGlnThrSerArgSerSerArgMetIleAlaValPheProAlaAsnGlyLys 640  
 Db 1861 AACCTGATGACAGACAGATAGATCCCGATGCTGGAGATTTTCCACCGAATGGAGAG 1920  
 Oy 641 MethIleSerThrValAspCysAsnGlyValValSerLeuValGlyLysProSerValPro 660  
 Db 1921 ATGCACACACAGTGTGATGCAATGTGTGTTCTTGGTGTGGAGACTTCAGTCTCT 1980  
 Oy 661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680  
 Db 1981 ACATCTGCTGTGTGACACTTCTGCAAGAGGTGATTAATAGAAACCACTACTGATGAC 2040  
 Oy 681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerPheHisValSer 700  
 Db 2041 AATGCAACACACATGAAATGAAATGAAAGAGAGAGGTCAGATTTTCCAGCTTTCC 2100  
 Oy 701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720  
 Db 2101 ATGACCTTTTAGAAGATCTTCCCAAGAGAGAGAGCAAGGATATGACGAGCATTTCTA 2160

QY 721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTyrTrpLys 740  
DB 2161 ACAAAATACAGTGAAGAACTTGAAGAAATCCAGCAGAAATGCCCACCTGGTGGTAA 2220  
QY 741 PheSerAsnIlePheLeuIleTrrPaspCysSerProTyrTrrPheLysValLysHisVal 760  
DB 2221 TTTCCAAACATATCTTAACTGGGAGCTGTCTCCATATGGTTAAAGTGAACATGTT 2280  
QY 761 ValAsnLeuValValMetLaspProPheValAspLeuValIleThrIleCysIleValLeu 780  
DB 2281 GTCACACCTGGTGTGATGAGACCATTTGTAACCTGGCATTCAACATCTGATTTGCTTA 2340  
QY 781 AsnThrIlePheMetAlaMetGluHisTyrPrometThrAspHisPheAsnValLeu 800  
DB 2341 AATCTCTTTCATGGCCATGAGCAGCTATCCATATGACGACCATTTCAATATGTCCT 2400  
QY 801 ThrValGluAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820  
DB 2401 ACAGTAGGAACCTGGTGTTCACCTGGATCTTACAGCAGAAATGTTCTGAAATATAT 2460  
QY 821 AlaMetAspProTyrTrrTyrPheGlnGluGlyTrrPasnIlePheAspGlyPheIleVal 840  
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QY 841 ThrLeuSerLeuValGluLeuGluLysLeuValAsnValGluGlyLeuSerValLeuArgSer 860  
DB 2521 ACCGTTAGCCTGGTAGAAGCTGGACCTGCCAATGTGGAAGATATATCTTCCCTG 2580  
QY 861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrrProThrLeuAsnMetLeuIle 880  
DB 2581 TTTTCATTTGCTCGAGTTTCAAGTTGCAAAATCTTGGCAACGTTAAATATGCTAA 2640  
QY 881 LysIleIleGlyAspSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900  
DB 2641 AAGATCATGCGCAATTCCTGGGGGCTCGGGAATTTAACCTCTCTGGGCATCATC 2700  
QY 901 ValPheIlePheAlaValAlaGlyMetGluLeuPheGlyLysSerTrrLysAspCysVal 920  
DB 2701 GCTTCATTTTGGCGTGGCTGGCATGACAGCTTGTGTAAAGCATCAAAAGATTGGTC 2760  
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QY 941 PheLeuIleValPheArgValLeuCysGlyLysIleGlyIleGluThrMetTrrPaspCysMet 960  
DB 2821 TTCCGATTTGCTTCGGCTGCTGCTGGGAGTGGATGATAGACATGCGACTGTATG 2880  
QY 961 GluValAlaGlyAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980  
DB 2881 GAGGTGGCTGTCAGGCAAGCTATGCTCTTACTGTCTCATGATGCTCATGATGGAA 2940  
QY 981 LeuValIleValLeuAsnLeuPheLeuAlaLeuLeu\*\*\*SerSerPheSerAlaAspAsnLeu 1000  
DB 2941 CTAGAGGCTCTGAATCTCTTTCGGCTTGTGCTTGTAGCTCATTTAGTGACACACT 3000  
QY 1001 AlaAlaThrAspAspAsnGlnMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020  
DB 3001 GAGGCACATGATGATATATGAATGAATATCTCCAAATTCCTGTGGATAGATGAC 3060  
QY 1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnInserPheIleArg 1040  
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QY 1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnLysLysAspSer 1060  
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QY 1061 CysMetSerAsnHisThr\*\*GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080  
DB 3181 TGTATGTCCATCATCATCAGCAAGAAATGGGAAAGATCTTGACTATCTTAAAGATGTA 3240

QY 1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100  
DB 3241 GGAACCTACAGTGTATAGAACTGGACACAGTGGTGAATAAATATATATGATGAAG 3300  
QY 1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120  
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QY 1141 SerLysGluLysLeuAsnGluSerSerSerSerSerGlySerThrValAspIleGly 1160  
DB 3421 AGCAAGAGAACTGATATGAAGCACTACTATGAAAGTAGCACTGTGGACATCGG 3480  
QY 1161 AlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCys 1180  
DB 3481 GCACCTGTGAGAAACAGCCCTAGTGAACCTGGAAGAACTTGAACAGAGCTTGT 3540  
QY 1181 PheThrGluGlyCysValGlnArgPheLysCysGlnIleAsnValGluGluArg 1200  
DB 3541 TTCACGGAAGCTGTGTACAAAGATTCAGATGTTGCAATCAATGTGGAAGAGCAG 3600  
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DB 3601 GGAAGAAATGGGGAACCTGAGAAAGAGCTGTTCCGATATCTTAACATACTGGT 3660  
QY 1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyValAlaLeuAlaPheGluAspIle 1240  
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DB 3721 TATATGATCAGGAAAGAGATTAAGAGATTTGGAATATCTGCACAAGTTTCACT 3780  
QY 1261 TyrIlePheIleLeuGluMetLeuLeuLysTrrPvalAlaTyrGlyTyrGlnThrTyrPhe 1280  
DB 3781 TACATTTTATCTTGGAATATGCTTCAAAATGGGTGGCATATGCTATCAACATATTC 3840  
QY 1281 ThrAsnAlaTrrPaspTrrPheLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300  
DB 3841 ACCAATGCTGCTGTGGCTGCTGCTTCTTATGATGATGATTCATGTCACATTA 3900  
QY 1301 AlaAsnAlaLeuGlyTrrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320  
DB 3901 GCAATAGCTTGGGTATACAGAACTTGAGCCATCAATCTCAGAGACATAAGAGCT 3960  
QY 1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValAlaAsnAlaLeu 1340  
DB 3961 CTGAGAGCTCTAAGAGCTTATCTCATTTGAAGGATGAGGTGGTGTGAATGGCT 4020  
QY 1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrrPheIle 1360  
DB 4021 TTAGAGCAATTCATCCATCATGATGATGCTCTGCTGTGCTTATATCTGCTAT 4080  
QY 1361 PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThr 1380  
DB 4081 TTCAGCATATGAGCGCTAATATTTGTTGGCGAAATTTACACAGTATTAACACACA 4140  
QY 1381 ThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIle 1400  
DB 4141 ACTGCTGACAGGTTGACATCGAAGAGCTGAATAATCATCTGATTCCTCAAAACATA 4200  
QY 1401 GluArgAsnGluThrAlaArgTrrPasnValLysValAlaAsnPheAsnValGlyPhe 1420  
DB 4201 GAAAGAAATAGACCTGCTGATGGAATAATGTGAAGATTAATTAATATGATGA 4260  
QY 1421 GlyTrrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrrPheAspIleMetTyrAla 1440  
DB 4261 GGGTATCTCTCTTGTCTTCAAGTGGCACATTCAAAGATGATGATTAATGATGCA 4320  
QY 1441 AlaValAspSerArgAsnValGluLeuGlnProLysTyrGluLeuSerLeuTyrMetTyr 1460

|    |      |   |      |
|----|------|---|------|
| Db | 4321 | GCAGTTGATTCAGAAATGTGGAACTCCAGCCTAGTAGAAGAAAGTCTGACATGAT         | 4360 |
| Qy | 1461 | LeuTyrPheValIlePheIleIlePheGlySerPheThrLeuAsnLeuPheIleGly       | 1480 |
| Db | 4381 | CTTACTTTGTGTAATTTTCAATCATCTTTGGTCCCTTCCTACCTGAACCTGTTTATGCT     | 4440 |
| Qy | 1481 | ValIleIleLeuAsnPheAsnGlnGlnIleLysIlePheGlyValGlnAspIlePheMet    | 1500 |
| Db | 4441 | GTCATCTAGTAGTAATTTTCAACCGACGAAAAAGAAATTGGAGGTTCAGACATCTTATG     | 4500 |
| Qy | 1501 | ThrGlnGlnIleLysIleLysTyrTyrAsnAlaMetLysLeuGlySerLysIleProL      | 1520 |
| Db | 4501 | ACAAAGAACGAGAAAGAAATCTATAATGCAAGAAAAATTAAGATTCAGAAAAACCGAA      | 4560 |
| Qy | 1521 | LysProIleProAlaGProGlyAsnLysPheGlnGlyMetValPheAspPheValThrArg   | 1540 |
| Db | 4561 | AAGCTTATACCTGCACGAGAAACAAATTTCAAGAAATGCTTTTGACTCTGTAACCGA       | 4620 |
| Qy | 1541 | GlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMetVal       | 1560 |
| Db | 4621 | CAATTTTGTGACATTAAGCATCATGATTTCTCATCTGCTTAACATGTCACATGATG        | 4680 |
| Qy | 1561 | GlnThrAspAspGlnSerGluTyrValIleThrIleLeuSerArgIleAsnLeuValPhe    | 1580 |
| Db | 4681 | GAACACATGACCGAGATGTAAATGTGAGCTACCATTTTGTCACGATCAATCTGGTGTTC     | 4740 |
| Qy | 1581 | IleValIleuPheThrGlnGlyGlyCysValIleuLysLeuIleSerLeuArgHisTyrTy   | 1600 |
| Db | 4741 | ATTGTGCTATTACTGGAGAGGTGTGACTGAAACATCATCTCTCTACGCCATTAATATTTT    | 4800 |
| Qy | 1601 | ThrIleGlyTyrPsnIlePheAspPheValValIleLeuSerIleValGlyMetPhe       | 1620 |
| Db | 4801 | ACCATTTGGAATGGAATATTTTGTATTTTGTTGGTTGTCATCTCTCCATTTGTAATGTTT    | 4860 |
| Qy | 1621 | LeuAlaGlnLeuIleGlyLysTyrTyPheValSerProThrLeuPheArgValIleArgLeu  | 1640 |
| Db | 4861 | CTTCCCGACGATGAGAAAGAAATGTTTCGTGTCCTCCCTACCCCTTCCGAGTGTCCGCTT    | 4920 |
| Qy | 1641 | AlaArgIleGlyArgGlyIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLeuLeu | 1660 |
| Db | 4921 | GCTAGATTTGGCCCAATCCCTACCTGTGATCAAGAGACCAAGGGATCCGACGCTGCTC      | 4980 |
| Qy | 1661 | PheAlaLeuMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPheLeuVal       | 1680 |
| Db | 4981 | TTTCTTTGATGATAGTCCCTTCTGCTGCTTTAAATGATGGCTCTTCTTCTCTATCTC       | 5040 |
| Qy | 1681 | MetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgGluValGly    | 1700 |
| Db | 5041 | ATGTTCATCTACGCGCATCTTTGGAGTCCCAACTTGTCCATGTAAAGAGGAAGTTGGG      | 5100 |
| Qy | 1701 | IleAspAspMetPheAsnPheGluTyrThrPheGlyAsnSerMetIleCysLeuPheGlnIle | 1720 |
| Db | 5101 | ATGCATGACATGTCAACTTTTGAGACCTTTGGCAACAGCATATCTGCTTATCCAAATT      | 5160 |
| Qy | 1721 | ThrThrSerAlaGlyTyrAspGlyLeuLeuAlaProIleLeuAsnSerLysProProAsp    | 1740 |
| Db | 5161 | ACAACCTCTGCTGGCTGGAGATGTGTCAGACACCATTTCTAAAGTAAGCACCGAC         | 5220 |
| Qy | 1741 | CysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsnProSer    | 1760 |
| Db | 5221 | TGTACCCCTATATAAAGTTAACCTCGGACACTCAGTTAAGGGAGACTGTGGCAACCATCT    | 5280 |
| Qy | 1761 | ValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValValAsnMet       | 1780 |
| Db | 5281 | GTTGCAATTTCTTTTGTGCACTATACATCAATCATCTTCCCTGCTGTGTGTAACATG       | 5340 |
| Qy | 1781 | TyrIleAlaValIleLeuGlnAsnPheSerValAlaThrGlnGluSerAlaGluProLeu    | 1800 |
| Db | 5341 | TACATCGCGGTCAATCCGAGGAACCTCATGTGCTACTGAAAGAAAGTCAGACCTCTG       | 5400 |
| Qy | 1801 | SerGlnAspAspPheGluMetCysPheTyrGluValTyrGluLysPheAspProAspAlaThr | 1820 |

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Db 5401 AGTACGAGTACCTTGGATGAGTTCATGAGCTTTGGGAGAACTTGAATCCCGATGCACACT 5460
OY 1821 GlnPheMetGlnPheGlnUlysLeuSerGlnPheAlaAlaLeuGlnProPheLeuAsn 1840
Db 5461 CAGTTCATGGAATTTGAAAAATATATCTCAGTTTGCAGCTGCGCTTGAACCGGCTCTCAAT 5520
OY 1841 LeuProGlnProAsnUlysLeuGlnLeuIleAlaMetLysLeuProMetValSerGlyAsp 1860
Db 5521 CTGGCCCAACCAACCAACCAACCCAGCTCATGCTCCATGATTTGCCCATGGTGAGTGAC 5580
OY 1861 ArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGlnSerGly 1880
Db 5581 CGGATCCAGCTGCTTGAATATCTTATTTGCTTTTACAAAGCGGGTTTGAAGAGAGTGCGA 5640
OY 1881 GluMetAspAlaLeuArgIleGlnMetGlnGlnUlyrPheMetAlaSerAspSerLys 1900
Db 5641 GAGATGGATGCTTCAGGAATACAGATGGAGAGGATTCATGGCTTCCAACTTCACAG 5700
OY 1901 ValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGlnGlnValSerAlaVal 1920
Db 5701 GTCCTCATACGACCAATCACTACTACTTTAAAGAAACAAAGAGGAGTATCTGCTTC 5760
OY 1921 IleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGlnAlaSerPhe 1940
Db 5761 ATTATTCACGCTGCTTCACACGCCACCTTTTAAAGCGAAGTGTAAACAAAGCTTCCTT 5820
OY 1941 ThrTyrAsnLysAsnLysIleLysGlyAlaAsnLeuLeuIleLysGlnAspMetIle 1960
Db 5821 AGCTACAAATTAACCAAAATCAAGTGGGCTTATCTTCTTATTAAGAAAGACATGATGA 5880
OY 1961 IleAspArgIleAsnGlnAsnSerIleThrGlnLys 1972
Db 5881 ATTGACAGATTAATGAAACCTGTATTACGAAAAA 5916

RESULT 4
US-09-930-871-3
; Sequence 3, Application US/09930871
; Patent No. US20020076780A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Daniel
; APPLICANT: Mathur, Brian
; TITLE OF INVENTION: No. US20020076780A1 Human Ion Channel Proteins and Polynuc
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0216-USA
; CURRENT APPLICATION NUMBER: US/09/930, 871
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225,989
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 5889
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-930-871-3

Alignment Scores:
Pred. No.: 0 Length: 5889
Score: 10124.50 Matches: 1961
Percent Similarity: 99.44% Conservative: 0
Best local Similarity: 99.44% Mismatches: 11
Query Match: 97.38% Indels: 11
DB: 10 Gaps: 1

US-09-930-871-12 (1-2009) x US-09-930-871-3 (1-5889)
OY 1 MetGlnGlnThrValLeuValProProGlyProAspSerPheAsnPheThrArgGlu 20
Db 1 ATGGAGCAACAGTGGCTTGTACCAAGGAGCTGACAGCTTCAACTCTTACACAGAGAA 60
21 SerValAlaAlaIleGlnUlyrArgIleAlaGlnGlnUlysAlaLysAsnProLysProAsp 40

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Db 61 TCCTGCGGCTATTGAAAGACGCAATTCAGAGAAAAGCCAAAGAAATCCCAACCAAGAC 120  
 QY 41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60  
 Db 121 AAAAAGATGACGACGAAAGGCCCCAAAGCAATATGACTGCGAAGCTGGAAAGAAC 180  
 QY 61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80  
 Db 181 CTTCATTTATTTATGAGACATTCCTCCACAGATGGGTGACAGCCCTGGAGACCTG 240  
 QY 81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100  
 Db 241 GACCCCTACTATATCAAAAGAAAACCTTTTATGATTAATTAAGGAGGCAATCTTC 300  
 QY 101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120  
 Db 301 CGGTTACGCGACCTGCGCCCTGACATTTAACTCCCTCAATCCCTTAGAGAAAATA 360  
 QY 121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140  
 Db 361 GCTATTAGATTTGGTACATTCATTTATTCAGCATGCAATATATGTCAGCTATTTGACA 420  
 QY 141 AsnCysValPheMetCysMetSerAsnProAspThrPheLysAsnValGluTyrThr 160  
 Db 421 AACTGTGTATTATGACAAATAGTAACCTCTGATTTGACAAAAGAAATGTAGAAATACAC 480  
 QY 161 PheThrGlyIleTyrThrPheGluSerIleuIleLysIleIleAlaArgGlyPheCysLeu 180  
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 QY 181 GluAspPheThrPheLeuArgAspProThrAsnThrLeuAspPheThrValIleThrPhe 200  
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 QY 201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220  
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 QY 221 LeuThrGluAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240  
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 QY 241 IleGluSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260  
 Db 721 ATCCAGCTGTGGAAGAGCTCTCAGATGTATGATCCGACTGCTGTCTGCTAGGCTA 780  
 QY 261 PheAlaLeuIleGlyLeuGluLeuPheMetGlyAsnLeuArgAsnLysCysIleGluThr 280  
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 Db 1021 GATCAGGCGCAATGTCCAGAGGAAATATATGTGTGAAGTGTGATAGAAATCCCAATATAT 1080  
 QY 361 GlyTyrThrSerPheAspThrPheSerTyrAlaPheLeuSerLeuPheArgLeuMetThr 380  
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 QY 381 GluAspPheThrProGluAsnLeuTyrGluLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400  
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 QY 401 IlePhePheValLeuValIlePheLeuGlySerPheTyrIleIleAsnLeuIleLeuAla 420  
 Db 1201 ATATTTTGTGTGTGTATTTCTTGGCTTATTCATCTTAATTAATTTGATCTGCT 1260  
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 QY 501 ArgLysLysArgLysGluLysGluGluGluGluGluGluGluGluGluGluGluGluGlu 520  
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 Db 1621 AACGATGTACATATGAAGAAGAGTACCTCCACACACAGCTTTGTGTGAGCATTCGT 1680  
 QY 561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgLysArg 580  
 Db 1681 GCGTCCCTATTTTCCCAAGGCGAAATAGCAGAAACACCTTTTACCTTTGAGAGGCGGA 1740  
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 QY 601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620  
 Db 1801 AACGAGACCGGTAGAGATTCCTTGTGTGGCCCCAGACAGCAGAGAGACGCAACAGC 1860  
 QY 621 AsnLeuSerGluThrSerArgSerSerArgMetLeuAlaValPheProAlaAsnGlyLys 640  
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 QY 641 MetHisSerThrValAspCysAsnGlyValIleSerLeuValGlyGlyProSerValPro 660  
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 QY 661 ThrSerProValGlyGluLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680  
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 Db 2068 ATGCACTTCTAGAGATCTCTCCAAAGGCAAGCAAGCAATGATGATGACGCAATTTCA 2120  
 QY 721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTyrPylLys 740  
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 QY 741 PheSerAsnIlePheLeuIleTyrAspCysSerProTyrThrPheLysValLysHisVal 760  
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QY 761 ValAsnLeuValAlaMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780  
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 Db 2308 AATACCTTTTCAATGCGCAAGAGACATATCCAAATGACGACCATTTCAATATGTCCTT 2367  
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 QY 821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTyrPheAsnIlePheAspGlyPheIleVal 840  
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 QY 841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860  
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 Db 2488 ACCCTTAGCCTGGTAGAACCTGACCTGCCAAATGTGGAAAGATTACTGTTCCGCTTCA 2547  
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 QY 881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900  
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 QY 1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020  
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 Db 3268 GATTAATGATCATATCATATCATATCATATCATATCATATCATATCATATCATATCATAT 3327  
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 Db 3568 GGAAGAACATGTGTGCAACCTGAGAAAGACGTTTCCGAATAGTTGAACATATGCTGTT 3627  
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 Db 3868 GCAATAGCCTTGGGTACTACTAGAACTTGGAGCCATCAAACTCTCAGAGACATCAAGCT 3927  
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 Db 3928 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGATGAGGCTGTGTGAATGACCTT 3987  
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 Db 4108 ACTGGTGACAGGTTTACATCATGAAAGACGTGAATTAATCATCTGATGCTCAAAACATA 4167  
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 Db 4168 GAAGAGAAATGAGCTGCTGATGAAATAATGTAAGATAAATCTTGATTAATGAGATTT 4227  
 QY 1421 GlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTyrPheAspIleMetTyrAla 1440  
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 Db 4228 GGGTATCTCTCTTGTCTCAAGTTGCCACATTCAAAGAGATGATGATTAATATGATGCA 4287  
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 Db 4288 GCAGTTGATTCAGAAATGTGGAATCCAGCTCAATATGAAAGAAAGTCTGTACATGTAT 4347  
 QY 1461 LeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIleGly 1480  
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 Db 4348 CTTTACTTTGTTATTTTCAATCATCTTGGGCTCTTCTCACTGAGCACTGTTATTTGT 4407  
 QY 1481 ValIleIleAspAsnPheAsnGlnGlnLysLysPheGlyGlyGlnAspIlePheMet 1500  
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Query Match: 81.268 Indels: 79  
 DB: 10 Gaps: 12  
 US-09-930-871-12 (1-2009) x US-09-917-800A-1604 (1-6822)

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 QY 21 SerLeuAlaIleGluArgArgIleAlaGluGluValAlaLysAsnProLysProAsp 40  
 DB 474 TCTCTGCTGCTATCGAAAGGGTCTCGAAGAGAAAGCCAGAAACCAGAAAGAG 533  
 QY 41 LysLysAspAspAspGluLysGluProLysProAsnSerAspLeuGluAlaGluLysAsn 60  
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 QY 61 LeuProPheIleTyrGluAspIleProGluMetValSerGluProLeuGluAspLeu 80  
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 QY 81 AspProTyrIleAsnLysThrPheIleValLeuAsnLysGluLysAlaIlePhe 100  
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 QY 101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120  
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 QY 281 ProThrAsnAlaSerLeuGluGluHisSerIleGluLys--AsnIleThrValAsn 299  
 DB 1254 CCCCCGAGCGANTGGCTTTGAAACCAACACTACTCTCTCAATGAGCAATGAGAT 1313  
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 QY 320 AspSerArgTyrHisTyrPheLeuGluGluPheLeuAspAlaLeuLeuCysGluYasnSer 339  
 DB 1374 GATGACAGTCACTTTATGCTGTGATGACAAAAAGATCCTTATCTGTGGAATATGGC 1433

QY 340 SerAspAlaGluGlnCysProGluGluTyrMetCysValLysAlaGluArgAsnProAsn 359  
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 QY 380 ThrGlnAspPheTyrGluAsnLeuTyrGlnLeuThrIleArgAlaAlaGluLysThrTyr 399  
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 DB 1674 GCTGTGTGGCCATGCTCATGAGAGAGCAACAGCCACACCTGAGAGAGGCTGACAG 1733  
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 QY 477 GlyArgLeuSerAspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGlu 496  
 DB 1848 GAGAGACTTCTGAGACAGTCTTCAGAACCTTCCAGATGAGACTCCAGAGTCTAAGAGAG 1907  
 QY 497 ArgArgAsnArgArgLysLysArgLysGlnLysGln-----SerGlyGluGluLys 515  
 DB 1908 TGGAGAAACCGGAGAAAGAGAGAGAGAGAGAGAACTTGGAGAGGAGAAACCAAGAGCC 1967  
 QY 516 AspGluAspGluPheGlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArg 535  
 DB 1968 GATGAGACAGGTTCCCAAGTCGGAATCGGAAGCACTGTCAAAAGAAAGAGCTTCTG 2027  
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 QY 556 LeuLeuSerIleArgGlySerLeuPheSerProArgArgAsnSerArgThrSerLeu 575  
 DB 2088 CTCTGATATACCGGGCTCTCCCTGTTTCCCAAGACCAATAGCAAAACGCAATTTTC 2147  
 QY 576 SerPheArgGlyArgAlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHis 595  
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 QY 596 SerThrPheGluAspAsnGlnSerArgArgAspSerLeuPheValProArgArgHisGly 615  
 DB 2208 AGCACCTTTCAGAGAGAGAGAGAGAGAGAGAGACTCCCTGTTTGTGCCACAGAGCTGGA 2267  
 QY 616 GluArgArgAsnSerAsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaPhe 635  
 DB 2268 GAGCAGCCACACAG----- 2282  
 QY 636 ProAlaAsnGlyLysMetHisSerThrValAspCysAsnGlyValSerLeuValGly 655  
 DB 2282 ----- 2282  
 QY 656 GlyProSerValProThrSerProValGlyGlnLeuLeuProGluValIleLeuAspLys 675  
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 QY 676 ProAlaThrAspAspAsnGlyThrThrThrGluThrGluMetArgLysArgArgSer 695  
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 QY 696 SerPheHisValSerMetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSer 715

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Db 2388 ATAGCCAGTATCCCTGACCAACACCATGAGAGACCTTAAAGAAATCTAACACAAATGCGCCA 2447
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RESULT 6  
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 ; Sequence 15, Application US/09930871  
 ; Patent No. US20020076780A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Turner, C. Alexander Jr.  
 ; APPLICANT: Mathur, Daniel  
 ; APPLICANT: Mathur, Brian  
 ; TITLE OF INVENTION: No. US20020076780A1 Human Ion Channel Proteins and Polynuci  
 ; TITLE OF INVENTION: Same  
 ; FILE REFERENCE: LEX-0216-USA  
 ; CURRENT APPLICATION NUMBER: US/09/930,871  
 ; PRIOR FILING DATE: 2001-08-14  
 ; PRIOR APPLICATION NUMBER: US 60/225,989  
 ; NUMBER OF SEQ ID NOS: 20  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 15  
 ; LENGTH: 4362  
 ; TYPE: DNA  
 ; ORGANISM: homo sapiens  
 ; US-09-930-871-15

Alignment Scores:  
 Pred. No.: 0 Length: 4362  
 Score: 7511.00 Matches: 1446  
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 Best Local Similarity: 100.00% Mismatches: 0  
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Db 3121 AAACAAAGATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3180  
QY 1061 CysMetSerAsnHisTrp\*\*\*GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080  
Db 3181 TGTATGTCATATCATCARCAGAAATGGGAAAGATCTTGATCATTTTAAAGATGATAAAT 3240

QY 1081 GlyThrThrSerGlyIleGlyThrCysSerSerValGluLysTyrIleIleAspCysLeuSer 1100  
Db 3241 GGAATCTACAGTGGTATGAGAACTGGCAGAGTGTGAAAATTAATTAATGATATAAAGT 3300  
QY 1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120  
Db 3301 GATTAATGATCATATTAACACACCCAGCTTACTGTGACTGTACCAATTCCTGTAGGA 3360  
QY 1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluIle 1140  
Db 3361 GAATCTGACTTGAATAATTTAAACACGAGACCTTACTAGATGATGATGATGATGATGATG 3420  
QY 1141 SerLysGluLysLeuAsnGlnSerSerSerSerSerGluGlySerThrValAspIleGly 1160  
Db 3421 AGCAAAAGAAATCTGAATGAAAGCAAGTGCATCAGATGAGATGAGATGAGATGAGATG 3480  
QY 1161 AlaProValGluGluGluProValValGluProGluGluThrLeuGluProGluLys 1180  
Db 3481 GCACCTGTAGAGAGAACACCCGCTAGTGGACCTGAGAGAACTCTTGAACCGAGACCTTGT 3540  
QY 1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg 1200  
Db 3541 TTCACTGAGGCTGTGTACAAAGATTCAGAGTGTCTCAATCAATGATGAGAGAGAGAGA 3600  
QY 1201 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe 1220  
Db 3601 GGAAGAACATGATGGAGAACCTGAGAGAGAGCTGTTCGAAATGATGAGAGAGAGAGAG 3660  
QY 1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240  
Db 3661 GAGACCTCATGTTTTCATATATCTCTTACTAGTGTGCTCTGCGCATTTGAGATATA 3720  
QY 1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr 1260  
Db 3721 TATATGATGACGCAAGAACATGATTAAGACGATGGAATGATGATGATGATGATGATG 3780  
QY 1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPhe 1280  
Db 3781 TACATTTTCATTTCTGGAATCTCTTAAATGAGGAGATGATGATGATGATGATGATGATG 3840  
QY 1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300  
Db 3841 ACCAATGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3900  
QY 1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320  
Db 3901 GCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3960  
QY 1321 LeuArgProLeuArgAlaLeuSerArgPheGluGluMetArgValValValAsnAlaLeu 1340  
Db 3961 CTGAGACCTCTTAAGACCTTATCTGATTTGAAGGATGAGGCTGCTGCTGCTGCTGCTGCT 4020  
QY 1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIle 1360  
Db 4021 TTAGAGCAATTCATCATCATATGATGATGATGATGATGATGATGATGATGATGATGATG 4080  
QY 1361 PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThr 1380  
Db 4081 TTCAAGCATCAAGGCGTAATTTGTTCTGCTGCAAAATCTCAACCTGATTAACACCA 4140  
QY 1381 ThrGluAspArgPheAspIleGluAspValAsnAsnHisTrpAspCysLeuLysLeuIle 1400  
Db 4141 ACTGCTGACAGGTTTGGATCATGAGAGAGCTGATATCTACTGATGATGATGATGATGATG 4200  
QY 1401 GluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyPhe 1420  
Db 4201 GAAAGAAATGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4260  
QY 1421 GlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetTyrAla 1440  
Db 4261 GGTATCTCTCTTGTCTCAAGTTGCCACATTCAAAGATGATGATGATGATGATGATGATG 4320

OY 1441 AlAlaValSerpArgasn 1446  
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 DB 4321 GCAAGTGGATCCAGAAAT 4338

## RESULT 7

US-09-930-871-5

Sequence 5, Application US/09930871

Patent No. US20020076780A1

## GENERAL INFORMATION:

APPLICANT: Turner, C. Alexander Jr.

APPLICANT: Mathur, Daniel

TITLE OF INVENTION: No. US20020076780A1 Human Ion Channel Proteins and Polynucleot

FILE OF INVENTION: Same

FILE REFERENCE: LEX-0216-USA

CURRENT APPLICATION NUMBER: US/09/930,871

CURRENT FILING DATE: 2001-08-14

PRIOR APPLICATION NUMBER: US 60/225,989

PRIOR FILING DATE: 2000-08-16

NUMBER OF SEQ ID NOS: 20

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO: 5

LENGTH: 4329

TYPE: DNA

ORGANISM: homo sapiens

US-09-930-871-5

## Alignment Scores:

|                        | Pred. No.: | Score: | Length: | Matches: | Mismatches: | Indels: | Gaps: |
|------------------------|------------|--------|---------|----------|-------------|---------|-------|
| Percent Similarity:    | 7438.50    | 1435   |         |          |             |         |       |
| Best Local Similarity: | 99.24%     | 0      |         |          |             |         |       |
| Query Match:           | 71.54%     | 11     |         |          |             |         |       |
| DB:                    | 10         |        |         |          |             |         |       |

US-09-930-871-12 (1-2009) x US-09-930-871-5 (1-4329)

OY 1 MetGluInThrValLeuValProProGluProAspSerPheAsnPhePheThrArgGlu 20  
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 DB 1 ATGGAGCAAAAGTCTGTTGACACAGACCTGACAGCTTCACTTCTCCACCGAGAA 60  
 OY 21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluValAlaLysAsnProLysProAsp 40  
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 DB 61 TCTCTGGCGGATATGAAAGACGATGCGAAGAAAGAAAGATCCCAACCGAGAC 120  
 OY 41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60  
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 DB 121 AAAAAAGATGACGAGAAAGATGCGCCCAAGCCCAATAGTGAAGCTGGAAGAAAGAAC 180  
 OY 61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAsnLeu 80  
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 DB 181 CTTCCATTATTTATGAGACATCTCCACAGATGCTGTCAGAGCCCTCGAGGACCTG 240  
 OY 81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100  
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 DB 241 GACCCCTACTATATCAATATGAACTTTATATGATTAATGAAAGGAGGAGCCATCTTC 300  
 OY 101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120  
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 DB 301 CGGTTCATGCGCACCTGCGCCCTGTACATTTTAACTCCCTTCAATCCCTCTAGCAAAATA 360  
 OY 121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140  
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 DB 361 GCTATTAAGATTTTGGTACATTCATTTATTCAGCATGCTATATATGCACTATTTTGGAC 420  
 OY 141 AsnGlyValPheMetThrMetSerAsnProProAspTyrPheThrLysAsnValGluTyrThr 160  
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 DB 421 AACTGTGTGTTATGACATATGATTAACCTCTGATTTGGACAAAGATTAATACATACACC 480  
 OY 161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180  
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 DB 481 TTCACAGAAATATATATCTTTGAAATCATTATATTAATTAATGCAAGGAGGATTCGTTTA 540

OY 181 GluAspPheThrPheLeuArgAspProTyrAsnThrPheAsnPheThrValIleThrPhe 200  
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 DB 541 GAAGATTTACTTCTCTGCGATCCAGAACTGGCTCGATTTCTCTCATATTAATTT 600  
 OY 201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220  
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 DB 601 GCGTACGTACAGAGATTTGTGACCTGGCCATGCTCCGCAATGTGAAACATTCACAGTT 660  
 OY 221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240  
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 DB 661 CTCGCGAGCATTTAGACGATTTCAAGCATTCAGAGCCCTGAAACCATTTGTGGAGCCCTG 720  
 OY 241 IleGluSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260  
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 DB 721 ATCCAGCTGTGAAAGAGCTCTCAGATTAAGATTCCTGACGCTGTCTGTGACCGTA 780  
 OY 261 PheAlaLeuIleGlyLeuGluLeuPheMetGlyAsnLeuArgAsnLysCysIleGluTyrP 280  
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 DB 781 TTTGCTATATTTGGCTGAGCTGAGCTGTCATGCGCAACCTGAGAAATATATATGATG 840  
 OY 281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300  
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 DB 841 CCTCCACCAATGCTTCTTGGAGGAAACATATATGAAAGAAATATATCTGATTAAT 900  
 OY 301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTyrPheSerTyrIleGluAsp 320  
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 DB 901 AATGGACACTATTAATAAGTCTCTTGGATTTGATGAGCAATATATTCAGAT 960  
 OY 321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLysCysGlyAsnSerSer 340  
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 DB 961 TCAAGATATCATTAATTTCTGAGAGGTTTTTATAGTGCATCTATGTGAAATATAGCT 1020  
 OY 341 AspAlaGlyGluCysProGluGlyTyrMetCysValLysAlaGlyLysArgAsnProAsnTyr 360  
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 DB 1021 GATCGAGGCAATGTCCAGAGGATATATGTGTGAAAGCTGTGAGAAATCCCATATAT 1080  
 OY 361 GlyTyrThrSerPheAspThrPheSerThrAlaPheLeuSerLeuPheArgLeuMetThr 380  
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 DB 1081 GGTCTACACAGTGTGATACCTTCAGTGGCTTTTCTCTTCTCTGCTGACTATAGACT 1140  
 OY 381 GluAspPheThrGluAsnLeuTyrGluLeuThrLeuAlaGlyLysThrTyrMet 400  
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 DB 1141 CAGGACTTCTGGGAAATCTTTATACACGATATACGTCGTCGCGGAAAGGATACATG 1200  
 OY 401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420  
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 DB 1201 AATATTTTGTGTTGCTATTTCTTGGGCTCATCTTCACTTAATTAATTTGATTCGCTG 1260  
 OY 421 ValValAlaMetAlaTyrGluGluGluLysGluAlaThrLeuGluGluAlaGluGluLys 440  
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 DB 1261 GTGGTGGCCATGCTTACAGAGAACAGAAATCAGGCCACCTTGGAGAAAGCAAGAAAGAAA 1320  
 OY 441 GluAlaGluPheGluGluMetIleGluGluLeuLysLysGluGluGluAlaAlaGluGlu 460  
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 DB 1321 GAGGCGCAATTTACACAGATGATTTGAACAGCTTAATAAAGCAACAGAGGACCTACAGC 1380  
 OY 461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480  
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 DB 1381 GCGAGCAAGGCAATGCTTCAAGATTCAGAGAGCCAGAGCCAGAGGAGGCTCTCA 1440  
 OY 481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500  
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 DB 1441 GACAGCTATCTGAAGCTCTTAAGTTGAGTTCAAGAGCTGCTAAGGAAAGAAAGAAATCGG 1500  
 OY 501 ArgLysLysArgLysGluLysGluGluGluGluGluGluGluLysAspGluAspGluPhe 520  
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 DB 1501 AGGAAGAAAGAAAGAAAGAAAGAGAGAGCTGTGGGGAAGAGAAAGATGAGATATATTC 1560  
 OY 521 GluLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540  
 |||||  
 DB 1561 CAAAAATCTGAATCTGAGAGACATCATCAGAGAGAAAGGTTTTCCCTTCCATTTGAAAGG 1620  
 OY 541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560

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Db 1621 AACGATGACATATGAAAAGAGTACTCCCTCCACACCGACTGTTGTTGAGCATCGCT 1680  
QY 561 G1ySerLeuPheSerProAlgaArgSerArgThrSerLeuPheSerPheArgGlyArg 580  
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Db 1681 GGCCTCATTTTCCACCAAGCCGAATAGCAGAACCAAGCTTTTCCAGTTTGAAGGGGGA 1740  
QY 581 AlAlaSerValG1ySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600  
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Db 1741 GCAGAGATGTGGCATCTGACAGACCTTCGCAATGATGACACAGCACCCTTGAGGAT 1800  
QY 601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisG1yGluArgArgAsnSer 620  
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Db 1801 AACAGAGCCGTAGATGATCTCTTTGTGCGCCGAGACAGCAGAGAGAGAGACAGACAGC 1860  
QY 621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValPheProAlaAsnGlyLys 640  
Db 1861 AACCTGAGTACAGACCATAGCTCATCCCGATGCTGCAGAGTTTCCAGCAATGGGAG 1920  
QY 641 MetHisSerThrValAspCysAsnGlyValValSerLeuValG1yGluProSerValPro 660  
Db 1921 ATGACAGACCATGTCGATGCAATGGTGGTTCTGTTGTTGATGACCTTCAGTTCTCT 1980  
QY 661 ThrSerProValG1yGluLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680  
Db 1981 ACATCGCTGTGGACAGCTTCTCCAGAG----- 2010  
QY 681 AsnGlyThrThrGluThrGluMetArgLysArgArgSerSerPheHisValSer 700  
Db 2011 ---GGAACAACCATGTAAGCAATGAGAAATGAGAAAGAGTCAAGTCTTCCAGTTTCC 2067  
QY 701 MetAspPheGluGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720  
Db 2068 ATGACATCTTCTAGAGATCTCTCCAAAGCAGACAGCAAGATGATAGCCAGATCTTA 2127  
QY 721 ThrAsnThrValG1yGluLeuGluGluSerArgGlnLysCysProProCysTyrTyrLys 740  
Db 2128 ACAAAATACAGTAGAAGAACTGGAAGATCCAGCAGCAAGAAATCCACCTGTTGTAATAA 2187  
QY 741 PheSerSerIlePheLeuIleTyrAspCysSerProTyrTyrPheLysValLysHisVal 760  
Db 2188 TTTTCCAACTATTTCTTAATCTGGGACTGTTCTCATATGTTTAAAGTGAACATGTT 2247  
QY 761 ValAsnLeuValAlaMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780  
Db 2248 GTCAACTGCTGTGATGAGACCCATTTGTTGACTGGCCATCACCATCTGATTTGCTTA 2307  
QY 781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800  
Db 2308 AATACCTTTTTCATGGCCATGAGACACTATCCAAATGACGGACATTTCAATATGCTCT 2367  
QY 801 ThrValG1yAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIle 820  
Db 2368 ACAGTAGAAACTGTTTCTACAGGGATCTTTACACAGAAATGTTCTGAAATATAT 2427  
QY 821 AlAlaMetAspProTyrTyrPheGlnGluGlyTyrAsnIlePheAspGlyPheIleVal 840  
Db 2428 GCCATGATCTTACTATTTATTTCCAGAAAGCCGGAATATCTTTGACGGTTTATTTGTC 2487  
QY 841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860  
Db 2488 ACCCTTAGCTGCTAGAACTGGACTGCGCAATGTGAGAGATATCTGTTCTCCGTTCA 2547  
QY 861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTyrProThrLeuAsnMetLeuIle 880  
Db 2548 TTTTCGATTTGCTGAGTTTTCAGTTGCAAAATCTTGGCCACGTTAAATATGCTATA 2607  
QY 881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValIleAlaIleIle 900  
Db 2608 AAGATCATCGGCAATTCGAGGGGGCTCTGGAAATTTAACCTTCGCTTGGCCATATTC 2667  
QY 901 ValPheIlePheAlaValAlaGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920  
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Db 2668 GTCTTCATTTTTCGCCGTGTCGGCATGACGCTCTTGTGTAAGCTACAAAGATTTGCTC 2727  
QY 921 CysLysIleAlaSerAspCysGlnLeuProArgTyrPheIleAsnAspPheHisSer 940  
Db 2728 TGCAAGATCGCAGCATGATGCAATCCACAGCGGCGCACAGAAATGACTTCTTCACATCC 2787  
QY 941 PheLeuIleValPheArgValLeuCysGlyGluTyrIleGluThrMetTyrAspCysMet 960  
Db 2788 TTCTGTATGTTGTTCCCGCTCTCTGTGGGAGTGGATAGACCATGTGGGACTGTATG 2847  
QY 961 GluValAlaGlyAlaAlaMetCysLeuThrValPheMetValMetValIleGlyAsn 980  
Db 2848 GAGGTGTGTGTCAAGCATGCTGCTTACTGCTTCAATGATGATGATGATGATGATGATG 2907  
QY 981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu\*\*SerSerPheSerAlaAspAsnLeu 1000  
Db 2908 CTACTGTCTCCGAATCTCTTCTGCTGCTTGTGATGATGATGATGATGATGATGATG 2967  
QY 1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnGluMetAsnIleAlaValAspArgMetHis 1020  
Db 2968 GCACCCACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3027  
QY 1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040  
Db 3028 AAAGGATGACTTATGTAAGAAAGAAATATGATATTTATTCACAGTCTTCATTATGG 3087  
QY 1041 LysGlnLysIleLeuAspGluIleLysProLeuAspLeuAsnAsnLysLysAspSer 1060  
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QY 1061 CysMetSerSerHisThr\*\*\*GluIleGlyLysAspLeuAspTyrIleLysValAsn 1080  
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Db 3208 GGAACCTCAAGTGTATAGGAATGAGCAGCTGTGAAATATCATATATGATGAAAGT 3267  
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Db 3268 GATTACATGTCAATCAAAACAAACCCAGCTTATCTGATCTGATCAACAAATGCTGTAGGA 3327  
QY 1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140  
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QY 1141 SerLysGluLysLeuAsnGluSerSerSerSerGluGlySerThrValAspIleGly 1160  
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QY 1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg 1200  
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Db 3688 TATATTCATGAGCAAGAAAGATTTAGACATGTGTGAATATGCTGCAAGGTTTACT 3747  
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Db 3748 TACATTTTCATTCGAAATAGCTTCTAAATGGGTGATGATGCTATCAACATATTTTC 3807

Oy 1 MetGlunIhrValLeuValProGlyProAspSerPheAsnPhetIhrArgIu 20  
 |||||  
 1 ATGAGCAACAGTGCCTGTACCAACAGGACCTGACAGCTTCACTTTCACCAAGAGAA 60

|    |      |   |      |
|----|------|---|------|
| OY | 21   | Seuenaiaaiaiegiuwaagylleialagluglulysalaysnprolyspasp           | 40   |
| Db | 61   | TCCTCTGGGCTATTGAAAGCGATTGCGAAGAAAGAAAGCCAAAGATCCCAACCGAGC       | 120  |
| OY | 41   | LyslyspaspaapagluasnngilyProlypPoaSnSeraspLeugluIaIaglylsasn    | 60   |
| Db | 121  | AAAAAGATGACGACGAAATGGGCCAAAGCCAAATAGTACCTTGGAACTGGAAAGAC        | 180  |
| OY | 61   | LeuProPheIIeTylGlyaspIIeProGlumetalSerGIuProleugluaspLeu        | 80   |
| Db | 181  | CTTCCATTATTTATTTGAGACATTTCCGCCAGATGGTGCAGAGCCCTCGAGGACCTG       | 240  |
| OY | 81   | AspProTyrTylleasnlyslsTthrPheIIeValleuasnlyslGlylsalIaIePhe     | 100  |
| Db | 241  | GACCCCTACATATCATTAAGAAAACCTTTATAGTATTGATTAAGGGAAGCCATCTTC       | 300  |
| OY | 101  | ArgPheSerAlaThrSerAlaLeuTylIleLeuThrProPheasnProLeuThrGlylsIe   | 120  |
| Db | 301  | CGGTTCAGTGGCACCTCGCCCTGGTACATTTTAACTCCCTCAATCTCTTAGGAAAAA       | 360  |
| OY | 121  | AlaIleLysIleLeuValIHisSerIleuPheSerMetIleIleMetysThrIleLeuThr   | 140  |
| Db | 361  | GCATTTAGATTTTGGTACATTCATTAATTCAGATCCTTAATTAATGCGACTTTTGGACA     | 420  |
| OY | 141  | AsnGlyValPheMetThrMetSerAsnProProAspTyrPThrLysAsnValGIuTyrThr   | 160  |
| Db | 421  | AACGTGTGTTTAGACAATAGAGTAACCCCTCGATTGGACAAAGATGTAGATATACAC       | 480  |
| OY | 161  | PheThrGlyIleTyrThrPheGIuSerIleLysIleIleAlaArgIlyPheCysLeu       | 180  |
| Db | 481  | TTTCACAGGAATATATACTTTTGAATCATCTTATTAATAATTAATGCAAGGCGATTCGTGTTA | 540  |
| OY | 181  | GIuSpPheThrPheLeuAgaAspProTAspTyrPLeuaspPheThrValIleThrPhe      | 200  |
| Db | 541  | GAAATTTTACTTCTTCCCTCGGATCCAGAGACCTGGCTCGATTTCCTGCTATTAACATT     | 600  |
| OY | 201  | AlaTyrValThrGIuPheValAspLeuGIyAsnValSerAlaLeuArgThrPheArgVal    | 220  |
| Db | 601  | GCGTACCTCACAGAGTTGGTGACCTGGGCAATGCTCGGCAATTCGAACTTCAGAGTT       | 660  |
| OY | 221  | LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGIyAlaLeu    | 240  |
| Db | 661  | CTCCGACATATGAAAGACGATTTCAGTCATATCCAGGCTCAAAAACCATTTGGAGCCCTG    | 720  |
| OY | 241  | IleGlnSerValIlyslsLysSerAspValMetIleLeuThrValPheCysLeuSerVal    | 260  |
| Db | 721  | ATCCAGCTGTGGAAGAGCGCTCAGATGTATAGTATCTCGATGCTGTCTGAGCGTA         | 780  |
| OY | 261  | PheAlaLeuIleGlyLeuGlnIleuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp   | 280  |
| Db | 781  | TTTTCTCTTAATGGCGTGGACGCTGTCATGTGGGCAACCTAGGAAATAAAGTTTACAAAGG   | 840  |
| OY | 281  | ProThrThrAsnAlaSerLeuGlnGluIHisSerIleGIuLysAsnIleThrValAsnTyr   | 300  |
| Db | 841  | CTCTCCACCAATGCTTCTCTTGAGAGAACATAGATATGAAAAAATATTACTGTGAATAT     | 900  |
| OY | 301  | AsnGIyThrLeuIleasnGluThrValPheGIuPheAspTyrIlySerTyrIleGlnasp    | 320  |
| Db | 901  | AATGCTACACTTAATTAATGAACTGTCTTGTGATTTGACTGGAAGCTAATATTTCCAAAT    | 960  |
| OY | 321  | SerArgTyrHisTyrPheLeuGluGlyIlyPheLeuAspAlaIleuLysCysLysnSerSer  | 340  |
| Db | 961  | TCAAGATATCATATTCTCCGAGGGGTTTTTATAGATGCCACTACTATGTGGAATATGCTCT   | 1020 |
| OY | 341  | AspAlaGIyLncysProGIuGIyTyrMetCysValIyAlaGIyArgAsnProAsnTyr      | 360  |
| Db | 1021 | GATCAGACGCAATGCTCCAGAGGAGTATATGTGTGTAAGACGTGTAGAAATCCCAATAT     | 1080 |
| OY | 361  | GIyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerIleuPheArgLeuMetThr   | 380  |
| Db | 1081 | GGCTACCAAGCTTGATTAACCTTCAGTGTGGGCTTTTGTTCCTGTCTTTCGACTAATGACT   | 1140 |

381 GlnAspPheTrpGlnAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400  
1141 CAGAGATTCTGGGAAATATCTTTATCAACTGACATTAAGTCTGCTCTGGGAAAGACTGAC 1200  
401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420  
1201 ATATTTTGTGTGTGTCATTTTCTTGGGGCTCATTTCTACCTAATAATTTGATCTGGCT 1260  
421 ValValAlaMetValaThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 440  
1261 GTGTGTGGCCATGGCTTACGAGGAGAACGAAATCAGGCCACCTGGAGAGAGAGAGAGAA 1320  
441 GluAlaGlnPheGlnGlnMetIleGlnGlnLeuLysGlnGlnGlnGlnGlnGlnGlnGln 460  
1321 GAGCGCGAATTTTCAGCAGATGATGAAACGCTTAAAAAGACAGAGAGAGAGAGAGAGAG 1380  
461 AlaAlaThrAlaThrAlaSerGlnHisSerArgGlnProSerAlaAlaGlyArgLeuSer 480  
1381 GCAGCAACGCAACCTCCACAGAACATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440  
481 AspSerSerSerGlnAlaSerLysLeuSerSerLysSerSerAlaLysGlnArgArgAsnArg 500  
1441 GACAGCTCATCTGAAGCCTTAAAGTGAAGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500  
501 ArgLysLysArgLysGlnLysGlnLysGlnLysGlnLysGlnLysGlnLysGlnLysGln 520  
1501 AGGAG 1560  
521 GlnLysSerGlnSerGlnLysAspSerIleArgArgLysGlyPheArgPheSerIleGly 540  
1561 CAAAAATCTGAATCTGAGCAGACATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620  
541 AsnArgLeuThrTyrGlnLysArgLysSerSerProHisGlnSerLeuLeuSerIleArg 560  
1621 ACCGATTGACAT 1680  
561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580  
1681 GGCTCCCTATTTTCCACAG 1740  
581 AlaLysAspValGlySerGlnAsnAspPheAlaAspAspGlnHisSerThrPheGlnAsp 600  
1741 GCAAGAGAGTGGGATCTGAG 1800  
601 AsnGlnSerArgArgAspSerLeuPheValProArgArgHisGlyGlnLysArgArgAsnSer 620  
1801 AACGAGAGCCGTAAGATCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1860  
621 AsnLeuSerGlnThrSerArgSerArgMetLeuAlaValPheProAlaAsnGlyLys 640  
1861 AACCTGAGTCAGACAGATGAGTCCGAGATCCGAGTGTTCACAGAGAGAGAGAGAGAGAG 1920  
641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyLysProSerValPro 660  
1921 ATGCACAGACATGTGATGCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1980  
661 ThrSerProValGlyLysLeuLeuProGlnValIleIleAspLysProAlaThrAspAsp 680  
1981 ACATCCCTCTGTGGACAGCTTCTGCCAGAGAGATATATATATATATATATATATATATAT 2040  
681 AsnGlyThrThrThrGlnThrGlnMetArgLysArgArgSerSerSerPheHisValSer 700  
2041 AATGAGAACACACCTGAATCTGAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2100  
701 MetAspPheLeuGlnAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720  
2101 ATGGACTTTCTGAGAAATCTTCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2160  
721 ThrAsnThrValGlnGlnLeuGlnGlnLysArgGlnLysCysProProCysTrpTyrLys 740  
2161 ACAAAATACAGTGAAGAACTGTGAAGAACTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2220  
741 PheSerAsnIlePheLeuIleThrAspCysSerProTyrTrpLeuLysValLysHisVal 760

2221 TTTTCCAAACATATCTTAATCTGGAGCTTTCTCCATATGCTTAAAGAGCAACATGTT 2280  
761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780  
2281 GTCAACCTGTGTGATGAG 2340  
781 AsnThrPheMetAlaMetGlnHisTyrProMetThrAspHisPheAsnAspValLeu 800  
2341 AATATCTTTTTCATAGCCAG 2400  
801 ThrValGlnLysLeuValPheThrGlyIlePheThrAlaGlnMetPheLeuLysIleIle 820  
2401 ACAGTAGAAGAACTGTGTTTCACTGAGGATCTTTACACAGAGAAATGTTTCTGAAATATAT 2460  
821 AlaMetAspProTyrTyrTyrPheGlnGlnGlyTrpAsnIlePheAspGlyPheIleVal 840  
2461 GCCATGATCTTACAT 2520  
841 ThrLeuSerLeuValGlnLeuGlyLeuAlaAsnValGlnLysLeuSerValLeuArgSer 860  
2521 ACCTTAGCCTGTGAGACTTGACTGCCAATGTGAGAGAGATATATATATATATATATATAT 2580  
861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880  
2581 TTTTCGATTTGCTGGAGAGTTTCAAGTTTGCAAAATCTTGCCCAACGTTAAATATGCTATA 2640  
881 LysIleIleGlnLysSerValGlyAlaLeuGlnLysLeuThrLeuValLeuAlaIleIle 900  
2641 AAGATCATCCGCAATATCCGAG 2700  
901 ValPheIlePheAlaValValGlnMetGlnPheGlnLysSerTyrLysAspCysVal 920  
2701 GTCTTCAATTTTGTGCGGAG 2760  
921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940  
2761 TGCAGAGATCCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2820  
941 PheLeuIleValPheArgValLeuCysGlyGlnTrpIleGlnThrMetTrpAspCysMet 960  
2821 TTCTTGATTTGTGTCCCGCTGT 2880  
961 GlnValAlaGlnGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980  
2881 GAGGTCTCTGTCAAGCAGATGCTTACTGTCTTCATGATGATGATGATGATGATGATGATGAT 2940  
981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu\*\*SerSerPheSerAlaAspAsnLeu 1000  
2941 CTAGTGTCTGATATCTTCTGAGCCTTCTTGTAGCTCATTTAGTGCAGACACACTT 3000  
1001 AlaAlaThrAspAspAspAsnGlnMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020  
3001 GCAGCCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3060  
1021 LysGlyValAlaIleValLysArgLysIleTyrGlnPheIleGlnGlnSerPheIleArg 1040  
3061 AAGGAGTACTTATGTAAG 3120  
1041 LysGlnLysIleLeuAspGlnIleLysProLeuAspAspLeuAsnLysLysAspSer 1060  
3121 AAACAAAGATTTTATGATGAATTAACCACTTGATGATGATGATGATGATGATGATGATGAT 3180  
1061 CysMetSerAsnHisThr\*\*GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080  
3181 TGTATGTCCATATCATACAGAGAAATGGGAAAGATCTTACATATATTAAGATGTAAT 3240  
1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGlnLysTyrIleIleAspGlnLys 1100  
3241 GGAACATCAAGTGTATGAGAACTGCGACAGAGTGTGAAATAATCATATATGATGAAAGT 3300  
1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120

Db 3301 GATTACATGTCATCATTAACAAACCCAGCTGTACTGTGACTGTACCAATTCGTGTAGA 3360  
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 Db 3361 GAATCTACTTTGAAATTTAAACACGAAAGACTTGTAGTGAATGCAATCGAATCGAAGAA 3420  
 Oy 1141 SerlySgluslyleuAsnGluSerSerSerSerSerGluGlySerThrValAsp1160  
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 Oy 1161 AlaprovAluGluGluInproValGluProGluGluThrLeuGluInproGluAlaCys 1180  
 Db 3481 GCACCTGTAGAGAGACCCGCTGTAGTGAACCTGAAGAACTTGTGAACGAGAGCTTGT 3540  
 Oy 1181 PheThrGluGlyCysValGlnArgPheGlyCysGlnLeuAsnValGluGluGlyArg 1200  
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 Oy 1261 TyrIlePheIleLeuGluMetLeuLeuGlySerGlyValAlaArgGlyValThrPhe 1280  
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 Oy 1301 AlaAsnAlaLeuGlyTrpSerGluLeuGlyAlaIleGlySerLeuArgThrLeuArgAla 1320  
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 Oy 1361 PheSerIleMetGlyValAsnLeuPheAlaGlyArgPheThrHisCysIleAsnThrThr 1380  
 Db 4081 TTGAGCAATGAGGCGTAATTTGTGTGCGCAATTCATCACTGATTAATTAACACACA 4140  
 Oy 1381 ThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLeuIle 1400  
 Db 4141 ACTGGTACAGGCC----- 4154  
 Oy 1401 GluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyPhe 1420  
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 Oy 1421 GlyTyrLeuSerLeuLeuGluValAlaThrPheGlyGlyTrpMetAspIle 1437  
 Db 4155 -----ACATTCAAAGCATGATGATATA 4178  
 RESULT 9  
 US-09-930-871-7  
 ; Sequence 7, Application US/09930871  
 ; Patent No. US20020076780A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Turner, C. Alexander Jr.  
 ; APPLICANT: Mathur, Daniel

; APPLICANT: Mathur, Brian  
 ; TITLE OF INVENTION: NO. US20020076780A1 Human Ion Channel Proteins and Polynuc  
 ; TITLE OF INVENTION: Same  
 ; FILE REFERENCE: JEX-0216-USA  
 ; CURRENT APPLICATION NUMBER: US/09/930, 871  
 ; PRIOR FILING DATE: 2001-08-14  
 ; PRIOR APPLICATION NUMBER: US 60/225, 989  
 ; NUMBER OF SEQ ID NOS: 20  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 7  
 ; LENGTH: 4146  
 ; TYPE: DNA  
 ; ORGANISM: homo sapiens  
 US-09-930-871-7  
 Alignment Scores:  
 Pred. No.: 0 Length: 4146  
 Score: 7108.50 Matches: 1381  
 Percent Similarity: 96.10% Conservative: 0  
 Best Local Similarity: 96.10% Mismatches: 1  
 Query Match: 68.37% Indels: 56  
 Gaps: 2  
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 Oy 1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPheThrArgGlu 20  
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 Oy 21 SerLeuAlaIleGluArgArgIleAlaGluGluGlyValAlaLysAsnProLysProAsp 40  
 Db 61 TCTCTGGCGCTATTGAAAGAGCGATTCGAGAGAAAGGCAAGAAATGCTGAGAAAGAAC 120  
 Oy 41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60  
 Db 121 AAAAAAGATGAGAGCAAGAAATGGCCCAAGCAATGACTGCTGAGAGCTGAGAAAGAC 180  
 Oy 61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80  
 Db 181 CTTCATTAATTAATTAAGAGACATTCCTCAGAGATGCTCAGAGCCCTGAGAGACCTG 240  
 Oy 81 AspProTyrTyrIleAsnLysLysThrPheIleValAsnLysGlyLysAlaIlePhe 100  
 Db 241 GACCCCTCTATATATAAAGAAATCTTTATGATTAATTAAGAGAGCCATCTTC 300  
 Oy 101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120  
 Db 301 CGGTTCACTGCGACCTCGCCCTGTACATTTAACTCCCTCAATCCTTAGAGAAATA 360  
 Oy 121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140  
 Db 361 GCTATTAAGATTTGGTACATTCATTAATTCAGCAATGCTTAATATGCAATTTTGACA 420  
 Oy 141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluThr 160  
 Db 421 AACTGTGTTTATAGCAATGATGATTAACCTCTGATTTGACAAAGAAATGATATACACC 480  
 Oy 161 PheThrGlyIleTyrThrPheGluSerLeuLeuLysIleIleAlaArgGlyPheCysLeu 180  
 Db 481 TTCACAGCAATATATATCTTTGAATCACTATATAAATTAATGCAAGGGAGATTCGTTTA 540  
 Oy 181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200  
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 Oy 201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220  
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 Oy 221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValAlaLeu 240  
 Db 661 CTCGAGCATTTGAGAGCAATTCAGTCAATCCAGGCTGAAACCATTCGTGGAGCCCTG 720





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Db 2908 CTATGTGGTCCGAAATCTCTTCTGCGCTTGTMTGACCTCAATTAAGGACACACCTT 2967
Oy 1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020
Db 2968 GCAGCCACTGATGATGATTAAGAAATGATATCTCCAAATTCGTGTGATGATGATGCAC 3027
Oy 1021 LysGlyValAlaArgValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040
Db 3028 AAAGGAGTAGCTATGTGAAAAGAAAATATATGATTAATTAACACAGCTTCCTCATTTAG 3087
Oy 1041 LysGlnIleLysIleLeuAspGluIleLysProLeuAspPheLeuAsnLysLysAspSer 1060
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Oy 1061 CysMetSerAsnHisThr**GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080
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Oy 1081 GlyThrThrSerGlyIleGlyTyrGlySerSerValGluLysTyrIleIleAspGluSer 1100
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Oy 1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValIle 1120
Db 3268 GATTACATGTCATTCATTAACCAACCAACCACTGCTGACTGATCAACCAATGCTGTAGA 3327
Oy 1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140
Db 3328 GAATCTACACTTGAATATTTAAACACGAAAGACTTACTGATGATGATGATGATGAAAGA 3387
Oy 1141 SerLysGluLysLeuAsnGluSerSerSerSerGluGlySerThrValAspIleGly 1160
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Db 3448 GCACCTGTACAGACAGCCCGTAGTGAACCTGAAGAACTCTTGAAACCAAGAGCTTGT 3507
Oy 1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg 1200
Db 3508 TTCACGTAAAGCTGTGTACAAAGATTCAGGTGTGTCAAAATGTGTGAAGAAAGCGCA 3567
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Oy 1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240
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Oy 1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGlnTyrAlaAspLysValPheThr 1260
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Oy 1261 TyrIlePheIleLeuGluMetLeuLeuLysTyrValAlaTyrGlyTyrGlnThrTyrPhe 1280
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Oy 1281 ThrAsnAlaTyrCysTyrPheLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300
Db 3808 ACCAAATGCGGTGGTGGCTGAGCTCTTAAATGATGATGATGATGATGATGATGATGATGAT 3867
Oy 1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320
Db 3868 GCAAAATGCGGTGGTGGCTGAGCTCTTAAATGATGATGATGATGATGATGATGATGATGAT 3927
Oy 1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValAlaAsnAlaLeu 1340
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Db 3928 CTGAGACCTCTTAAGACCTTATCTGATTTGAAGGATGAGGCTGTGTAACCCCTT 3987
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Oy 1361 PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThr 1380
Db 4048 TTCACATCATGAGGAGTAAATTTGTTGCTGCAAAATCTACACTGATTTAAACCCACA 4107
Oy 1381 ThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIle 1400
Db 4108 ACTGGTGACAGGCC----- 4121
Oy 1401 GluArgAsnGluThrAlaArgTyrLysAsnValLysValAsnPheAspAsnValGlyPhe 1420
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RESULT 10
US-09-930-871-19
: Sequence 19, Application US/09930871
: Patent No. US20020076780A1
: GENERAL INFORMATION:
: APPLICANT: Turner, C. Alexander Jr.
: APPLICANT: Machuz, Daniel
: APPLICANT: Machuz, Brian
: TITLE OF INVENTION: No. US20020076780A1 Human Ion Channel Proteins and Polynuc
: TITLE OF INVENTION: Same
: FILE REFERENCE: LEX-0216-USA
: CURRENT APPLICATION NUMBER: US/09/930,871
: PRIOR FILING DATE: 2001-08-14
: PRIOR APPLICATION NUMBER: US 60/225,989
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 19
: LENGTH: 4197
: TYPE: DNA
: ORGANISM: homo sapiens
: US-09-930-871-19

Alignment Scores:
Pred. No.: 0
Score: 7105.50
Percent Similarity: 98.43%
Best Local Similarity: 98.43%
Query Match: 68.34%
Gaps: 10
Matches: 4197
Conservative: 1377
Mismatch: 0
Indels: 22

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Db 61 TCTCTTCGCGCTATTTGAAGACGATGTCAGACAAAGGCAAGAAATGCCAAAGCCAGAC 120
Oy 41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
Db 121 AAAAAGATGACGACGAAATGCGCCCAAGCCAAATAGTGAAGCTGGAAGCTGGAAGAAC 180
Oy 61 LeuProIleLysArgLysAspIleProProGluMetValSerGluProLeuGluAspLeu 80
Db 181 CTTCATTTATTTATGAGACATTCCTCCAGAGATGTGTGACAGCCCGGAGAGACCTG 240
Oy 81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
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Db 301 CGGTTCAGTCCACCTCTGCTGATCAATTTTAACTCCCTTCAATCCCTTTAGGAAATA 360  
QY 121 AlaIleIleValIleValHisSerIlePheSerMetIleMetCysThrIleLeuThr 140  
Db 361 GCTATTAAAGTTTGGTACATTCATTATTCAGATGCTAATATATGTCACATTTTGACA 420  
QY 141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluThr 160  
Db 421 AACTGTGTGTTATGACAAATAGTAACCCCTGATTTGACAAAGATGTAAGATACAC 480  
QY 161 PheThrGlyIleThrThrPheGluSerIleIleLysIleIleAlaArgGlyPheCysLeu 180  
Db 481 TTTCACAGGAATATATCACTTTTGAATCACTTATAAAAATATATTCAGAGGGATCTGTTA 540  
QY 181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200  
Db 541 GAAGATTTTACTTCTCTCGGAGATTCAGATGCACTGGCTGATTTCACTGTCATTAATTT 600  
QY 201 AlaThrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220  
Db 601 GCTAGCTCAGACAGATTTGTGGACCTGGCAATGTCTCGCATTTGAGAAATCAGAGTT 660  
QY 221 LeuArgAlaLeuThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240  
Db 661 CTCGAGACATGAGAGCATTTCAATTCAGATTCAGAGCTGAAACCATTTGGAGAGCCCTG 720  
QY 241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260  
Db 721 ATCCAGCTGTGAGAGAGCTCTCAGATGTAATATCTGATCTGTCTGTCTGACAGCTA 780  
QY 261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280  
Db 781 TTTCCTCTATTTGGCTGAGCTGTTCATGAGGCAACCTGAGAAATATGATATACATG 840  
QY 281 ProProThrAsnAlaSerLeuGluGlnHisSerIleGlnLysAsnIleThrValAsnTrp 300  
Db 841 CCTCCACCAATGCTCTCTGGAGAACATGATAGAAAGAAATATCACTGGAATTTAT 900  
QY 301 AsnGlyThrLeuIleAsnGlnThrValPheGluPheAspTrpLysSerTrpIleGlnAsp 320  
Db 901 AATGTACACTATTAATAGAACTGTCTTGAATTTGACTGGAAGCATATATTCAGAT 960  
QY 321 SerArgTrpHisThrPheLeuGlnGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340  
Db 961 TCAGATATCATATATTTCTGTGGAGGCTTTTATGATGACACTATGATGGAATATACCTCT 1020  
QY 341 AspAlaGlyGlnCysProGluGlnGlyTrpMetCysValLysAlaGlyArgAsnProAsnTrp 360  
Db 1021 GATGAGGCCAATGTCAGAGGGATATATGTGTAAAGCTGTGGTGAATAATCCCAATTTAT 1080  
QY 361 GlyTrpThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380  
Db 1081 GGCTACACAGCTTTGATACCTTCACTGGGCTTTTGTTCCTGTTTGAGCAATAGACT 1140  
QY 381 GlnAspPheTrpGluAsnLeuTrpGlnLeuThrLeuArgAlaAlaGlyLysThrTrpMet 400  
Db 1141 CAGGACTTCTGGGAAATCTTTATATCAATGCAATTCAGCTGTGGGAAACGTAACAG 1200  
QY 401 IlePhePheValLeuValIlePheLeuGlySerPheTrpLeuIleAsnLeuIleLeuAla 420  
Db 1201 AATATTTTGTGTGTCTATTTCTTGGGCTCATTTCTACATTAATTAATTTGATCCGGCT 1260  
QY 421 ValValAlaMetAlaTrpGluGlnAsnGlnAlaThrLeuGlnGluAlaGlnLys 440  
Db 1261 GTGTGTGGCCATGTCCACAGAGCAAGATTCAGGCCACTTGGAGAACACAGAACAGAA 1320  
QY 441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysGlnGlnGlnAlaGlnGln 460  
Db 1321 GAGGCCGAATTTTCAGATGATGATGAACGTTTAAAAACCAACAGAGGACCTCAGCAG 1380

---

QY 461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyLeuSer 480  
Db 1381 GCAGCAACGGCAACTCTCTCAGAACATTTCCAGAGAGCCAGTCCAGAGAGGAGCTTCA 1440  
QY 481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgAsnArg 500  
Db 1441 GACAGCTCATTCAGACCTCTAAGTTGAGTTCCAGAGTCTTAAGGAAGCAATATCGG 1500  
QY 501 ArgLysLysArgLysGlnLysGlnLysSerGlyGlyGluLysAspGluAspGluPhe 520  
Db 1501 AGGAGAAAGAAAGAAAGAGAGAGAGTCTGTGGGGAGAGAAAGATGAGATGATTC 1560  
QY 521 GlnLysSerGluSerLysAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540  
Db 1561 CAAAAATCTGAATCTAGAGACACATCAGAGAGAGAAAGCTTTTGCCTTCATTTGAAGG 1620  
QY 541 AsnArgLeuThrTrpGluLysArgTrpSerSerProHisGlnSerLeuSerIleArg 560  
Db 1621 AACCGATTGACATATGAAAGAGTACTCTCCACACAGTCTTGTGTGACATCTCGT 1680  
QY 561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580  
Db 1681 GGCTCCCTATTTTACCAAGGCGAAATAGCAGAAACAGCCTTTTCACTTACAGGGCGA 1740  
QY 581 AlaLysAspValGlySerLysAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600  
Db 1741 GCAGAGATGTGGAGATCTAGAGACACTTCGAGAGATGACAGACACACTTTTGGAGAT 1800  
QY 601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgAsnSer 620  
Db 1801 AACGAGGCCGTAGAGATTCCTTGTGTGTGCCCCGACGACAGAGAGAGAGACCAACAC 1860  
QY 621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValPheProAlaAsnGlyLys 640  
Db 1861 AACCTGAGCAGACACAGTGTATCCCGATCTGGAGTGTTCACAGCAATGGAGAG 1920  
QY 641 MetHisSerThrValAspLysAsnGlyValAlaSerLeuValGlyLysProSerValPro 660  
Db 1921 ATGCACAGCACTGTGATGCAATGCTGTGTCTCTGTGTGTGTGTGTGTGTGTGTGTGT 1980  
QY 661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680  
Db 1981 ACATGCCCTGTGGACAGCTTCTGCCAGAGGTATATATAGCAGCTACTGATGAC 2040  
QY 681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700  
Db 2041 AATGGAACAACACAGTAACCTGAAATGAGAAAGAGAGCAAGTCTTCCACGTTTCC 2100  
QY 701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720  
Db 2101 ATGAGACTTCTAGAGATCTCTCCCAAGGCAACGAGCAATGATGTATGCCACATTTCA 2160  
QY 721 ThrAsnThrValGluGlnLeuGlnLeuSerArgGlnLysCysProProCysTrpTrpLys 740  
Db 2161 ACAAAATACAGTGAAGAACTTGAAGATCCAGGCAAAATGCCACCTGTGTGTAATA 2220  
QY 741 PheSerAsnIlePheLeuIleTrpAspCysSerProTrpTrpLeuLysValHisVal 760  
Db 2221 TTTTCCAACTATTTCTATCTGGGACTGTCTCCATATGTGTAAAGAGAAACATGTT 2280  
QY 761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValIle 780  
Db 2281 GTCAACCTGTGTGATGACCACTTTGTGACCTGTGGCAATCCCATCTGTATGTCTTA 2340  
QY 781 AsnThrLeuPheMetAlaMetGluHisTrpPrometThrAspHisPheAsnValLeu 800  
Db 2341 AATACTCTTTATGAGCATGAGACATTCATGAGAGGACATTTCAATATATGCTT 2400  
QY 801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820  
Db 2401 ACAGTAGGAACCTGTTTCACTGGAGATTTTACAGCAGAAATGTTTCTGAAATATAT 2460

|    |      |   |      |
|----|------|---|------|
| OY | 821  | AlaMetAspProCysTyrTyrPheGlnGluGlyTyrAsnIlePheAspGlyPheIleVal    | 840  |
| Db | 2461 | GCCAGGAACTCTTACATATATATTCACAAAGAGCGTGAATAATCTTGACGGTTTATTTG     | 2520 |
| OY | 841  | ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer    | 860  |
| Db | 2521 | ACGCTTACCTGGGTAGAACTTGGACCTGCCAATGTGGAAAGATTATCTGTCTCCGTTCA     | 2580 |
| OY | 861  | PheArgLeuLeuArgValPheLysLeuAlaLysSerTyrProThrLeuAsnMetLeuIle    | 880  |
| Db | 2581 | TTTCGATGCTGCAGAGTTTCAAGTTTGGCAAAATCTTGCCCAACGTTAAATGTCAATA      | 2640 |
| OY | 881  | LysIleIleGlyAsnSerValGlyValaLeuGlyAsnLeuThrLeuValLeuAlaIleIle   | 900  |
| Db | 2641 | AAGATCAATCGGCAAATCTCGTGGGGCGCTCTGGAAATTAACCTCGCTTGCCCAATATC     | 2700 |
| OY | 901  | ValPheIlePheAlaValaValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal   | 920  |
| Db | 2701 | GCTTCATTTTGGCCGTGGTGGCGATCAGCTCTTTGGTAAAGCTCAAAAGATTGTGTG       | 2760 |
| OY | 921  | CysLysIleAlaSerAspCysGlnLeuProArgTyrPheLysAsnAspPhePheLysSer    | 940  |
| Db | 2761 | TGCAAGATCGCCAGATGATGTCAACCTCCACGCTGGCACATGAATGACTCTTCACATCC     | 2820 |
| OY | 941  | PheLeuIleValaPheArgValaLeuCysGlyGluTyrIleGluThrMetTyrAspCysMet  | 960  |
| Db | 2821 | TTCTCGATTGTGTCCCGCTGCTGTGGGAGATGATAGAACCATGTGGACATGTATG         | 2880 |
| OY | 961  | GluValaIaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn    | 980  |
| Db | 2881 | GAGGTGCTGGTCAAGCATGTGCTTACTGTCTTATATATGTGTATGTGTATGTGAAC        | 2940 |
| OY | 981  | LeuValValLeuAsnLeuPheLeuAlaLeuLeu**SerSerPheSerAlaAspAsnLeu     | 1000 |
| Db | 2941 | CTAGAGGTGCTGAATCTCTTTGCGCCCTGCTTGTAGCTCAATTATAGCAAGACAACCT      | 3000 |
| OY | 1001 | AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValaAspArgMetHis   | 1020 |
| Db | 3001 | GCACCCACTGTATGTATGATTAAGAAATGAATAATCTCCAAATGTCTGTGATGATGCAC     | 3060 |
| OY | 1021 | LysGlyValaIaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg    | 1040 |
| Db | 3061 | AAAGCAGTACCTTATGTGAAAGAAAGAAATATGAATTAATTCACAGCTCTCAATTAGG      | 3120 |
| OY | 1041 | LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnLysLysAspSer       | 1060 |
| Db | 3121 | AAACAAAGATTTAGATGAATTAAGAAATTAACCCCTGATGATCTAAACACAGAAGACAGT    | 3180 |
| OY | 1061 | CysMetSerAsnHisIleThr**GluIleGlyLysAspLeuAspTyrIleuLysAspValAsn | 1080 |
| Db | 3181 | TGTATGTCCAAATCATACARAGAAATGTGGAAAGATCTTGACTATCTTAAAGATTAAT      | 3240 |
| OY | 1081 | GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleGlnAspGlnSer    | 1100 |
| Db | 3241 | GGAACTACAACTGATATAGCACTGGCAGAGGTGTGAAAATATCACTTATGTGATTAAGT     | 3300 |
| OY | 1101 | AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly    | 1120 |
| Db | 3301 | GATTACATGTCATCATTAACCAACCCCAAGCTTACTGTGACTGATGTCACAAATGTGTAG    | 3360 |
| OY | 1121 | GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGlu       | 1140 |
| Db | 3361 | GAATCTGACTTGGAAATTTTAAACAGCGAAGACTTTATAGATCGGATCTCGAGAGAA       | 3420 |
| OY | 1141 | SerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGly    | 1160 |
| Db | 3421 | AGCAAGAGAACTGATAGAGAGAGAGCTCATCGAAGGTAGACATGTGTGACATCTGGC       | 3480 |
| OY | 1161 | AlaProValGluGluGlnProValaValaGluProGluGluThrLeuGluProGluAlaCys  | 1180 |
| Db | 3481 | GCACCTGTAGAGAAAGACCCCGTAGTGGAAACCTGGAAGAAATCTTGAAACCAAGAGCTTCT  | 3540 |
| OY | 1181 | PheThrGluGlyCysValaGluArgPheLysCysCysGlnIleAsnValaGluGluGlyArg  | 1200 |

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Db      3541  TTCACGGAAGGCTGTCACAAAGATTCAGAGCTTCTCAAAATCAATGTCGAAGAAGCACA 3600
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QY      1201  GLYVSGINTPTPTPASLLEuAqgThrGysPhearqIleVLIghuHSasntPpHe 1220
|||
Db      3601  GGAANAACATGTTGGAACCTGAGAAGACGCTTTCCGAATAGTGAACATTAAGTTT 3660
|||
QY      1221  GIuThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluASPHe 1240
|||
Db      3661  GAGACCTTCATGTTTCATGATTCCTTAGTAGTGGTGGCTGGCATTTGAAGATATA 3720
|||
QY      1241  TYrIleaspGlnaGlyThrIleLysThrMetLeuGluIYrAlaAspIYrValPheThr 1260
|||
Db      3721  TATATGTATCAGCCGAAACGATTAAAGCGATGTTGGAAATAGCTGCACAAAGTTTCAC 3780
|||
QY      1261  TYrIlePheIleLeuGluMetIleLeuLeuYsrPAlaIATyrGlyTYrGlnThrTYrPhe 1280
|||
Db      3781  TACATTTTCATTCCTGGAATAGCTTCTAAATAGGTGGCCTATGCTATCAACATATTTTC 3840
|||
QY      1281  ThrAsnAlaIrcPcYsrTPLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300
|||
Db      3841  ACCAATGCGCTGGTGTGGCTGCAGCTTCTTAATGTGATGTTTCATTTGGTCAATTAACA 3900
|||
QY      1301  AlAsnAlaIleuGlyTYrSerGluLeuGlyAlaIleLysSerLeuArqThrLeuAlaGla 1320
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Db      3901  GCAAATGCGCTGGGTACTGACAACTTGAGACCCATCAAACTCTCAGAGACACTAAGAGCT 3960
|||
QY      1321  LeuArqPcLeuArqAlaIleuSerArqPheGluGluMetIYr 1334
|||
Db      3961  CTGAGACCTCTTAAGAGCTTATCTGCATTTGAAGGATGAGGACATATCTGCTCCAACT 4020
|||
QY      1335  -----ValValValAsnAl 1339
|||
Db      4021  TCGATGGGTGGAGCGCTGTTCTCCCTGAGCCCTTATATAGGTGGTGTGAATGC 4080
|||
QY      1339  aLeuLeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLe 1359
|||
Db      4081  CCTTTAGACCAATTCATCATCATGAAATGCTCTGTTGTCTTATATTCTGGCT 4140
|||
QY      1359  uIlePheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTYrHisCysIle 1377
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Db      4141  AATTTTCAGATCATGGCGTAAATTTGTTGGCTGGCAAAATTCACCACTGTAAAT 4195
|||

RESULT 11
US-09-930-871-9
; Sequence 9, Application US/09930871
; Patent No. US20020076780A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Machur, Daniel
; APPLICANT: Machur, Brian
; TITLE OF INVENTION: No. US20020076780A1el Human Ion Channel Proteins and Polynuc
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0216-USA
; CURRENT APPLICATION NUMBER: US/09/930, 871
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225, 989
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 4164
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-930-871-9

Alignment Scores:
Pred. No.: 0 Length: 4164
Score: 7033.00 Matches: 1366
Percent Similarity: 97.64% Conservative: 0
Best Local Similarity: 97.64% Mismatches: 0
Query Match: 67.64% Indels: 33
DB: Gaps: 2

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US-09-930-871-12 (1-2009) x US-09-930-871-9 (1-4164)

QY 1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20  
DB 1 ATGGACCAAAACAGTGGTGTGACACAGGACGTGACAGCTTCAACTTCTTCCACCAAGAA 60  
QY 21 SerLeuAlaAlaIleGluArgArgGluLeuGluGluValAsnProLysProAsp 40  
DB 61 TCTCTTGGCGCTATTCAGAACACGCTTGCAGAAAGGAAAGAAATCCCAACCGAC 120  
QY 41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60  
DB 121 AAAAAAGATGACACGCAAAAATGGCCAAAGCCAAATAGTACTTGGAAAGCTGGAAAGAAC 180  
QY 61 LeuProPheIleThrGlyLysPheProProGluMetValSerGluProLeuGluAspLeu 80  
DB 181 CTTCATTTATTTATGAGACATTCCTCCAGACATGGTGTACAGAGCCCTGGAGGACCTG 240  
QY 81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100  
DB 241 GACCCCTACTATATCAATAAGAAACTTTATATGATATGAATTAAGGAGGACCATCTTC 300  
QY 101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120  
DB 301 CGGTTACAGCCACCTGCGCTGACATTTTAACCTCCCTTCAATCCTTAGGAAATA 360  
QY 121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140  
DB 361 GCTATTAAATATTTGGTACATTCATTATTCAGATGATGATTAATATATGTCACATTTTACA 420  
QY 141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160  
DB 421 AACTGCTGTTTATGACATGATGATTAACCTCCGATTTGCAGAAAGATGAGATACACC 480  
QY 161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180  
DB 481 TTCACGGAATATATCTTTGAAATCACTTAATAAATATATTCAGAGGGATTCGTGTTA 540  
QY 181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAsnPheThrValIleThrPhe 200  
DB 541 GAAGATTTACTCTCTCGGGATTCATGGACATGGCTGCTGATTCCTGCTCATTTACATTTT 600  
QY 201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220  
DB 601 GGGTACGTACAGAGTTGTGGACGTGGGCAATGCTCGGCAATGGAACATTCAGAGCT 660  
QY 221 LeuAlaGluLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240  
DB 661 CTCGCGACATTCAGACATTCATTCAGATTCAGAGGCTGAAACCATTTGGGAGGCCCTG 720  
QY 241 IleGluSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260  
DB 721 ATCCACTGTGTAGAGAGCTCTCAGATGATATATCTCTGCTGTCTGTGAGCGTA 780  
QY 261 PheAlaLeuIleGlyLeuGluIleuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280  
DB 781 TTTGCTCTAATTTGGGCTGACGCTTCATGGGCACTGAGGAAATATATATACATG 840  
QY 281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300  
DB 841 CCTCCACCAATGCTTCTCTGGAGAACATAGATAGAAAAGAAATTAATCTGGAATTA 900  
QY 301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGluAsp 320  
DB 901 ATGTGTACTTATTAATAAAGACGTCTTGTAGAGTTGACTGGAGACATATATATCAAGAT 960  
QY 321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuGlyAsnSerSer 340  
DB 961 TCAAGATATCATTAATTTCTCGAGGGGTTTTTAGATGCACTATATGTGAATATACCTC 1020  
QY 341 AspAlaGlyGluCysProGluGlyTyrMetCysValLysAlaGlyLysAsnProAsnTyr 360  
|||||

DB 1021 GATGACAGCCCAATGTCCAGAGGATATATGTGTGTAAGAGCTGGTAGAAATCCCAATTAT 1080  
QY 361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheAlaGluMetThr 380  
DB 1081 GGTACACAAAGCTTTGTATACCTTCAAGTTGGGCTTTTGTCTTTTGTTCATCAATAATGACT 1140  
QY 381 GluAspPheTrpGluAsnLeuTyrGluIleuThrLeuArgAlaAlaGlyLysThrTyrMet 400  
DB 1141 CAGGACTTGGGAAATCTTTATCAATGTACATTAACCTGCTGCTGGAAAGCTACATG 1200  
QY 401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420  
DB 1201 ATATTTTGTGTGTGATTTCTTGTGGCTCATTTCACTTAATTAATTTGATTCCTGGCT 1260  
QY 421 ValValAlaMetAlaTyrGluGluGluAsnGluAlaThrLeuGluGluValAlaGluGlnLys 440  
DB 1261 GTGGTGCCATGGCTTACAGAGAACAGAAATCAGGCCACTTGGAAAGAGCAAGAAAGAA 1320  
QY 441 GluAlaGluPheGluGluMetIleGluGluLeuLysGluGluGluAlaAlaGluGln 460  
DB 1321 GAGGCCAATTTACAGCAGATGATTAACACCTTAAAAAGCAACAGAGGACCTCAGCAG 1380  
QY 461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480  
DB 1381 GCAGCAAGGCAACTGCTCAGAAACATTCAGAGAGCCAGTGCGAGCAGGCGAGCTCTCA 1440  
QY 481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluValArgAsnArg 500  
DB 1441 GACAGCTCATCTGAAGCTTAAAGTTGATCCAAAGAGTCTTAAGAAAGAAAGAAACGG 1500  
QY 501 ArgLysLysArgLysGluLysGluGluSerGlyGlyGluLysAspGluAspGluPhe 520  
DB 1501 AGCAGAAAGAAAGAAAGAAAGAGCACTGTGGGGGAAAGAAAGATGAGATGCAATTC 1560  
QY 521 GluLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540  
DB 1561 CAAAAATCTGAATCTGAGCAGACATCAGAGAGAAAGTTTGCTTCCTCATTAAGAGG 1620  
QY 541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560  
DB 1621 AACGATTCATATGAAAGAGAGTCTCTCCACACAGCTTTGTTGAGACATCCGT 1680  
QY 561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580  
DB 1681 GGCTCCCTATTTCCACCAAGCAATAGCAGAAACAAAGCTTTTACCTTAAGGCGCA 1740  
QY 581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600  
DB 1741 GCAAAGATGCTGGATCTGAGAACGACTTCGAGATGATGAGCAGACAGCACTTTGAGGAT 1800  
QY 601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluValArgAsnSer 620  
DB 1801 AACGAGAGCCGTAGAAATCTCTGTTGTGCCCCGAGACAGCAGAGAGAGACCAACAG 1860  
QY 621 AsnLeuSerGlnThrSerArgSerArgMetLeuAlaValPheProAlaAsnGlyLys 640  
DB 1861 AACCTGAGTACAGCAGTAGAGTATCCCGATCTGTGCACTGTTCCAGCGAATGGGAG 1920  
QY 641 MetHisSerThrValAspCysAsnGlyValIleSerLeuValGlyGlyProSerValPro 660  
DB 1921 ATGCACAGCACTGTGATGATGATGCTGTGCTTCTGTGGTGGTGAGCACTTCAAGTTCC 1980  
QY 661 ThrSerProValGlyGluLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680  
DB 1981 ACATCCCTGTGTGACAGCTTGTGCGAGAG----- 2010  
QY 681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerPheHisValSer 700  
DB 2011 ---GGAACAACCACTGAATCTGAATAGAGAAAGAGAGAGCAAGTCTTCCAGCTTCC 2067  
QY 701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720  
DB 2068 ATGGACTTCTTGAAGATCTCTCCCAAGGCAAGCAGCAATGATATGACCAAGCATTTCTA 2127  
|||||



|   |      |   |       |
|---|------|---|-------|
| QY  | 1081 | GLYTHRTHRserglylleglythrglySerSerValglulysTyrilleaspgluser      | 1100  |
| Db  | 3208 | GGAACTACAAGTGGTATAGGAACCTGGCAGACAGTGTGAAATAATCATTTTGGATGAAAGT   | 3267  |
| QY  | 1101 | AspTyrMetSerPheilleasnasnProSerLeuThrValThrValProIleIleValgly   | 11202 |
| Db  | 3268 | GATTTCATGTATTCATTAACAAACCCAGCTTACTGTATGATACGTGACCAATTCCTGTAGGA  | 33227 |
| QY  | 1121 | gluserAspPhegluaenleuAsnThrGluAspPheSerSerGluuserAspIleuglu     | 11440 |
| Db  | 3328 | GAATCTGACTTTGGAATAATTTAAACAGGAGACTTTAGTAGTAAGTAACGGATCTGGAGAGA  | 3387  |
| QY  | 1141 | SerlysglyslleuasngluserSerSerSerSerGlyglySerThrValAspIlegly     | 11660 |
| Db  | 3388 | AGCAAAAGAAACGTAATGAAACAGACAGTCTATCCAGAAAGTAGACACTGTGGACATCGGC   | 3447  |
| QY  | 1161 | AlaProValGluIugluInProValGluProGluIugluThrIleugluProGluIuIacys  | 11860 |
| Db  | 3448 | GCACCTGTAGAGAGAACAGCCCGTAGTGAACCTGGAAGAAACCTTGGAAACAAACACTGT    | 3507  |
| QY  | 1181 | PheThrGluIuglyCysValGlnArgPheIysCysCysGlnIleAsnValGluIuglyArg   | 12000 |
| Db  | 3508 | TTCACTGAAGGCTGTGTACCAAAATTCMACTGTGTTCCTCAAAATCAATGTGGAGAAAGCAGA | 3567  |
| QY  | 1201 | GlyIysGlnTyrPTrPasnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe   | 12220 |
| Db  | 3568 | GGAAACAAATGCTGGAACTGAGAGAAGAGAGCTGTTCCGAATAGTTGAACATATACGGTTT   | 3627  |
| QY  | 1221 | GluThrPheIleValPheMetIleleuLeuSerSerGlyAlaLeuAlaPheGluAspIle    | 12400 |
| Db  | 3628 | GAGACCTTCATGTTTTCATGATTCCTTACTAGTAGGGCTCTGGCAATTCGAAATATA       | 3687  |
| QY  | 1241 | TyrIleAspGlnArgIysThrIleIysThrMetLeuGluTyrAlaAspIysValPheThr    | 12660 |
| Db  | 3688 | TATATTGATCGCGGAAGACGATTAAGACAGTGTGGATATGCTGACAAAGGTTTTCT        | 3747  |
| QY  | 1261 | TyrIlePheIleleuGluMetleuLeuIysTyrValAlaTyrGlyTyrGlnThrTyrPhe    | 12880 |
| Db  | 3748 | TACATTTTCATTTGCGAAATGCTTTCAAAATAGGGTGGCATATGGCATCAACATATTC      | 3807  |
| QY  | 1281 | ThrAsnAlaTyrPcyStrPleuAspPheIleuIleValAspValSerIeuValSerLeuThr  | 13000 |
| Db  | 3808 | ACCAATGCTCGGTGTGGCGGACTTCTTAATTGTGAGATTTCATTGGTCAGTTTACA        | 3867  |
| QY  | 1301 | AlaAsnAlaIleuGlyTyrSerGluIleuGlyAlaIleIysSerLeuArgThrIleuArgIa  | 13200 |
| Db  | 3868 | GCAATGCTCTGGTGTACTACAGAACTTGGAGGCATCAAAATCTCAGACACTAAGAGCT      | 3927  |
| QY  | 1321 | LeuArgProLeuArgAlaLeuSerArgPheGluIuglyMetArg-----               | 13340 |
| Db  | 3928 | CTGAGACCTCTAAGAGCCTTATCTGATTTGAAAGGATGAGGATAACTTGCCTCAACT       | 3987  |
| QY  | 1335 | -----ValValAlaAsnAl   | 13390 |
| Db  | 3988 | TGATGGGGGTGAGCGCTGGTTCCTCCCTCGAGCCCTTATATGAGGTGGTGTGAATGC       | 4047  |
| QY  | 1339 | AlenIleuGlyAlaIleProSerIleMetAsnValIleuValuIcysIleuIlePheTrpIe  | 13590 |
| Db  | 4048 | CCCTTTAGAGCAATTCACATCCATCAATGAAATGGCTTGTGTTCTCTTAATATCTCGCT     | 4107  |
| QY  | 1359 | uilePheSerTlleMetGlyValAsnLeuPheAlaGlyIysPheTyrHisCysIle        | 1377  |
| Db  | 4108 | AATTTTCAGCATCATGGGGGTAAATTTGTTTCTGTGGCAATTTCTACCACTGATT         | 4162  |
| RESULT 12   |      |   |       |
| US-09-840-125-3   |      |   |       |
| ; Sequence 3, Application US/09840125                                     |      |   |       |
| ; Patent No. US20020061524A1  |      |   |       |
| ; GENERAL INFORMATION:  |      |   |       |
| ; APPLICANT: Splawski, Igor   |      |   |       |
| ; APPLICANT: Keating, Mark T.   |      |   |       |
| ; TITLE OF INVENTION: ALTERATIONS IN THE LONG QT SYNDROME GENES KVLQ1 AND |      |   |       |
| ; TITLE OF INVENTION: SCN5A AND METHODS FOR DETECTING SAME                |      |   |       |



FILE REFERENCE: 2323-155  
 CURRENT APPLICATION NUMBER: US-09/840,125  
 CURRENT FILING DATE: 2001-04-24  
 PRIOR APPLICATION NUMBER: 09/634,920  
 PRIOR FILING DATE: 2000-08-09  
 PRIOR APPLICATION NUMBER: 60/147,488  
 PRIOR FILING DATE: 1999-08-09  
 NUMBER OF SEQ ID NOS: 4  
 SOFTWARE: Patent In Ver. 2.0  
 SEQ ID NO 3  
 LENGTH: 6048  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (1)..(6048)  
 US-09-840-125-3

Alignment Scores:  
 Pred. No.: 0 Length: 6048  
 Score: 6312.00 Matches: 1287  
 Percent Similarity: 72.72% Conservative: 230  
 Best Local Similarity: 61.70% Mismatches: 386  
 Query Match: 60.71% Indels: 184  
 DB: 10 Gaps: 30

US-09-930-871-12 (1-2009) x US-09-840-125-3 (1-6048)

QY 6 LeuValProPogIyProaSPSerPheAsnDhePheThrArgIuSerLeuAlaIle 25  
 DB 13 CTATTACCTGGGGGACAGCAGCAGCTCCGAGTTCACAGCGAGGAGTCCGAGCAGCATC 72  
 QY 26 GluArgTrgIleaglIuGlulysAlaIysAsnProIysProAspIysAsp----- 43  
 DB 73 GAGAAAGCGATGGCGGAGAAAGCAAGCCCGGCTCAACACCTTCGAGAGAGCGGAGAG 132  
 QY 44 -----AspAspGluAsnGlyProIysProAsnSerAspLeuGluAlaIyAsnLeu 61  
 DB 133 GGGCTGGCCGAGGAGGAGGCTCCCGGCGCAGCTGAGACCTGCGAGGCTCCAAAAGCTG 192  
 QY 62 ProPheIleIyTrgIyAspIleProPogIuMetValSerGluProLeuGluAspLeuAsp 81  
 DB 193 CCAGATCTCATGATGCAATCCACCCCAAGAGCTCATCGAGAGCGCCCTGAGAGACTGGAC 252  
 QY 82 ProTyrTrIleAsnIySlyThrPheIleValIleAsnIySglySAlaIlePheArg 101  
 DB 253 CCTTCTATAGCACCCAAAAGACTTTCATGCTGATGAATAAAGCAAGACCATCTCCGG 312  
 QY 102 PheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgIySAlaIle 121  
 DB 313 TTCAGTCCACCAAGCGCTGTATGCTCAGTCCCTCCACCAAGTTCGAGAGCGGCT 372  
 QY 122 IleIyAlleuValIleIleSerLeuPheSerMetLeuIleMetCysThrIleLeuThrAsn 141  
 DB 373 GTGAAGTGTGTGCTCCTGCTTCATCATGCTCATGTCAGACCATCTCACCAC 432  
 QY 142 CysValPheMetThrMetSerAsnProPogIyProIyThrIyAsnValIyIyThrPhe 161  
 DB 433 TGGCTGTATAGGCCCGCAGCAGACCTCCACCTGAGCAAGATGTGCGATACCTTC 492  
 QY 162 ThrGlyIleIyThrPheGluSerIleuIleIySAlleIleAlaArgIyPheCysIleGlu 181  
 DB 493 ACCGCACTTACACCTTGTAGTCTGTGCAAGATTCGTGCTCGAGCTTCGCTGCTCAC 552  
 QY 182 AspPheThrPheLeuArgAspProIyThrIyAsnThrIyAsnValIleIyThrPheAla 201  
 DB 553 GCGCTCACTTCCCTGCGGAGCCATGCACTGCGTGAATGATTAATCATGCA 612  
 QY 202 TyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgValIleu 221  
 DB 613 TACACAACTAATTTGGAGACCTGGGCAATGTCTACACCTTCAGCACTTCGAGTCTC 672  
 QY 222 ArgAlaLeuIySlyThrIleSerValIleProGlyLeuIySlyThrIleValIyAlaLeuIle 241

DB 673 CGGGCCCGGAAATATATCTATCTATTCAGGCTTCAGAGACCATCTGGGGCCCTGATC 732  
 QY 242 GluSerValIySlyLeuSerAspValMetIleLeuThrValIyPheCysIleSerValPhe 261  
 DB 733 CAGTGTGGAAGAAGCTGTGATGTGATGTGCTTCACAGTCTTCGCTCAGAGTCTTT 792  
 QY 262 AlaLeuIleGlyLeuGluLeuPheMetGlyAsnLeuArgAsnIySlyIleGlnTrpPro 281  
 DB 793 GCGCTCATGCGCTGACACTCTTCATGCGCAACTAAGGCACAGTGTGT----- 843  
 QY 282 ProThrAsnAlaSerIleuGluIleHisSerIleGlyIyAsnIleIyThrValIyAsnTrp 301  
 DB 844 -----CGCACTTCACAGCG-----CTCAC 864  
 QY 302 GlyThrIleuIleAsnGluThrValPheGluPheAsp-----TrpIySer----- 316  
 DB 865 GGCAC-----AACGGCTCGGTG-----GAGCGCAGCGGCTTCGTGGAATCCCTGAGC 915  
 QY 317 ---TyrIleGlnAspSerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeu 335  
 DB 916 CTTCACCTCAGTATCCAGAAATTAATCTGCTCAAGAACGCACTCTGATGTGTACTG 975  
 QY 336 CysGlyAsnSerSerAspAlaGlyGlnCysProGluIyTrpMetCysValIySAlaGly 355  
 DB 976 TGTGGAAACACTGTGACCTGGGACATGTCCGAGGAGCTTACCGGCTTAAAGCGAGGC 1035  
 QY 356 ArgAsnProAsnIyTrgIyThrSerPheAspThrPheSerTrpAlaPheLeuSerLeu 375  
 DB 1036 GAGAAACCCGACACGCGCTACACAGCTGATTCGCTTCGCTGGGCTTCCTTGACATC 1095  
 QY 376 PheArgIleuMetThrGlnAspPheTrgIyAsnLeuTyrGlnLeuThrIleValAlaAla 395  
 DB 1096 TTCGCTGTATGACGAGGAGCTGTGTGGAGCGCTCATACAGACCTCAGCTCCGCA 1155  
 QY 396 GlyIyThrTrpMetIlePhePheValIlePheLeuGlySerPheTyrIleuIle 415  
 DB 1156 GGGAAAGTCAATGATCTTTCATGCTGTATCTCTTCCTGGGCTTCCTTACCTGTG 1215  
 QY 416 AsnLeuIleuValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGlu 435  
 DB 1216 AACCTGATCTCGCGCTGTGCGCAATGCTATGAGGAGAAACCAAGCACCATCGCT 1275  
 QY 436 GluAlaGluGlnIySlyAlaGluPheGlnMetIleGluIleuIySlyGlnGln 455  
 DB 1276 GAGACCGAGGAGAAAGAAAGCGCTTCAGAGCGCATGGAATGCTCAAGAAAGAACAC 1335  
 QY 456 GluAlaIleGlnIleAlaIleThrAlaSerGluHisSerArgIuProSerAla 475  
 DB 1336 GAGGCCCTCACACATCAGGCGTGTGATACCTGCTCCGT----- 1374  
 QY 476 AlaGlyArgLeuSerAspSerSerGluAlaSerIySlySerIySerAlaIyS 495  
 DB 1375 -----ACCTCCTTGAGATGTCCTTCGCTTCGCGCAAGTAAACAGCAT 1416  
 QY 496 GluArgTrgAsnArgTrgIySlyArgIySAlaGluIleGluIleGluIyS 515  
 DB 1417 GAGAGAAAGAAAGCAAGAGAAAGAGAG-----TCTTCAGAGAACTGAGAGTGT 1467  
 QY 516 AspGluAspGluPheGlnIySlySerGluSerIyAspSerIleArgTrgIySlyPheArg 535  
 DB 1468 GGGGAGAGACAGGCTCCCAAGTGTGACTAGAAAGTGTCCAGACAAATG----- 1518  
 QY 536 PheSerIleGluIySlyAsnArgLeuThrTrgIySlyArgTrgIySerSerProIySlnSer 555  
 DB 1519 -----AATCATCTCAGCCTCAGCCCTGCGCTCAGCAGCACTTATGAAAG 1563  
 QY 556 LeuLeuSerIleArgGlySerLeuPheSerProIyArgAsnSerArgThrIySerLeuPhe 575  
 DB 1564 CCAAGTTCAGCGCGGAGACATTTTACACTTTCGAGG----- 1602  
 QY 576 SerPheArgIyArgAlaValIySerGluAspPheAlaAspArgIySln 595

Db 1603 -----CGAGACCTGGGTCTGAAGCAGATTTCAGATGATGAAAAC 1644  
 Oy 596 SerThrPheGluAspAsnIuSerArgAspSerLeuPheValProAlaArgHisGly 615  
 Db 1645 AACACAGCGCGGAGAGAGAGCCACACACATCACTGCTGGTGC-----TGGCCC 1698  
 Oy 616 GluArgAspSerAsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaPhe 635  
 Db 1699 CTGGCCCGGACAGAGTCCAGGAGCAGCCAGTCCCGGAACCTCGGCTCTGCCCCACG-- 1756  
 Oy 635 eProAlaAsnGlyLysMetHisSerThrValAspCysAsnGlyValSerLeuValG1 655  
 Db 1757 -CCCTC-CATGGCAAAAGAACAGACACTGTGACTGCATAGGGGTGTCTCATTTCTGGG 1814  
 Oy 655 Y---GlyProSerValProThrSerProValGlyGlnLeuLeuProGlnValIleLeu 674  
 Db 1815 GGCAGGCGCAGCAGAGCCACATCCAGAGAACCCACCTCCGCCCTGTATGTATGATA 1874  
 Oy 674 PLSProAlaThrAspAsnGlyThrThrThrGlnThrGlnMetArgLysArgArgSe 694  
 Db 1875 GCACCG-----CCAGACAGCAGCAGCCATCGAGAGCCAGCGCGCCCGCCAGATGCT 1928  
 Oy 694 rSerSerPheHisValSerMetAspPheGlnIuAspProSerGlnArgGlnArgAla 714  
 Db 1929 GACCTCCAGGCTCGGTGTGTAGATGCTTGCAGAGGCGCAGAGCAGCAGCGGCGCCCT 1988  
 Oy 714 tSerIleHisSerIleLeuThrAsnThrValGlnGlnGlnGlnGlnGlnGlnGlnGln 734  
 Db 1989 CAGCGCAGTCAAGCTGTCTACAGCGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2048  
 Oy 734 sProProCysTrpTyrLysPheSerAsnIlePheLeuIleTyrPAPCysSerProTyrTr 754  
 Db 2049 TCCACCATCTCGAAGCCGTCTGCCAGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2108  
 Oy 754 PLeuLysValLysHisValValAsnLeuValValMetAspProPheValAspLeuAla 774  
 Db 2109 GATGTCCATCAAGCAGGAGGAGTGAAGTGGTGTCTCATGAGCCGTTACTGACCTCACCAT 2168  
 Oy 774 eThrIleCysIleValIleAsnThrLeuPheMetAlaMetGlnHisTyrPromethAs 794  
 Db 2169 CAGTATGTGCATGTGATCAACACACTCTCTGAGCGCGAGCAGCTCAACATATCAAG 2228  
 Oy 794 PHisPheAsnAsnValLeuThrValGlyAsnLeuValPheThrGlyIlePheThrAlaG1 814  
 Db 2229 TGAATTCGAGGAGATGCTGCGAGAGTGGAACTGGTCTTCACAGGAGATTTTCACAGCAGA 2288  
 Oy 814 uMetPheLeuLysIleIleAlaMetAspProTyrTyrTrpPheGlnGlnGlyTrpAsnI1 834  
 Db 2289 GATGACCTTCAGATCATTTGCCCTGACCCCTACTACTACTCAACAGGCGCTGGAACAT 2348  
 Oy 834 ePheAspGlyPheIleValThrLeuSerLeuValGlnGlnGlyLeuAlaAsnValGlnG1 854  
 Db 2349 CTTCACACGATCATCTGATCTTACGATGAGAGCTGGGCGCTGCTCCCGCATAGCAA 2408  
 Oy 854 yLeuSerValLeuArgSerPheArgLeuLeuArgValPheLysLeuAlaLysSerTrpR 874  
 Db 2409 CTGTGCGGTGGCGCTCTCTCCGCTGCTGGGTCTTCACAGCGGCAATCATGAGCC 2468  
 Oy 874 oThrLeuAsnMetLeuLysIleIleGlyAsnSerValGlyAlaLeuGlnGlyAsnLeuTh 894  
 Db 2469 CACCTTGAAACACTCATCAAGATCATCGGAACTCACTGGGGGAGCTGGGGAACCTTAC 2528  
 Oy 894 rLeuValIleAlaIleIleValPheIlePheAlaValValGlyMetGlnLeuPheGlyLys 914  
 Db 2529 ACTGGTGTAGCATCATGATGATCTTGTGCTGTGGGAGCAGCTCTTTGGCAA 2588  
 Oy 914 sSerTyrLysAspCysValLysLysIleAspSerAspCysGlnLeuProAlaTrpPheHis 934  
 Db 2589 GAACACTACGAG-----CTGAGGAGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2642  
 Oy 934 tAsnAspPhePheHisSerPheLeuIleValPheArgValLeuCysGlyGlnTrpIleG1 954  
 Db 2643 GATGACTTCTTTCATGCTTCTTCAATCATCTTCGCGCATCTCTGTGAGAGTGGATGGA 2702

Oy 954 uThrMetTrpAspCysMetGlnValAlaGlyGlnAlaMetCysLeuThrValPheMetMe 974  
 Db 2703 GACCATGTGGAGATGATGAGGTGTGGGGCAGTATTTGGCTGTGCTGCTTGTGCT 2762  
 Oy 974 tValMetValIleGlyAsnLeuValValLeuAsnLeuPheLeuAlaLeuLeu\*\*\*SerSe 994  
 Db 2763 TGTATGTGATTTGGCAACCTTGTGTGCTGAAATCTTCTGAGCTGTGCTGCTGCTGCT 2822  
 Oy 994 rPheSerAlaAspAsnLeuAlaValThrAspAspAsnGlnMetAsnAsnLeuGlnI1 1014  
 Db 2823 CTTCAGTGCAGACAACTCATACAGCCCTGATGAGAGAGAGATGATACAACTCCAGCT 2882  
 Oy 1014 eAlaValAspArgMetHisLysGlyValAlaArgValLysArgLysIleTyrGlnPheI1 1034  
 Db 2883 GGCCTGGCGCCCATCCAGAGGGGCGCTGTGTTCAGAGCGGACCACTGGGATTTCTG 2942  
 Oy 1034 eGlnGlnSerPheIleArgLysGlnLysIleLeuAspGlnIleLysProLeuAsp---As 1053  
 Db 2943 CTGTGTCTCTGCGGACAGCGCTCAG-----AAGCCGCGACCGCTTGC 2987  
 Oy 1053 PLeuAsnAsnLysLysAspSerCysMetSerAsn-----HisTrp 1066  
 Db 2988 CCGCCAGGCGCAGCTGCCAGGTGCATGTGCACCCCTACTCCCGCCACCCCGCAGAGAC 3047  
 Oy 1066 r\*\*\*GlnIleGlyLysAspLeuAspTyrLeuLysAspValAsnGlyThrThrSerGlyI1 1086  
 Db 3048 GGAGAGAGGCTCTCCACCCGCAAGAAACAGTTTGAGAGAGGAGGAGCAGCAGCAGCA 3107  
 Oy 1086 eGlyThrGlySerSerValGlnLysTyrIleIleAspGlnSerAspTyrMetSerPheI1 1106  
 Db 3108 GGGCAGCCCGGGGAGTCCAGAG----- 3129  
 Oy 1106 eAsnAsnProSerLeuThrValThrValProIleAlaValGlyGlnSerAspPheGlnAs 1126  
 Db 3130 -----CCGCTGTGTGCTGCATCGCTGTGTGGCGGATCAGACACATGA 3173  
 Oy 1126 nLeuAsnThrGlnAspPheSerSerGlnSerAspLeuGlnGlnGlnGlnGlnGlnGln 1146  
 Db 3174 C---CAAGAAAGAGATGAGAGAGACAGCTGGGACGAGAGAGAGTCCAGCAAGCAGA 3230  
 Oy 1146 nGlnSer----- 1148  
 Db 3231 GGAATCCAGCTGTGTGCTGCGGCTGCGCCAGAGCGCTCCGATTCAGAGACTGGAGCCA 3290  
 Oy 1148 ----- 1148  
 Db 3291 GGTGTACGACTGCTCTCTGAGCGCAGGCGAGTGCATGACGCGGAGCTGGCGGA 3350  
 Oy 1149 -----SerSerSe 1152  
 Db 3351 GCAGTGGAAAGCGGAACCCAGGCGCCAGGCTGCGGTGAGAGCCCGAGAGAGATGTGCTC 3410  
 Oy 1152 rGlnGlySerThrValAspIleGlyValAlaProValGlu-----GlnGlnProValValG1 1170  
 Db 3411 CGAGGCGACACAGACATACCAACACCGCTGAGCTCTGAGACACATCCCTGACT 3470  
 Oy 1170 uProGlnGlnThrLeuGlnProGlnAlaCysPheThrGlnGlnGlyCysValGlnArgPheLys 1190  
 Db 3471 CGGCGAGATGTCAGAGACCCAGAGACTGCTTCACTGAAGCTGTGCTGGCGGTGCTC 3530  
 Oy 1190 sCysCysGlnIleAsnValGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 1210  
 Db 3531 CTGCTGTGCGGTGAGCACACACAGCCCGCAGGAGGAGTCTGTGCTGCTGCTGCTGCTG 3590  
 Oy 1210 rCysPheArgIleValGlnHisAsnTrpPheGlnThrPheIleValPheMetIleLeu 1230  
 Db 3591 CTGTACACATCTGTGAGACAGCTGTGCTCAGACATTCATCATCTTCTATATCTTACT 3650  
 Oy 1230 uSerSerGlyAlaLeuAlaPheGlnAspIleTyrIleAspGlnArgLysThrIleLysTrp 1250  
 Db 3651 CAGCAGTGGAGGCTGCGCTTGCAGAGACATCTACTAGAGAGGAGGAGGAGGAGGAGGAG 3710

1250 mletleuglntyrAlaaspysValpheThrTyrIlepheIleuglmetleuLeuLy 1270  
Db 3711 TCCTCTGAGATGCGCAGAGATGTTACATATGCTGTGCTGAGATGCTGCA 3770  
1270 strValAlaTyrGlyTyrGlnThrTyrPheThrAsnAlaTrpCysTrpLeuAspPheLe 1290  
Db 3771 GTGGGTGGCCACGCTGACAGAGATGCTACCAATGCTGCTGCTGCTGCTGCT 3830  
1290 uileValAspValSerLeuValSerLeuThrAlaAsnAlaLeuGlyTyrSerGluLeuAl 1310  
Db 3831 CATGTGAGAGCTCTCTGTGGACGCTGTGGCCACACCTGGGCTTGGCGGATGG 3890  
1310 yAlaIleLysSerLeuArgThrLeuArgAlaLeuArgProLeuArgAlaLeuSerArgph 1330  
Db 3891 CCCATCAAGTACATGGGAGCGGCGGTGCATCCGCTGCTGAGACCTCTGTACAGATT 3950  
1330 egluglyMetArgValValValAsnAlaLeuGlyAlaIleProSerIleMetAsnVa 1350  
Db 3951 TGAGGGCATGGGTGGTGGTCATGCTGTGGCGCCATCCCTCATCATGAACGT 4010  
1350 lleuLeuValCysleuIlePheThrPheIlePheSerIleMetGlyValAsnLeuPheAl 1370  
Db 4011 CCTCTGCTGCTGCTCTCTGTGGCTGTGCTCATCTCATGATGAGGCGCTGAACCTTCTTGC 4070  
1370 aglyLysPheThrHisCysIleAsnThrThrThrGlyAsp---ArgPheAspIleGluAs 1389  
Db 4071 GGGGAAATTTGGAGGTGATCATCAACGACGAGGAGATTTGGCTTGAACATACCAT 4130  
1389 pValAsnAsnHisThrAspCysleuLeuIleGluArgAsnGluThrAlaArg----- 1407  
Db 4131 CGTGACACACAGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4181  
1408 -TrpLysAsnValLysValAsnPheAsnAsnValGlyPheGlyTyrIleuSerleuLeuGl 1427  
Db 4182 CTGACCAAGGTGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCA 4241  
1427 nValAlaThrPheLysGlyTrpMetAspIleMetTyrAlaAlaValAspSerArgAsnVa 1447  
Db 4242 GGTGGCAACATTTAAAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 4301  
1447 lGluLeuGlnProLysTyrGluLeuSerLeuTyrMetTyrLeuTyrPheValIlePheAl 1467  
Db 4302 TGAAGACACGCTGAGGGAATACACCTCATGATGATGATGATGATGATGATGATGAT 4361  
1467 eilePheGlySerPhePheThrLeuAsnLeuPheIleGlyValIleleAspAsnPheAs 1487  
Db 4362 CATCTTTGGGTCTTCTTCTTCACTGCAACCTTATTTGCTGATCATTTACAACTTCA 4421  
1487 nglnGlnLysLysLysPheGlyGlyGlnAspIlePheMetThrGluGlnLysLysTyr 1507  
Db 4422 CCAACAGAAAGAAAGTTAGGGGCGCCAGACATCTTCATGACAGAGAGCAAGAAAGTA 4481  
1507 rTyrAsnAlaMetLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 1527  
Db 4482 CTACAAAGCCATGAAAGAGTGGGCTCCAGAAAGCCCAAGCCCAAGCCCAAGCCCAAG 4541  
1527 yAsnLysPheGlnGlyMetValPheAspPheValThrArgGlnValPheAspIleSerI 1547  
Db 4542 GAACAGATACAGAGGCTCTATTTGATGATGATGATGATGATGATGATGATGATGATGAT 4601  
1547 emetIleLeuIleCysLeuAsnMetValThrMetMetValGluThrAspAspIleSerI 1567  
Db 4602 CATGTTTCTGATCTGCTGTAATATGATGATGATGATGATGATGATGATGATGATGATG 4661  
1567 uTyrValThrThrIleLeuSerArgIleAsnLeuValPheIleValLeuPheThrGlyG 1587  
Db 4662 TGAAGAAATCAACATCTGGCCAGAGATCAACCTGCTTGTGGCATCTTCAACAGGCA 4721  
1587 uCysValLeuLysLeuIleSerLeuArgHisTyrTyrPheThrIleGlyTrpAsnIlePh 1607  
Db 4722 GTGTATTTGCAAGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 4781  
1607 eAspPheValValValIleLeuSerIleValGlyMetPheLeuAlaGluLeuIleGluLy 1627  
4782 CGACTGTGGTGTGATCCCTCATGCTGAGGAGCTGTGCTGCTGAGCATCATCCAGAA 4841  
1627 strPheValSerProThrLeuPheArgValIleArgLeuAlaArgIleGlyArgIleLe 1647  
Db 4842 GTACTTCTTCCCGCCGAGGCTTCCGAGTCATCCGCTGCTGCTGCTGCTGCTGCTGCT 4901  
1647 uArgLeuIleLysGlyAlaLysGlyIleArgThrLeuPheAlaLeuMetMetSerLe 1667  
Db 4902 CAGACTATCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4961  
1667 uProAlaLeuPheAsnIleGlyLeuLeuPheLeuValMetPheIleTyrAlaIlePh 1687  
Db 4962 GCGTGGCCCTTCAACATCGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5021  
1687 eglYMetSerAsnPheAlaTyrValLysArgGlnValGlyIleAspAspMetPheAsnph 1707  
Db 5022 TGGCATGGCCAACTTCTTATGCAAGTGGAGAGGCTGGCATGAGCAGCATGTTCAACT 5081  
1707 egluThrPheGlyAsnSerMetIleCysLeuPheGlnIleThrThrSerAlaGlyTrpAs 1727  
Db 5082 CCAGACCTTGCCACAGCATGCTGTGCTTCCATCATCAACACGTCGGCGGCTGGGA 5141  
1727 pGlyLeuLeuAlaProIleLeuAsnSerLysProProAspCysAspProAsnLysValAs 1747  
Db 5142 TGGCTCTCTCAAGCCCATCTCTCAACACTGGGCGCCCTTACTGCAATGCTCATCTT 5201  
1747 nProGlySerSerValLysGlyAspCysGlyAsnProSerValGlyIlePhePhePheVa 1767  
Db 5202 CAGCAATGGCTCT---CGGGGGGAGCTCGGGAGCCAGCGTGGGCAATCTTCTTCAAC 5288  
1767 lSerThrIleIleIleSerPheLeuValValAsnMetTyrIleAlaValIleLeuGl 1787  
Db 5259 CACCTCATCATCATCTCTCTCTCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5318  
1787 uAsnPheSerValAlaThrGlnGlnSerAlaGluProLeuSerGlnLysAspPheGluMe 1807  
Db 5319 GAACCTCAGGCTGGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5378  
1807 tPheTyrGlnValTrpGlnLysPheAspProAspAlaThrGlnPheMetGluPheGluLy 1827  
Db 5379 GTTCTATGAGATCTGGGAGAAATTTGACCAAGGCGCACATGATTTATGATGATGCT 5438  
1827 sLeuSerGlnPheAlaIleAlaLeuGluProProLeuAsnLeuProGlnProAsnLysI 1847  
Db 5439 CTGCTGACTTTCGACAGCCCTGCTGTGAGCACTCCGATGCTCCAGACCCAGCAT 5498  
1847 uGlnLeuIleAlaMetAspLeuProMetValSerGlyAspArgIleHisCysLeuAspI 1867  
Db 5499 AACCTCATCAACATGAGACCTGCCCATGATGATGATGATGATGATGATGATGATGAT 5558  
1867 eLeuPheAlaPheThrTyrArgValLeuGlyGlnSerGlyGlnMetLysAlaLeuArgI 1887  
Db 5559 TCTCTTTCCTTCAACCAAAAGGCTCTGAGGAGTGGGAGAGTGGAGTGGAGTGGAGT 5618  
1887 eGlnMetGlnGlnArgPheMetAlaSerAsnProSerLysValSerTyrGlnProIleTh 1907  
Db 5619 CCGATGAGAGAGAGTTCATGAGCAGCAACCATCCATCAACATCTCCATCAAGCCATCAC 5678  
1907 rThrThrLeuLysArgLysGlnGlnValSerAlaValIleIleGlnArgAlaTyrArg 1927  
Db 5679 CACCAACCTCGGGGAG 5738  
1927 gArgHisLeuLeuLysArgThrValLysGlnAlaSerPheThrTyrAsnLysAsnLysI 1947  
Db 5739 CAGGCACTGGCTCAACGCTTGTGAAGCATGCTCTTCTTCTTCTTCTTCTTCTTCTT 5798  
1947 eLysGlyGlyAlaAsnLeuLeuIleLysGlnAsp-----MetIleI 1961  
Db 5799 CAGCGGC-----CTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5846  
1961 eAspArgIleAsnGluAsn-----SerIleThrGlnLysThrAspLeuThrMetSe 1978

Db 5847 CTACGTGATGAGTGAACCTCTCCGACCCCTGGCCACCCCTCCAGCTCTCCATCTC 5906  
Oy 1978 rThralalaGysProProserTytrAspArgValhlyrProIleValGlnLysHisG1 1998.  
Db 5907 CTCGACTTCCTCCACCCCTCTATGACGTGTACTGTAGCCACCGCATTAACCTCA 5966  
Oy 1998 uGlnGluGlyLysASP 2003  
Db 5967 GGTGGGGGGTCTGAC 5982  
RESULT 13  
US-09-896-994-1  
Sequence 1, Application US/0986994  
Publication No. US20030074024A1  
GENERAL INFORMATION:  
APPLICANT: Ken Stokes  
TITLE OF INVENTION: SYSTEMS AND METHODS FOR ENHANCING CARDIAC  
SIGNAL SENSING BY CARDIAC PACEMAKERS THROUGH GENETIC TREATM  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. US20030074024A1r1s  
STREET: One Liberty Place - 46th floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: U.S.A.  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/896,994  
FILING DATE: 02-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/514,907  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Paul K. Legard  
REGISTRATION NUMBER: 38,534  
REFERENCE/DOCKET NUMBER: MEDT-0029/P-3586  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6048 bases  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-896-994-1  
Alignment Scores:  
Pred. No.: 0 Length: 6048  
Score: 6310.00 Matches: 1286  
Percent Similarity: 72.72% Conserved: 231  
Best Local Similarity: 61.65% Mismatches: 386  
Query Match: 60.69% Indels: 184  
Gaps: 30  
US-09-930-871-12 (1-2009) x US-09-896-994-1 (1-6048)  
Oy 6 LeuValProGlyProAspSerPheAsnPhethrArgGluSerLeuAlaIle 25  
Db 13 CTATTAACCTGGGGACACAGAGCTTCGCCAGTTCAACGGGAGTCCCTGGACCCATC 72  
Oy 26 G1uAArg1leAlaGlnGlnLysAlaLysAsnProLysProAspLysLysAsp----- 43  
Db 73 GAGAAAGGCGATGGCGGAGAAAGACCCGCGCTCAACACCTTGCAGAGAGACCGAGAG 132

Oy 44 -----AspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsnLeu 61  
Db 133 GGGCTGCCGAGAGAGAGAGCTCCGGCCAGCTGGAGCTCGAGCTCCAAAGCTG 192  
Oy 62 ProPheIleArgLysAspIleProGluMetValSerGluProLeuGluAspLeuAsp 81  
Db 193 CCAGATCTGTAGGCAATCCACCCCAAGAGCTCATCGAGAGACCCCTGGAGAGCTCGAC 252  
Oy 82 ProTyrTyrIleAsnLysLysThrPheIleValLeuAsnGlyLysAlaIlePheArg 101  
Db 253 CCTTCTATGACCAACCAAAAGACTTTCATGCTGATTAAGCAAGCAAGCAACTTCCGG 312  
Oy 102 PheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIleAla 121  
Db 313 TTCAGTCCACCAAGAGCTGTATGCTCCTGCTCCCTCCAGTCCAGTGGAGAGCGCT 372  
Oy 122 IleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThrAsn 141  
Db 373 GGAAGATTCGTGTCACGCTGCTTCACATCATCATCATGACCATCTCCACCAAC 432  
Oy 142 CysValPheMetThrMetSerAsnProProAspTyrPheLysAsnValGluTyrThrPhe 161  
Db 433 TCGGTGTCATGCGCCAGCAGCAGCACCCTCCAGCAAGTATGTGAGTACACCTTC 492  
Oy 162 ThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeuGlu 181  
Db 493 ACCGCCATTACACCTTGATGCTGTGTCAGAGATTGCGAGCTTGTGCTGCTGCAC 552  
Oy 182 AspPheThrPheLeuArgAspProTyrAsnTyrPheAspPheThrValIleThrPheAla 201  
Db 553 GCGTTCACCTTCCTCGGAGACCAAGCAAGTACGCGAGCTTATGATGATATCATGGA 612  
Oy 202 TyrValThrGluPheValAspLeuGlnLysAsnValSerAlaLeuArgThrPheArgValLeu 221  
Db 613 TCACAACTGATTTGTGACCTGGGCAATGTCTACAGCTTACGACCTTCGAGACTCCTC 672  
Oy 222 ArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeuIle 241  
Db 673 CGGGCCCTGAAACATATATCATGCTATTCAGGGCTGAAAGACCATGCTGGGGCCCTGATC 732  
Oy 242 GlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerValPhe 261  
Db 733 CAGTGTGGAAGAACTGGCTGATGTGATGTGCTCAGACAGTTCCTGCTCAGCTCTTT 792  
Oy 262 AlaLeuIleGlyLeuGlnLeuPheMetGlnLysLeuArgAsnLysCysIleGlnTyrPro 281  
Db 793 GCCCTCATCGGCTGACACTCTTCACTGGGCAACTAAGGCAACAGTGTGTG----- 843  
Oy 282 ProThrAsnAlaSerLeuGlnGluHisSerIleGluLysAsnIleThrValAsnTyrAsn 301  
Db 844 -----GSCACCTTCACAGCG---CTCAAC 864  
Oy 302 GlyThrLeuIleAsnGluThrValPheGluPheAsp-----TyrLysSer----- 316  
Db 865 GGCAC-----AAGGCTCGGTG---GAGGCCAGAGGCTGTGCTGGGAATCCCTGGAC 915  
Oy 317 ---TyrIleGlnAspSerArgTyrHisTyrPheLeuGlnGlyPheLeuAspAlaLeu 335  
Db 916 CTTTACCTAGATGATCCAGAAATTAATTAATCTGCTCAAGAGGACACCTGTGATGTACTG 975  
Oy 336 CysGlyAsnSerSerAspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGly 355  
Db 976 TGTGGGAACGCTGTGACGTGGGACATGTCCGAGGCTACCGGTGCTTAAGGACAGGC 1035  
Oy 356 ArgAsnProAsnTyrGlyTyrThrSerPheAspThrPheSerTyrPheLeuSerLeu 375  
Db 1036 GAGAAACCCGACACAGGCTACACAGCTTCATTCCTTGTGCTGCTTCTTCTGACATC 1095  
Oy 376 PheArgLeuMetThrGlnAspPheThrPheGluAsnLeuTyrGlnLeuThrLeuArgAlaAla 395  
Db 1096 TTCCGCTCATGATGACGACAGACTGCTGGAGAGCGCTCTATGACAGAACCTCAGGTCCGCA 1155  
Oy 396 GlyLysThrTyrMetIlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIle 415

|    |      |  |      |
|----|------|--|------|
| Db | 1156 | GGGAAATCTACATGATCTCTTCATCTTCATCTGTCAATCTCTCGGGGCTCTTACTACTGGTG | 1215 |
| QY | 416  | ASPLELLELEMLAVALVALAMETATATYCTUGLUGLNSGGLNALATHLEUGL           | 435  |
| Db | 1216 | AACTATCTCTGCGCGGTGGTCAGATGGCTATAGAGCAAAACCAAGCCATCTCT          | 1279 |
| QY | 436  | GLUALAGLUGLINSYGLUALAGLUPHPEGLNGIMETLEUGLUGLINSYGLUGL          | 455  |
| Db | 1276 | GAGCCGAGAGAGAGAAAGCCGCTCCAGAGGCCATGMAATCTCAGAAAGAAC            | 1335 |
| QY | 456  | GLUALALAGLINALALATHRALATHLASERGLNHISERATGGLUPROSERALA          | 475  |
| Db | 1336 | GAGGCGCTCAACATCAAGGGGTGGATACCGATCTCCCGT                        | 1374 |
| QY | 476  | ALAGLYATGLEUSERASPSESERSETSERGLALASERLYSEUSERSELYSERALYS       | 495  |
| Db | 1375 | -----AACTCCCTTGAGATGTCTCCCTTTGGCCCAAGTAAACAGCAT                | 1416 |
| QY | 496  | GLUATGATGASNAATGATGLYSATGLYSGLINSYGLUGLINSERGLYGLUGLULYS       | 515  |
| Db | 1417 | GAGAGAAAGCAAGAGAGAGAAACGATG-----TCTTCAGAACTGAGAGATGT           | 1467 |
| QY | 516  | ASPGULASPGULUPHEGLINSYSEGLINSERGLUNASPSERILLEATGATGLYGLYPHEATG | 535  |
| Db | 1468 | GGGAGAGACAGGCTCCCAAGTGTACTCGAAGATGTGCCAAGGACATG-----           | 1518 |
| QY | 536  | PHESERILEGLUGLYASNAATGLEUTHRTYGLULYSATGTYTSESERPROHISGLNSER    | 555  |
| Db | 1519 | -----AATCATCTGAGCTCAACCCGTGGCTCAGACAGACTTCTATGAG               | 1563 |
| QY | 556  | LEULSERILLEATGGLYSERLEUPHESERPROATGATGASNSERATGYSERLEUPHE      | 575  |
| Db | 1564 | CCAGCTTCAGCCCGCGGAGCAATTTTCACCTTCGCGAG-----                    | 1602 |
| QY | 576  | SERPHATGATGATGALVALYSAPVALGLSERGLUNASPSRHEALASAPAGLUNIS        | 595  |
| Db | 1603 | -----CGAGACTGGGTCTTGAAACAAATTTTGCAATGATGAAAC                   | 1644 |
| QY | 596  | SERTHPHGLUNASPSANGLUSERATGATGASPSERLEUPHEVALPROATGATGINSGLY    | 615  |
| Db | 1645 | AGCAGCGCGGAGAGCGAGACCCACACATCATCTGCTGGGCC-----TGAGCC           | 1698 |
| QY | 616  | GLUATGATGASNSERANLEUSERGLNTHRSERATGSESRARGMETLEMLAVALPH        | 635  |
| Db | 1699 | CTGCGCGGAGACATGCCCCAGGACACGCCATGCCGGAACCTCGGCTCTGGCGAGC--      | 1756 |
| QY | 635  | EPROALANGLYLYSMETHISSETHRALVALASPCYASNGLYVALVALSERLEUVALGL     | 655  |
| Db | 1757 | -----CCCTC-CATGGCAAAAAGAACAGCACTGTGGATCGAATGGGGTGTCTCATTAACGGG | 1814 |
| QY | 655  | Y-----GLYPROSERVALPROTHSERPROVALGLYGLINSLEUPROGLUNALLEAS       | 674  |
| Db | 1815 | GGCAGCGAGCCAGAGAGCCACATCCAGAGAACCACTCTCCGCCCTGTATGTGTAGA       | 1874 |
| QY | 674  | PLYSPROALATHRASAPASNGLYTHRTYTHRTYGLNTHRTYGLIMETATGYSATGATGSE   | 694  |
| Db | 1875 | GCACCG-----CCAGACACAGCAACCCATGATGGAGAGACCCAGCGGCCCCCAATGCT     | 1928 |
| QY | 694  | TSERSEPRHEHIVALSETMETASPRHELEUGLUNASPROSERGLNATGALAME          | 714  |
| Db | 1929 | GACCTCCAGGCTCCCTGTGTAGATGGCTTGAGAGAGCCAGAGACAGCGAGCGGCGCT      | 1988 |
| QY | 714  | TSERILEALASERILLEATHRASPHRYALIGLUGLUNGLINSYGLINSYGLINSY        | 734  |
| Db | 1989 | CAGCGCAGTCAAGGCTCTCAACAGCCATCGGAAGAGTTAGAGAGATCTGCCACAAGTG     | 2048 |
| QY | 734  | SPROFCTSTPTTYLYLSPHESERANILEPHELEULETTPASPCYSERPROTYT          | 754  |
| Db | 2049 | TCCACCATCTGGAACCGCTGCCAGAGGCTACGTGATGTGGAGATGCGCCGCGCTG        | 2108 |
| QY | 754  | PLEULYSVALYSHLSVALVALANLEUVALVALIMETASPRPROPHVALASPLEUALAL     | 774  |

|    |      |   |      |
|----|------|---|------|
| Dh | 2109 | GATGTCCATCAAGCAGGGAGTGAAGTTGGTGGTCACTGAGACCCTTACAGACTCAACAT     | 2166 |
| Oy | 774  | eThrlleCysllleValleuasnhrleuPheMetalaMetGlnHisTryPromethras     | 794  |
| Dh | 2169 | CACATATGTGCATCTGACCAACACACTCTTCATGCGCCCTGAGCACTCAACATCTCAAG     | 2228 |
| Oy | 794  | PhlshPheasnhrValleuThrValGlyasnleuValPheThrGlyIlePheThrAlaGl    | 814  |
| Dh | 2229 | TGAATTCAGAGAGATGCTGCAGGCTCGAAGAACCTGGTGCTTCACAGGGAATTTTCACAGCA  | 2288 |
| Oy | 814  | uMetPheleuLyslllellealameLaspProTryTyrTyrPheGlnGluGlyTyrAsnll   | 834  |
| Dh | 2289 | GATGACCTTCAAGATCATGTGCGCTCGACCCCTACTACTACTTCCAAACAGGGCTGGAACT   | 2344 |
| Oy | 834  | ePheAspGlyPheIleValIhrleuSerleuValGluLeuGlyleuAlaAsnValGluCl    | 854  |
| Dh | 2349 | CTTGACAGCATCATCTGATCTCTTACCTCCATGGAGAGCTGGGCTCTCCGAGTGCAG       | 2408 |
| Oy | 854  | YleuSerValleuArSerPheArGleuLeuArGValPheLysleuAlaGlySerTyrP      | 874  |
| Dh | 2409 | CTTGCGGTGCTGGCGCTCTTCGCGCTCGCGGCTTCACACTGGCCAAATCATGGCC         | 2466 |
| Oy | 874  | oThrleuAsnMetleuIleLyslllelleGlyasnSerValGlyAlaIleGlyAsnleuTh   | 894  |
| Dh | 2469 | CACCTGAAACACTCATCAAGATCATCGGGAACCTAGTGGGGGCACTGGGGAACCTGCAC     | 2528 |
| Oy | 894  | rleuValleuAlallelleValPheIlePheAlaValAlaValGlyMetGlnleuPheGlyly | 914  |
| Dh | 2529 | ACTGGTGCTACCCATCATCTGTCATCTTGTGCTGTGGTGCGCATCCTCTTGCGCA         | 2588 |
| Oy | 914  | sSerTyrLysAspCysValCysLysIleAlaSerAspCysGlnleuProArGTrPHisMe    | 934  |
| Dh | 2589 | GAACATCTCGAG-----CTGAGGAGCAGCAGCTACAGGCTGCTCGTCCGTGGGACAT       | 2642 |
| Oy | 934  | tAsnAspPhePheHisSerPheleuIleValIlePheArGValleuCysGlyGluTrrPleGl | 954  |
| Dh | 2643 | GATGACTCTTCTATGCTCTTCCATCAATCTTCGCACTCTGTGGAGAGTGAATGCA         | 2702 |
| Oy | 954  | uThrMetTrpAspCysMetGluValAlaGlnGlnAlaMetCysleuThrValPheMetMe    | 974  |
| Dh | 2703 | GACCATGTGGAGCATGATGGAGGTGTCGGGGGCACTAATATGCTGCTGCTTCTTCTCT      | 2766 |
| Oy | 974  | tValMetValIlelleLysleuIleuValleuAsnleuPheleuAlaIleuLys***SerSe  | 994  |
| Dh | 2763 | TGTTATGTGCTATGGCAACCTTGTGTGCTCGAATCTCTCTCGCTTCCTCTCACTTC        | 2822 |
| Oy | 994  | rPheSerAlaAspAsnleuAlaIhrTrpAspAspAsnGluMetAsnleuGlnIle         | 1014 |
| Dh | 2823 | CTTCAGTGCACACACTCATACCCCTGATGTGGGACAGAGAGATGAACACTTCACCT        | 2882 |
| Oy | 1014 | eAlaValAspArGMetHisLysGlyValAlaIhrValLysArGlyLysIleTyrGluPheI   | 1034 |
| Dh | 2883 | GGCCCTGTCCCGCATCCAGAGGGGCGCTTGTTCAGAGCGGACACCTGGGATTTCTG        | 2942 |
| Oy | 1034 | eGlnGlnSerPheIleArGlyGlnIleLysIleleuAspGluIleLysProleuAsp--As   | 1053 |
| Dh | 2943 | CTGTGTCTCTCTGGCGACCGCGCCTGAG-----AAAGCCGACGCCCTTGC              | 2987 |
| Oy | 1053 | pleuAsnAsnLysLysAspSerCysMetSerAsn-----HisTh                    | 1066 |
| Dh | 2988 | CGCCAGAGGCGAGCTGCCAGGTGCATGTGCACCCCTACTCCCGCACCCCGAGAAC         | 3047 |
| Oy | 1066 | r***GluIleGlyLysAspLeuAspTyrleuLysAspValAsnGlyThrThrSerGlyI     | 1086 |
| Dh | 3048 | GGAGAAAGTGTCTCCACCGCGCAAGAAACAGATTGGAGAGGCGAGAACACAGGCCA        | 3107 |
| Oy | 1086 | eGlyThrGlySerSerValGlyLysTyrIleIleAspGlnSerAspTyrMetSerPheI     | 1106 |
| Dh | 3108 | GGGACACCCCGGAGTCCAGAC-----                                      | 3129 |
| Oy | 1106 | eAsnAsnProSerleuThrValIhrValProIleAlaValGlyLysSerAspPheGlnAs    | 1126 |
| Dh | 3130 | -----GGCGTGTGTGTGCCATATCGTGTGGCGGAGTGCAGACAGATGA                | 3173 |

QY 1126 nleuanthrGlunaspheserSerGluserAspLeuGlunSerLysGluLysLeuAs 1146  
 Db 3174 C-----CAAGAAAGAGATAGAGAGAACACCTGGGACGAGAGAGAGATCCAGCAACAGCA 3230  
 QY 1146 ngLuser----- 1148  
 Db 3231 GGATCCACAGCTGTGTGCGGCTGGCCAGAGGCGCTCCGGATTCCAGAGACTGGAGCCA 3290  
 QY 1148 ----- 1148  
 Db 3291 GGTGTACGACTGCTCTCTGTAGGCCGAGGCCATGTCATCGAGGCGGACTGGCGCA 3350  
 QY 1149 -----SerSerSer 1152  
 Db 3351 GCAGTGGAAAGCGGACCCAGGCGCCAGGGGTGGAGACCCAGAGAGACATGCTGCTC 3410  
 QY 1152 rgluglySerThrValAspIleGlyAlaProValGlu-----GluGlnProValValGlu 1170  
 Db 3411 CGAGGGGACGACAGCAGACATGACCAACACCGGCTGAGCTCTCTGGAGCAGATCCCTGACCT 3470  
 QY 1170 uproglugluThrLeuGluProGluAlaCysPheThrGluGlyCysValGlnArgPheLys 1190  
 Db 3471 CGGCGAGGATGTCAAGAGACCAGAGGACTGCTTCACTGAAGGCTGTGCCGCGCTGTCC 3530  
 QY 1190 scYsYsGlnIleAsnValGluGluArgGlyLysGluThrProAsnLeuArgThr 1210  
 Db 3531 CTGCTGTGCGGTGACACACACAGGCCCCAGGAGAGGCTGTGGGGGTGGCCCAAGAC 3590  
 QY 1210 rCyPheArgIleValGlnHisAsnTrpPheGluThrPheIleValPheMetIleLeu 1230  
 Db 3591 CTGCTACCATGCTGTGGAGCAGAGCTGTTCGAGACATTCATATCTTCATGATCTTACT 3650  
 QY 1230 userSerGlyAlaLeuAlaPheGluAspIleTyrIleAspGlnArgLysThrIleLysThr 1250  
 Db 3651 CACAGTGGAGGCGCTGCTCGGAGACATCTACCTAGAGAGGAGGAGCAACATCAAGGT 3710  
 QY 1250 rMetLeuGluThrAlaAspLysValPheThrTyrIlePheIleLeuGluMetLeuLys 1270  
 Db 3711 TGTGCTGTGATGTGCGACAGAGATTCACATATGCTTGTGTGGAGATGCGCTCAA 3770  
 QY 1270 strValAlaTyrGlyGlnThrTyrPheThrAsnAlaTrpCysTrpLeuAspPhe 1290  
 Db 3771 GTGGGGGCGCTACGGCTCAAGAAATCTTACCAATGCTGTGGTGGCTGCGCTTCT 3830  
 QY 1290 uIleValAspValSerLeuValSerLeuThrAlaAsnAlaLeuGlyTyrSerGluLeuGlu 1310  
 Db 3831 CACGTGAGACGCTCTCTGTGTAGCGCTGTGGCCACACCCCTGGGCTTGGCCGAGATGGG 3890  
 QY 1310 yAlaIleLysSerLeuThrPheThrArgAlaLeuArgProLeuArgAlaLeuSerArgPh 1330  
 Db 3891 CCCCATCATACCTGTGGAGGCGCTGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3950  
 QY 1330 egluglyMetArgValValValAlaAsnAlaLeuGlyAlaIleProSerIleMetAsnVal 1350  
 Db 3951 TGAGGGCATAGAGGT 4010  
 QY 1350 IleuLeuValCysLeuIlePheThrLeuIlePheSerIleMetGlyValAsnLeuPheAl 1370  
 Db 4011 CTTCTGCTGT 4070  
 QY 1370 agLylLysPheThrLysCysIleAsnThrThrThrLysPhe-----ArgPheAspIleGluAs 1389  
 Db 4071 GGGGAACTTTGGGAGGTGATCAACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4130  
 QY 1389 rValAsnAsnHisThrAspCysLeuLysLeuIleGluArgAsnGluThrAlaArg----- 1407  
 Db 4131 CCGTGAACACACAG 4181  
 QY 1408 -TrpLysAsnValLysValAsnPheAspAsnValGlyPheGlyTyrIleLeuSerLeuLeuGlu 1427  
 Db 4182 CTGGACCAAGAGTGAAGTCAATTTGTGACAAAGTGGGGGCGGGGTACTGGCCCTTCTGCA 4241

QY 1427 nValAlaThrPheLysGlyTrpMetAspIleMetTyrAlaAlaValAspSerArgAsnVal 1447  
 Db 4242 GGTGGCAACATTTAAAGCTGTGATGACATTTATGTATGACAGCTGTGGACTCCAGGGGGTA 4301  
 QY 1447 lGluLeuGlnProLysTyrGluGluSerLeuLysTyrMetTyrLeuTyrPheValIlePheIle 1467  
 Db 4302 TGAGAGCAGCCTCAGTGGGAATACACCTCTACATGATGATCATTTTGTATTTCAT 4361  
 QY 1467 eIlePheGlySerPhePheThrLeuAsnLeuPheIleGlyValIleIleAspAsnPheAs 1487  
 Db 4362 CATCTTGGGCTTCTTCCACCTGACCTCTTATTTGTGTGCATCATTTGACAACTTCAA 4421  
 QY 1487 nglnglnLysLysPheGlyGluAspIlePheMetThrGluGlnLysLysTyr 1507  
 Db 4422 CCACAGAAAGAAAGATTAGGGGGCCAGAGACTTCTTCATGACAGAGAGACAGAAAGTA 4481  
 QY 1507 rTyrAsnAlaMetLysLysLeuGlySerLysLysProGlnLysProIleProArgProGlu 1527  
 Db 4482 CTACAAATGCCATGAGAAAGAGTGGGCTCCAGAGAGCCCAAGAGCCATCCAGGCGCT 4541  
 QY 1527 yAsnLysPheGlnGlyMetValPheAspPheValThrArgGlnValPheAspIleSerIle 1547  
 Db 4542 GAACAAAGTACACAGGCGCTCATATTCGACATTCGTGACCAAGAGAGCGCTTGGACCTCACCAT 4601  
 QY 1547 eMetIleLeuIleCysLeuAsnMetValThrMetMetValGluThrAspAspGlnSerGlu 1567  
 Db 4602 CATGTTTGTGATCTGCTGTGAATATGTGACCATGATGTGGAGACAGATGACAAAGTCC 4661  
 QY 1567 uTyrValThrThrIleLeuSerArgIleAsnLeuValPheIleValPheThrGlyGlu 1587  
 Db 4662 TGAGAAATCAACATCTGGCCAGAGATCAACCTGCTCTTGTGGGCATCTTCACAGGGA 4721  
 QY 1587 uCysValLeuLysLeuIleSerLeuArgHisTyrTyrPheThrIleGlyTyrAsnIlePhe 1607  
 Db 4722 GTGATTTGTCAAGGCGCTGCGCTGCGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4781  
 QY 1607 eAspPheValValIleLeuSerIleValGlyMetPheLeuAlaGluLeuIleGlyLys 1627  
 Db 4782 GCAGCTGTGCTGTGATCTTCATCTCTCATCTGCTGTGGGCTGCTGCTGCTGCTGCTGCTGCT 4841  
 QY 1627 strPheValSerProThrIlePheArgValIleArgLeuAlaArgIleGlyArgIle 1647  
 Db 4842 GTACTTCTTCCCGGAGCGCTTCCGAGTCACTCGGCTGGCCGAAATAGCGCGATCT 4901  
 QY 1647 uArgLeuIleLysGlyAlaLysGlyIleArgThrLeuLeuPheAlaLeuMetSerIle 1667  
 Db 4902 CAGACTGATCCGAGGGGCGCAAGGGGATCCGACGCTGCTTGTGGCCATGATGTCCCT 4961  
 QY 1667 uProAlaLeuPheAsnIleGlyLeuLeuPheLeuValMetPheIleTyrAlaIlePhe 1687  
 Db 4962 GCGTGGCCTCTTCAACATCGGAGCTGTGCTCTCTCTCTCAATGTTCACTACTCCATCTT 5021  
 QY 1687 eglYMetSerAsnPheAlaTyrValLysArgGluValGlyIleAspAspMetPheAsnPh 1707  
 Db 5022 TGGCATGGCCAACTCGCTTATGTCAGAGTGGAGGCTGGCATTCAGCATGTTCACTT 5081  
 QY 1707 egluThrPheGlyAsnSerMetIleCysLeuPheGlnIleThrThrSerAlaGlyTyrPhe 1727  
 Db 5082 CCAGAGCTTCCGCCAACACAGATGCTGTGCTCTTCCAGATTCACAGCTGCGGCGGTGGGA 5141  
 QY 1727 pglYLeuLeuAlaProIleLeuAsnSerLysProProAspCysAspProAsnLysValAs 1747  
 Db 5142 TGGCTCTCTCAAGCCCATCTCCAACTAGGCGCGCTTACTGAGCCCACTGTGCCAA 5201  
 QY 1747 nProGlySerSerValLysGlyAspCysGlyAsnProSerValGlyIlePhePhePheVal 1767  
 Db 5202 CAGCAATAGGCTCT---CGGGGGAGCTGGGGAGGCCAGCCAGCTGGGCAATCTTCTTCCAC 5258  
 QY 1767 lSerTyrIleIleIleSerPheLeuValValValAsnMetTyrIleAlaValIleLeuGlu 1787  
 Db 5259 CACCTTACATCATCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 5318  
 QY 1787 uAsnPheSerValAlaThrGluGluSerAlaGluProLeuSerGluAspAspPheGluMet 1807



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Db 5319 GAACTTACAGTGGCCAGGAGAGAGACACCCCTGAGTGGAGACTGATAT 5378
Qy 1807 tethyrtgluvaltrpglulyspheasproaspalathrlnphemetglupheglu 1827
Db 5379 GTCTATGAGACTGGAGAAATTTGACCAGAGGCCACTGATTTATGAGATTCGG 5438
Qy 1827 sleuserglnphealalaleuclupropoleuanleuproglnprobsnlyste 1847
Db 5439 CCGTGTGACTTGGCCAGCCCTGCTGTGAGCCACTCCGTATGCCAAGCCCAACAGAT 5498
Qy 1847 uclnleuilealameasleuprometvalserglaspargilehsicysleuasp11 1867
Db 5499 AAGCCTCATCAACATGAGACTGCCATGGAGTGGAGATGGAGCCATCATGATGACAT 5558
Qy 1867 eleuphealapherthlyarthyaleuclugluserglglumetaspalaleuar 1887
Db 5559 TCTCTTGGCTTCCACCAAAAGGTCTGGGGAGTCTGGGGAGATGAGCCCTGAAGAT 5618
Qy 1887 eglmetglulargphemetlaseranproserlysvalsestertgluprolleph 1907
Db 5619 CCGATGGAGGAGAAATTTATGCGACCAACCATCCAGATCTCTACAGGCCATCAC 5678
Qy 1907 rthrtthleuylsargylsnglulvalseralavalleilegluarphlatyaf 1927
Db 5679 CACACACTCCGGCCAGACAGAGAGGTGTCGCCATGTTATCCAGAGACCTTCG 5738
Qy 1927 garthslleuylsargylthlyvalysglinalaserpherthlyasnllyasnl 1947
Db 5739 CAGGACCCGCTGCACAGCTCTTGAAGATGCCCTCTCTCCGTCAGAGCGGG 5798
Qy 1947 elysgllyalalaenleuilelysgluasp-----metleil 1961
Db 5799 CAGCGGC-----CTCTCCGAGAGATGCCCTGACCGAGAGGCCCTCATCCG 5846
Qy 1961 easparglyleasn-----serlethrghlysthraspleuthmetse 1978
Db 5847 CTACGTGATGAGTACACTTCTCCGACCCCTTGGCCACCCCTCAGCTCCATCTC 5906
Qy 1978 rthralaaiacysproprosettyrtyrparvalthlysploilevalglulysl 1998
Db 5907 CTCCTCTCTTCCCACTCTCTATGACGTGACTAGAGCCAGCAGGATTAACCTCCA 5966
Qy 1998 uclnngllylasp 2003
Db 5967 GGTGGGGGGTCTGAC 5982

RESULT 14
US-09-864-761-10189/C
: Sequence 10189, Application US/09864761
: Patent No. US20020048763A1
: GENERAL INFORMATION:
: APPLICANT: Penn, Sharon G.
: APPLICANT: Rank, David R.
: APPLICANT: Hanzel, David K.
: APPLICANT: Chen, Wensheng
: TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
: TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
: FILE REFERENCE: Aecmca-X-1
: CURRENT APPLICATION NUMBER: US/09/864,761
: PRIOR APPLICATION NUMBER: 2001-05-23
: PRIOR FILING DATE: 2000-02-04
: PRIOR APPLICATION NUMBER: US 60/207,456
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: US 09/632,366
: PRIOR FILING DATE: 2000-08-03
: PRIOR APPLICATION NUMBER: GB 24263.6
: PRIOR FILING DATE: 2000-10-04
: PRIOR APPLICATION NUMBER: US 60/236,359
: PRIOR FILING DATE: 2000-09-27
: PRIOR APPLICATION NUMBER: PCT/US01/00666
: PRIOR FILING DATE: 2001-01-30

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: PRIOR APPLICATION NUMBER: PCT/US01/00667
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00664
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00669
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00665
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00668
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00663
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00662
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00661
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00670
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: US 60/234,687
: PRIOR FILING DATE: 2000-09-21
: PRIOR APPLICATION NUMBER: US 09/608,408
: PRIOR FILING DATE: 2000-06-30
: PRIOR APPLICATION NUMBER: US 09/774,203
: PRIOR FILING DATE: 2001-01-29
: NUMBER OF SEQ ID NOS: 49117
: SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
: SEQ ID NO 10189
: LENGTH: 1992
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: MAP TO AC010127.3
: OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.6
: OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.4
: US-09-864-761-10189

Alignment Scores:
Pred. No.: 1,1e-201 Length: 1992
Percent Similarity: 2037.00 Matches: 442
Best Local Similarity: 70.74% Conservative: 27
Query Match: 66.67% Mismatches: 79
DB: 19.59% Indels: 116
Gaps: 12

US-09-930-871-12 (1-2009) x US-09-864-761-10189 (1-1992)
Qy 1371 glylspheyrhiscysileasnthrthrglyaspargpheasplilegluaspval 1390
Db 1984 GGATCCTTTCAGAAATGACAGAACATACATTAATGATATTAATAAATTTAGCTGG 1925
Qy 1391 Asn-----AsnHsthraspCysleuylsleuilegluargsnlgurth 1405
Db 1924 AATTTAAGTAACTACCAAGATCATGCGGAGATGAAAGTACATCAAAAGCTACCAAT 1865
Qy 1406 Alaargtrpysasnvalylvalasnphespaspvalglphedglytyrleusleu 1425
Db 1864 TTCACATGAGAAAGCAAGTAATAGCAATTTAGCAATGCAATT----- 1820
Qy 1426 leuglnvalalathrphelysglytrpmetasplilemettyralalavalaspseratg 1445
Db 1820 ----- 1820
Qy 1446 AsnValgluleucluprollystyglnugluserleutyrmetyrleu----- 1461
Db 1819 -----TCAGAAAGATCAGCTATATATAAAGCTTGTACC 1784
Qy 1462 tyyphevalillephelellephedglyserpneperthleuasnleuhe---llegly 1480
Db 1783 TATACGTGGGCTGCTGACTGTTCCGCCAAATGTCATTTTAACTATTTCTTTTAA 1724
Qy 1481 Valilleleaspasnphespasnnglnlystlyspheglyglylnaspillepemet 1500
Db 1723 ATTCTGACTTGGACTTACATTAATAAAGTATTAATAAATCT----- 1676

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: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00662
: PRIOR FILING DATE: 2001-01-30
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: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00670
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: US 60/234,687
: PRIOR FILING DATE: 2000-09-21
: PRIOR APPLICATION NUMBER: US 09/608,408
: PRIOR FILING DATE: 2000-06-30
: PRIOR APPLICATION NUMBER: US 09/774,203
: PRIOR FILING DATE: 2001-01-29
: NUMBER OF SEQ ID NOS: 49117
: SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
: SEQ ID NO 18334
: LENGTH: 1194
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: MAP TO AC010127.2
: OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.1
: OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.87
: OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.3
: OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
: OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 7.9
: OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.6
: OTHER INFORMATION: EXPRESSED IN HEEL, SIGNAL = 1.3
: OTHER INFORMATION: EXPRESSED IN HB100, SIGNAL = 2.3
: OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.94
: OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
: OTHER INFORMATION: NT HIT: M91803.1, EVALUATE 0.00e+00
: OTHER INFORMATION: SWISSPROT HIT: P04774, EVALUATE 0.00e+00
: OTHER INFORMATION: EST_HUMAN HIT: AL120392.1, EVALUATE 1.00e-129
: US-09-864-761-18334

Alignment Scores:
Pred. No.: 7.6e-195 Length: 1194
Score: 1967.50 Matches: 390
Percent Similarity: 96.56% Conservative: 3
Best Local Similarity: 95.82% Mismatches: 1
Query Match: 18.92% Indels: 13
Gaps: 3
DB: 10

US-09-930-871-12 (1-2009) x US-09-864-761-18334 (1-1194)
QY 1599 TyrPhehrlleGlyTTPan-----lLePheaspheValValleleuSer 1615
DB 1191 TTTCTTCACT---GGTTCGTATTCATCATGTTATTC----- 1159
QY 1616 lLeValGlYmetPheleuAlaGluLeuIlleGluYstYrPheValSerProThrleuPhe 1635
DB 1158 ---ATAGATATGTTCTTCCGCGAGCTATGAGAAAAGATTTCTGTCCTTACCTGTTTC 1102
QY 1636 ArgValIleArgleuAlaArgIleGlyArgIleleuArgleuIleYsgIalAlaYsgIy 1655
DB 1101 CGAGTGTATCGTCTGTAGATGATGGCGAATCTACGTCTGATCAAGGAGCAAGGAGG 1042
QY 1656 lLeArgThrleuLeuPheAlaLeuMetSerleuProAlaLeuPheAsnIlleGlyleu 1675
DB 1041 ATCCGCAACGCTGCTCTTGGTTTGATGATGTCCTTCCTCGTTGTTTAAACATCGGCTTC 982
QY 1676 leuLeuPheleuValMetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrVal 1695
DB 981 CTACTCTCTCTACTCATGTTCACTACGCAATCTTTGGGATGTCCAACTTTCCTTATGTT 922
QY 1696 LysArgGluValAlaGlyIleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIle 1715
DB 921 AAGAGGGAAGATGGGATCGATGACATGTCACTTTGAGACCTTTGGCAACAGCATGATC 862
QY 1716 CysleuPheGlnIlePheThrSerAlaGlyTyrAspGlyleuLeuAlaProIleleuAsn 1735
DB 861 TGGCTATTCACAAATTAACAACCTCTGCTGGGATGATGATGTAGACCACTTCTCAAC 802

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QY 1736 SerLysProProAspCysAspProAsnLysValAsnProGlySerSerValIleYsgIasp 1755
DB 801 AGTAAGCAACCCGACTGTGACCTTATTAAGTTAAACCTGGAAAGCTTAAGGAGAAC 742
QY 1756 CysGlyAsnProSerValGlyIlePhePhePheValSerTyrIleIleSerPheleu 1775
DB 741 TGTGGAAACCACTCTGTGGAAATTTCTTTTGTGACATTCATATCATATCTTCTCTG 682
QY 1776 ValValValAsnMetTyrIleAlaValIleleuGluAsnPheSerValAlaThrGluIle 1795
DB 681 GTTGGTGAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 622
QY 1796 SerAlaGluProLeuSerGluAspAspPheGluMetPheTyrGluValTyrGluYsphe 1815
DB 621 AGTCGAGACCTCTGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 562
QY 1816 AspProAspAlaThrGluPheMetGluPheGluIleYsgIleuSerGluPheAlaAlaLeu 1835
DB 561 GATCCCATGCACTCACTCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 502
QY 1836 GluProProLeuAsnLeuProGluProAsnLysleuGluIleAlaMetAspLeuPro 1855
DB 501 GAACCGCTCTCAATCTGCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 442
QY 1856 MetValSerGlyAspArgIleHisCysleuAspIleleuPheAlaPheThrLysArgVal 1875
DB 441 ATGGGATGTGTGACCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 382
QY 1876 LeuGlyGluSerGlyGluMetAspAlaLeuArgIleGluMetGluGluArgPheMetAla 1895
DB 381 CTAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 322
QY 1896 SerAsnProSerLysValSerTyrGluProIleThrThrleuLysArgLysGlnIle 1915
DB 321 TCCATCTCTTCCAAAGGTCTCTATCAGCAATCACTACTACTTAAACGAACAAAGAG 262
QY 1916 GluValSerAlaValIleIleGluArgAlaTyrArgHisIleuLeuLysArgThrVal 1935
DB 261 GAGTATCTGTGTCATTAATTCAGGCTGTACAGAGCCACCTTTTAAAGCAACTGTA 202
QY 1936 LysGluAlaSerPheThrTyrAsnLysAsnLysIleYsgIyAlaAsnLeuIle 1955
DB 201 AAACAGCTCTCTTACGTACATAAACAACAAAGTGGGCTTAATCTTCTTATA 142
QY 1956 LysGluAspMetIleIleAspArgIleAsnGluAsnSerIleThrGluLysThrAspLeu 1975
DB 141 AAAGAGACATGATTAATTGACAGATAAATGAAACCTATTACAGAAAAAATGATCTG 82
QY 1976 ThrMetSerThrAlaAlaCysProProSerTyrAspArgValThrLysProIleValGlu 1995
DB 81 ACATATCTCTGACGCTGTGACCTTCTATGACGAGGATGACAAAGCAATTTGTGAA 22
QY 1996 LysHisGluGlnGluGlyLys 2002
DB 21 AAACATGAGCAAGAGGAAA 1

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Search completed: April 23, 2003, 04:57:45  
 Job time : 651 secs

GenCore version 5.1.4.p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 23, 2003, 02:49:16 ; Search time 7546 Seconds

(without alignments)  
7748.150 Million cell updates/sec

Title: US-09-930-871-12

Perfect score: 2009  
Sequence: 1 MEGTALVPPGPDSENFRTRE.....TKPIVEKHGSGKDEKAKGK 2009

Scoring table:

|        |      |         |      |
|--------|------|---------|------|
| OLIGO  | 60.0 | Xgapert | 60.0 |
| Xgapop | 60.0 | Ygapert | 60.0 |
| Fgapop | 6.0  | Fgapert | 7.0  |
| Delop  | 6.0  | Delext  | 7.0  |

Searched: 2054640 seqs, 14551402878 residues

Word size: 1

Total number of hits satisfying chosen parameters: 4106490

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

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-Q/cgnt\_1/USPTO.spool/US09930871/runat\_16042003\_114925\_8986/app\_query.fasta\_1.2183  
-DB-GenBml -OPMT-fastap -START-1 -END-1 -MATRIX-oligo -TRANS-human40.cdl  
-LOOEXT-0 -UNITS-bits -START-1 -END-1 -MATRIX-oligo -TRANS-human40.cdl  
-LIST-45 -DOCALLIG-200 -THR SCORE-quality -THR MIN-1 -ALIGN-15 -MODE-LOCAL  
-OUTPM-PTC -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-2000000000  
-USRR-US09930871.ecgn\_1\_1\_5394\_etunat\_16042003\_114925\_8986 -NCPU-6 -ICPU-3  
-NO\_ALPRY -NO\_MMAP -LARGESUBSTRY -NES-SCORES-0 -WAIT -LONGLOC -DEV-TIMEOUT-120  
-WARN-TIMEOUT-30 -THREADS-1 -XGAPOP-60 -XGAPEXT-60 -FGAPOP-6 -FGAPEXT-7  
-YGAPOP-60 -YGAPEXT-60 -DELOP-6 -DELEXT-7

Database :

GenBml: \*  
1: gb\_ba: \*  
2: gb\_hlg: \*  
3: gb\_in: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pr: \*  
10: gb\_ro: \*  
11: gb\_sts: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_vl: \*  
15: em\_ba: \*  
16: em\_fun: \*  
17: em\_hum: \*  
18: em\_in: \*  
19: em\_jnu: \*  
20: em\_om: \*  
21: em\_or: \*  
22: em\_ov: \*  
23: em\_pat: \*  
24: em\_ph: \*  
25: em\_pl: \*  
26: em\_ro: \*  
27: em\_sts: \*  
28: em\_un: \*

29: em\_vl: \*  
30: em\_hlg\_hum: \*  
31: em\_hlg\_inv: \*  
32: em\_hlg\_other: \*  
33: em\_hlg\_mus: \*  
34: em\_hlg\_pln: \*  
35: em\_hlg\_trod: \*  
36: em\_hlg\_mam: \*  
37: em\_hlg\_vrt: \*  
38: em\_sy: \*  
39: em\_hlgo\_hum: \*  
40: em\_hlgo\_mus: \*  
41: em\_hlgo\_other: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| 1          | 2007  | 99.9        | 6030   | 6     | AX391140 Sequence  |
| 2          | 1970  | 98.1        | 5922   | 6     | AX391142 Sequence  |
| 3          | 1733  | 86.3        | 8378   | 6     | AX164171 Sequence  |
| 4          | 1447  | 72.0        | 8378   | 6     | AX164172 Sequence  |
| 5          | 1444  | 71.9        | 4362   | 6     | AX391144 Sequence  |
| 6          | 1382  | 68.8        | 4179   | 6     | AX391146 Sequence  |
| 7          | 1332  | 66.3        | 4197   | 6     | AX391148 Sequence  |
| 8          | 1326  | 66.0        | 5997   | 6     | AX391130 Sequence  |
| 9          | 1289  | 64.2        | 5889   | 6     | AX391132 Sequence  |
| 10         | 1126  | 56.0        | 6046   | 9     | AY043484 Homo sapi |
| 11         | 947   | 47.1        | 8131   | 9     | AF225985 Homo sapi |
| 12         | 763   | 38.0        | 4329   | 6     | AX391134 Sequence  |
| 13         | 701   | 34.9        | 4146   | 6     | AX391136 Sequence  |
| 14         | 670   | 33.3        | 4164   | 6     | AX391138 Sequence  |
| 15         | 403   | 20.1        | 1269   | 9     | HSSCN1A            |
| 16         | 403   | 20.1        | 1269   | 9     | HOMSDOPCHA         |
| 17         | 392   | 19.5        | 190066 | 9     | AC010127           |
| 18         | 392   | 19.5        | 191194 | 2     | AC021673           |
| 19         | 375   | 18.7        | 8398   | 10    | RATNCHI            |
| 20         | 375   | 18.7        | 8398   | 10    | RATNCHI            |
| 21         | 329   | 16.4        | 164928 | 2     | AC129458           |
| 22         | 329   | 16.4        | 206895 | 2     | AL844526           |
| 23         | 318   | 15.8        | 3403   | 6     | AX164202           |
| 24         | 232   | 11.5        | 2659   | 10    | MUSSC3R            |
| 25         | 161   | 8.0         | 1531   | 10    | MUSSC3R            |
| 26         | 161   | 8.0         | 8552   | 10    | RATNCHI            |
| 27         | 161   | 8.0         | 8553   | 10    | RATNCHI            |
| 28         | 139   | 6.9         | 6328   | 9     | HOMBRAX            |
| 29         | 139   | 6.9         | 8349   | 6     | AX164203           |
| 30         | 139   | 6.9         | 8349   | 6     | AX164204           |
| 31         | 127   | 6.3         | 163106 | 2     | AP002375           |
| 32         | 120   | 6.0         | 163551 | 2     | AC015777           |
| 33         | 119   | 5.9         | 3700   | 6     | AX164234           |
| 34         | 119   | 5.9         | 4337   | 9     | F327224S23         |
| 35         | 119   | 5.9         | 154141 | 2     | AC121042           |
| 36         | 119   | 5.9         | 175830 | 2     | AC094721           |
| 37         | 119   | 5.9         | 188616 | 9     | AC011303           |
| 38         | 114   | 5.7         | 163551 | 2     | AC015777           |
| 39         | 103   | 5.1         | 458    | 10    | RNO277391          |
| 40         | 99    | 4.9         | 6822   | 6     | AX401928           |
| 41         | 99    | 4.9         | 6822   | 10    | RNSCIII            |
| 42         | 96    | 4.8         | 965    | 6     | AX164187           |
| 43         | 94    | 4.7         | 677    | 6     | AX164197           |
| 44         | 94    | 4.7         | 1556   | 9     | S71446             |
| 45         | 94    | 4.7         | 163106 | 2     | AP002375           |

RESULT 1

## ALIGNMENTS

AX391140 Sequence  
AX391142 Sequence  
AX164171 Sequence  
AX164172 Sequence  
AX391144 Sequence  
AX391146 Sequence  
AX391148 Sequence  
AX391130 Sequence  
AX391132 Sequence  
AY043484 Homo sapi  
AF225985 Homo sapi  
AX391134 Sequence  
AX391136 Sequence  
AX391138 Sequence  
X63632 Homo sapi  
M91803 Homo sapi  
AC010127 Homo sapi  
AC021673 Homo sapi  
X03638 Rat brain m  
M2253 Rattus norv  
AC129458 Rattus no  
AL844526 Mus muscu  
AX164202 Sequence  
I42339 Mus musculu  
I42341 Mus musculu  
M2254 Rattus norv  
X03639 Rat brain m  
M94055 Human volta  
AX164203 Sequence  
AX164204 Sequence  
AP002375 Homo sapi  
AP002377 Homo sapi  
AC015777 Homo sapi  
AX164234 Sequence  
AF327224S23 Homo sapi  
AC121042 Rattus no  
AC094721 Rattus no  
AC011303 Homo sapi  
AC015777 Homo sapi  
AJ277391 Rattus no  
AX401928 Sequence  
Y00766 Rat mRNA fo  
AX164187 Sequence  
AX164197 Sequence  
S71446 SCNA-brain  
AP002375 Homo sapi

| LOCUS   | AX391140   | 6030 bp       | DNA  | linear | PAT 19-MAR-2002 |
|---|--|---------------|------|--------|-----------------|
| DEFINITION                                    | Sequence 11 from Patent WO0214498.                                     |               |      |        |                 |
| ACCESSION                                     | AX391140   |               |      |        |                 |
| VERSION                                       | AX391140.1   | GI:19584237   |      |        |                 |
| KEYWORDS                                      |  |               |      |        |                 |
| SOURCE  | human.   |               |      |        |                 |
| ORGANISM                                      | Homo sapiens   |               |      |        |                 |
| REFERENCE                                     | 1  |               |      |        |                 |
| AUTHORS                                       | Turner,C.A., Mathur,B. and Mathur,D.                                   |               |      |        |                 |
| TITLE   | Novel human ion channel proteins and polynucleotides encoding the same |               |      |        |                 |
| JOURNAL                                       | Patent: WO 0214498-A 11 21-FEB-2002;                                   |               |      |        |                 |
| FEATURES                                      | Lexicon Genetics Incorporated (US)                                     |               |      |        |                 |
| source  | 1..6030  |               |      |        |                 |
| BASE COUNT                                    | 1786 a 1190 c 1345 g 1706 t  |               |      |        | 3 others        |
| ORIGIN  |  |               |      |        |                 |
| Alignment Scores:                             |  |               |      |        |                 |
| Pred. No.:                                    | 0  | Length:       | 6030 |        |                 |
| Score:  | 2007.00  | Matches:      | 2009 |        |                 |
| Percent Similarity:                           | 100.00%  | Conservative: | 0    |        |                 |
| Best Local Similarity:                        | 100.00%  | Mismatches:   | 0    |        |                 |
| Query Match:                                  | 99.90%   | Indels:       | 0    |        |                 |
| Db:   | 6  | Gaps:         | 0    |        |                 |
| US-09-930-871-12 (1-2009) x AX391140 (1-6030) |  |               |      |        |                 |
| QY  | 1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhenThrArgGlu           | 20            |      |        |                 |
| Db  | 1 ATGGAGCAAAACAGTCTCTGTACACACAGACCTGCACACTTCTTACACAGAGAA               | 60            |      |        |                 |
| QY  | 21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluGluValAlaValAsnProGlyProasp     | 40            |      |        |                 |
| Db  | 61 TCTCTGGGGCTATTGAAAGAGCGCAATGCAGAGAAAGGCAAGAAATCCAAACCAAC            | 120           |      |        |                 |
| QY  | 41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn        | 60            |      |        |                 |
| Db  | 121 AAAAAAGATGACGAGAGAAATAGGCCCAAGCAATATGACTTGGAAAGTGAAGAAC            | 180           |      |        |                 |
| QY  | 61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu        | 80            |      |        |                 |
| Db  | 181 CTTCATTATTATTATGAGACATTCCTCCACAGATGGTGTGACAGCCCTCGAGAGACCTG        | 240           |      |        |                 |
| QY  | 81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyValAlaIlePhe        | 100           |      |        |                 |
| Db  | 241 GACCCCTACTATATCAATAGAGAAACCTTTATAGATTGAATTAAGGAGAGCCATCTTC         | 300           |      |        |                 |
| QY  | 101 ArgPheSerAlaIleThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle    | 120           |      |        |                 |
| Db  | 301 CGGTTCAGTGGCACCTGCGCCCTGCATTTTAACCTCCCTCAATCCCTTAGAGAAATA          | 360           |      |        |                 |
| QY  | 121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr       | 140           |      |        |                 |
| Db  | 361 GCTATTAGATTGGTATGATCATCTTATATTCAGATGCTAAATATGTGCATATTATTGACA       | 420           |      |        |                 |
| QY  | 141 AsnGlyValPheMetThrMetSerAsnProProAspTyrThrLysAsnValGluTyrThr       | 160           |      |        |                 |
| Db  | 421 AACGTGTGTTTATGACATAGTATACCTCTCTGATTTGGACAAAGAAATGATGATACACC        | 480           |      |        |                 |
| QY  | 161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu       | 180           |      |        |                 |
| Db  | 481 TTCACAGGAATATATCTTTGGAATCACTTATAAAAAATTTATGCAAGGGGATCTGTTA         | 540           |      |        |                 |
| QY  | 181 GluAspPheThrPheLeuArgAspProTyrPasnThrLeuAspPheThrValIleThrPhe      | 200           |      |        |                 |
| Db  | 541 GAAATATTTACTCTTCCTGGGATCCATGAAAGCGCTCGATTTCACTGTCATTACATTT         | 600           |      |        |                 |

|    |      |   |      |
|----|------|---|------|
| QY | 201  | AlAtYrValThhGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal    | 220  |
| Db | 601  | GGTACGTCACAGAGATTGTGGACCTGGGCAATGCTCTGGCATGAGAACATTCACAGATT     | 660  |
| QY | 221  | LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu    | 240  |
| Db | 661  | CTCCGAGCATTTGAAACACATTTTCAGTCTCCAGGCGCTGAAGAACCATTTGGGAGCCCTG   | 720  |
| QY | 241  | IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal    | 260  |
| Db | 721  | ATCCAGTGCTGTGAAGAACCTCTCAGATGTATATGATCCTGACTGCTGTCTGTGAGCGTA    | 780  |
| QY | 261  | PheAlaLeuIleGlyLeuGlnLeuPheMetLysLeuArgAsnLysCysIleGlnTrp       | 280  |
| Db | 781  | TTTGTCTTAATTTGGGCTCCACTGTTCATGGGCAACCTGAGGAATAATGTATACAAATGG    | 840  |
| QY | 281  | ProPheThrAspAlaSerLeuGlnGlnHisSerIleGlyLysAsnIleThrValAsnTrp    | 300  |
| Db | 841  | CCCTCCACCAATGCTCTCTTGAGAGAACATAGTATGAAAAAGAAATTAATCACTGGAATTAT  | 900  |
| QY | 301  | AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTrpIleGlnAsp    | 320  |
| Db | 901  | AATGTACACTATTAATAAGAAACGTGTTTATGTTAGTTACGGAAGCATATATTCAGAT      | 960  |
| QY | 321  | SerArgTrpHisTrpPheLeuGlnGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer    | 340  |
| Db | 961  | TCMAATATTCATTTATTTCTCGAGGGTTTTTAATGACACTACATATGTGAATTAACCTCT    | 1020 |
| QY | 341  | AspAlaGlyLysCysProGlnGlyTrpMetCysValLysAlaGlyArgAsnProAsnTrp    | 360  |
| Db | 1021 | GATGCAGGCGCAATGCCCAGAGGAAATATATGTGTGAAGCACTGGTGAATATCCCAATTAT   | 1080 |
| QY | 361  | GlyTrpThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr    | 380  |
| Db | 1081 | GGCTACACAGAGTTTGATACCTTCAGTTGGGCTTTTTTGTCCTGTTTGACATAAGACT      | 1140 |
| QY | 381  | GlnAspPheTrpGluAsnLeuTrpGlnLeuThrLeuArgAlaAlaGlyLysThrTrpMet    | 400  |
| Db | 1141 | CAGGCTTCCTGGGAAAACTTTATCAACATGCAATTAAGTCTCTGGGAAAAAGTCAATG      | 1200 |
| QY | 401  | IlePhePheValIleValIlePheLeuGlySerPheTrpLeuIleAsnLeuIleLeuAla    | 420  |
| Db | 1201 | ATATTTTGTGTGGTGCATTTTCTTGGGCCATTCACCTAATTAATTTGATCCGGCT         | 1260 |
| QY | 421  | ValValAlaMetAlaTrpGluGlnGlnAsnGlnAlaThrLeuGlnGluAlaGlnGlnLys    | 440  |
| Db | 1261 | GTGGTGGCCATGGGCTACGAGGAACAACAATCAGGCCACTTTGGAAGACAGACAGAA       | 1320 |
| QY | 441  | GluAlaGluPheGlnGlnMetIleGlnGlnLeuLysGlnGlnGluAlaAlaGlnGln       | 460  |
| Db | 1321 | GAGGCGGAATTTACAGCAGATGATTTGAACACCTTAAAAAGCAACAGAGGACGCTCAGCAG   | 1380 |
| QY | 461  | AlaAlaThrAlaThrAlaSerGlnHisSerArgGluProSerAlaAlaGlyArgLeuSer    | 480  |
| Db | 1381 | GCAGCAACGGCACTGCCCTCGAACAATTCAGAGAGGCCAGTCAACAGGACGGCTCTTA      | 1440 |
| QY | 481  | AspSerSerSerGluAlaSerLysLysLeuSerSerLysSerAlaLysGlnArgArgAsnArg | 500  |
| Db | 1441 | GACAGCTCATCTGAAGGCTCTTAAGTTGAGTTCCAAAGAGTGTCTAAGGAAGAAGAAATCGG  | 1500 |
| QY | 501  | ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGlnGluLysAspGluAspGluPhe    | 520  |
| Db | 1501 | AGGAAGAAAAAAGAAAAAGCAAGCAGCTGTGTGGGGAAGAGAAATATAGATGATAATTC     | 1560 |
| QY | 521  | GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGlnGly    | 540  |
| Db | 1561 | CAAAAACTGAATCTGAGACAGCATCAGGAGGAAGGTTTTGCTTCTCCATTAAGAGG        | 1620 |
| QY | 541  | AsnArgLeuThrTrpGluLysArgTrpSerSerProHisGlnSerLeuLeuSerIleArg    | 560  |
| Db | 1621 | AACGATTAACATATGAAGAAAGAGTACTCTCCACACACAGCATGCTTTGTTGACATCCCT    | 1680 |
| QY | 561  | GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgLysArg    | 580  |

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Db 1681 GGCTCCCTATTTTCACCAAGGGAATAGAGAACAGCTTTTCAGCTTTAGAGGCCA 1740
QY 581 AlaIAspValIglSerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600
Db 1741 GCAAAGAGTGTGGAGCTGTGGAACGACTTCGCAGATGATGACAGCAGCCACTTTGAGGAT 1800
QY 601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgAsnSer 620
Db 1801 AACGAGAGCCGATAGAGATTCCTGTTGTGCCCCGACGACGACGAGAGAGAGCAACACC 1860
QY 621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValPheProAlaAsnGlyHis 640
Db 1861 AACCTAGTCAGACAGCTAGTGTATCCCGATCTGCGAGTGTTCACAGGAATGGGAAG 1920
QY 641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660
Db 1921 ATCCACAGCAGCTGTGATTCAGATGGTGTGGTTCCTTGTTGGTGGACCTTCAGTTCCT 1980
QY 661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680
Db 1981 ACATGCCCTGTGGACAGCTTGTGCCAGAGGTGATATATAGATAGCCACTACTGATGAC 2040
QY 681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700
Db 2041 AATGGAGAACACCACTGAACCTGAATGAGAGAAAGAGGTCAAGTCTTCCACGCTTCC 2100
QY 701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleLeaSerIleLeu 720
Db 2101 ATGGACTTTCAGTAATATCTTCCCAAGCAAGCAGCAATGATATGACAGCATTTCA 2160
QY 721 ThrAsnThrValGlnGluGluGlnGluSerArgGlnLysCysProProCysTrpTrpLys 740
Db 2161 ACAATACAGATGAGAAACCTTGAGAGATCCAGGACAGAAATGCCACCCGTGTGATATAA 2220
QY 741 PheSerAsnIlePheLeuIleTrpAspCysSerProTrpTrpLeuLysValHisVal 760
Db 2221 TTTTCCACATATTTCTTAATCTGGGACTTCTCCATATGTTGTTAAAGTGAACATGTT 2280
QY 761 ValAsnLeuValAlaMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780
Db 2281 GTCACACCTGGTGTGTGATGAGCCCATTTGTTGACCTGGCCATCACCTGTATATGCTTCA 2340
QY 781 AsnThrLeuPheMetAlaMetGluHisTrpPrometThrAspHisPheAsnValLeu 800
Db 2341 AATACTCTTTTCACTGGCCATGAGCACTATCCAAATGACGACCATTTCAATATGCTT 2400
QY 801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820
Db 2401 ACAGTAGGAACCTGTGTTTCACTGGGACTTTACGAGCAAAATGTTCTGAAATATAT 2460
QY 821 AlaMetAspProTrpTrpTrpPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840
Db 2461 GCCATGAGATCCTTACTATATATTTCCAAAGAGCTGGAATATCTTGACAGGTTTATG 2520
QY 841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGlnGlyLeuSerValLeuArgSer 860
Db 2521 AGGCTTAGCTGTGTAACCTTGAGACTGCGCAATGAGGAAGATATATCTGTCTCCGCTCA 2580
QY 861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880
Db 2581 TTTCGATGCTCGAGATTTCAAGTTGGCAAAATCTTGCGCAACGTTAAATGCTAATA 2640
QY 881 LysIleIleGlyLysAsnSerValGlyAlaLeuGlnLysAsnLeuThrLeuValIleLeuIle 900
Db 2641 AAGATCATCTGCGCAATTTCCCTGGGGGCTCTGGGAAATTTAAACCTGTCTTGCCATCAT 2700
QY 901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlnLysSerTrpLysAspCysVal 920
Db 2701 GCTTCATATTTTGGCGTGGCTGCGACGCTCTTTGGGAAAGCTACAAATATGCTGTC 2760
QY 921 CysLysIleLeaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940
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Db 2761 TGCAAGATGCCAGCTATATGTCAACTCCACGCTGCGACATGATGACTTCTCCACTCC 2820
QY 941 PheLeuIleValPheArgValAlaCysGlyGluTrpIleGluThrMetTrpAspCysMet 960
Db 2821 TTCTCATATGTTGTTCCGCTGCTGTGGGAGAGGATGATGAGACCATGCTGGAGCTGTATG 2880
QY 961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValIleGlyAsn 980
Db 2881 GAGGTGCTGTGCTAAGCCATGCTCTTACTGTCTTCATGATGGTCATGAGTGGATGGAAAC 2940
QY 981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu**SerSerPheSerAlaAspAsnLeu 1000
Db 2941 CTAGTGTCTGTGATCTCTTCTGCGCTTCTTGTAGCTCATTTAGTGCAGACACCTT 3000
QY 1001 AlaIleThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020
Db 3001 GCAGCCACTGATGATGATGATGATGAAATGAAATCTCCAAATGTGCTGGATGAGATGCAC 3060
QY 1021 LysGlyValAlaLeuValLysArgLysIleTrpGluPheIleGlnGlnSerPheIleArg 1040
Db 3061 AAGAGATGAGCTTATGTGAAAGAAAATATATGAAATTTATCAACAGTCTTCATTTAGC 3120
QY 1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnLysLysAspSer 1060
Db 3121 AATCAAAAGATTTTATGATGAAATTTAAACCACTGATGATGATTTAAACAAAGAAAGACGT 3180
QY 1061 CysMetSerAsnHisThr**GluIleGlyLysAspLeuAspTrpLeuLysAspValAsn 1080
Db 3181 TGTATGTCACATCATATCARGACAGAAATGGGAAAGATCTTCATATGATTAAGATGTAAT 3240
QY 1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTrpIleIleAspGluSer 1100
Db 3241 GGAATCTACAGAGTGTATGAGAACTGGACAGAGTGTGAAAAATATATGATGTAAGAAAT 3300
QY 1101 AspTrpMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120
Db 3301 GATTAATATGTCATCTTAATAACCAACCCAGCTTACTGTACTGATACCAATGCTGTAGGA 3360
QY 1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140
Db 3361 GAATCTGACTTTGAAATTTAAACAGGAAGACTTATGATGATGAATCGCATCGAAGAA 3420
QY 1141 SerLysGluLysLeuAsnGlnGluSerSerSerSerSerGlnGlySerThrValAspIleGly 1160
Db 3421 AGCAAAAGAAATGATGATGAAAGCACTAGCTCATCAAGAAAGTGCACCTGTGACATCGGC 3480
QY 1161 AlaProValGluGlnGlnProValValGluProGluGluThrLeuGluLupProGluAlaCys 1180
Db 3481 GCACCTGTAGAAACAAAGACCCGATAGTGAACCTGAAAGAACTTTGAAACCAAGACTTGT 3540
QY 1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg 1200
Db 3541 TTCACGGAAGGCTGTGTACAAAGATTCAGATGTTGTCAATCAATGAGGAAGAAAGCAAG 3600
QY 1201 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe 1220
Db 3601 GGAAGAAACAAATGTGTGAACCTGAGAAAGAGCTGTTTCCGAATACTTGAACCTAAGCTG 3660
QY 1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyValAlaLeuAlaPheGluAspIle 1240
Db 3661 GAGACCTTCATGTTTTCATGATGATCTCTTCTAGTAGTGCTCTTGCCATTTGAGATATA 3720
QY 1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTrpAlaAspLysValPheThr 1260
Db 3721 TATATTTGATCAGCAAGAAAGATTAAGATGATGATGATGATGATGATGATGATGATGAT 3780
QY 1261 TyrIlePheIleLeuGlnMetLeuLeuLysTrpValAlaTrpGlyTrpGlnThrTrpPhe 1280
Db 3781 TACATTTTCATCTGTGAATATGCTTCAAAATGGGTGGCATATGATGATGATGATGATGAT 3840
QY 1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300
Db 3841 ACCATGCTGCTGTGTGCTGACCTTTAATTTGATGATGATGATGATGATGATGATGATGAT 3900
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|----|------|--|------|
| OY | 1301 | AlaasnalaleuglytrSerGlnLeuGlyValIleIysSerLeuArgThrLeuArgAla      | 1320 |
| Db | 3901 | GCAAAATGCCCTGGGGTCTACTCGAAACTTGGAGCCATCAAAATCTCTCAGGACATAAGAGACT | 3960 |
| OY | 1321 | LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValAlaAsnAlaLeu     | 1340 |
| Db | 3961 | CTGAGACCTCTAAGACCCTTATCTCGATTGGAAAGGATGAGGGGTGTGTAAATCCCTT       | 4020 |
| OY | 1341 | LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIle     | 1360 |
| Db | 4021 | TTAGAGCAAAATTCATCCATCATCATGAATGCTCTCGGTGTGCTTATATCTGGCTAAT       | 4080 |
| OY | 1361 | PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheThyHisCysGlyLeasnThrThr   | 1380 |
| Db | 4081 | TTACACATCAATGGCGTAAATATTGTTGGCGGAAATTTCCACACATGTAATTAACCCACA     | 4140 |
| OY | 1381 | ThrGlyAspArgPheAspIleGluAspValAlaAsnAsnIleThrAspCysLeuIysLeuIle  | 1400 |
| Db | 4141 | ACTGGTGACAGTTTGAACATCGAAGACGTAAATATCATACATGATTCGCTAAACATAATA     | 4200 |
| OY | 1401 | GluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyPhe     | 1420 |
| Db | 4201 | GAAGAAATATGAGACTGCTCGATGGAAAAAGTAAAGTAACCTTGATATGTAGAAATT        | 4260 |
| OY | 1421 | GlyTrpLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetTrpAla     | 1440 |
| Db | 4261 | GGGTATCTCTCTTTCCTTCAAGTTGCCACATTTAAAGATGGATGATATATATGATCA        | 4320 |
| OY | 1441 | AlaValAspSerArgAsnValGluLeuGlnProLysTrpGluGlnSerLeuTrpMetLys     | 1460 |
| Db | 4321 | GCAGTTGATTTCCAAAAATGTGAACCTCCACCTAATGAAGAAAGTCTGATCATGTAT        | 4380 |
| OY | 1461 | LeuTrpPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIleGly     | 1480 |
| Db | 4381 | CTTTACTTGTATTTTCAATCATCTTGGGTCTCTTCACTTGAACCTGTTATATGCT          | 4440 |
| OY | 1481 | ValIleIleAspAsnPheAsnGlnGlnLysLysPheGlyGlyGlnAspIlePheMet        | 1500 |
| Db | 4441 | GTCATCATAGATAATTTCAACACAGCAAGAAAAAAGATTGGAGGTCAAGACATCTTATG      | 4500 |
| OY | 1501 | ThrGluGlnLysLysTrpTrpAsnAlaMetLysLysLeuGlySerLysLysProGln        | 1520 |
| Db | 4501 | ACAAGAAAGCAAGAAATATCTAATATGCATGTAAAAATTATGTAGTCAGAAAAACCGCA      | 4560 |
| OY | 1521 | LysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheValThrArg     | 1540 |
| Db | 4561 | AAGCTTATCTCGACAGGAACAAATTTCAAGGATGTCTTGACTGTGTAACACAGA           | 4620 |
| OY | 1541 | GlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMetLeuVal     | 1560 |
| Db | 4621 | CAAGTTTTTGACATAACATCATGATTCATCTGCTTAAACATGTCACAAATGATGGTG        | 4680 |
| OY | 1561 | GluThrAspAspGlnSerGlyTrpValThrThrIleLeuSerArgIleAsnLeuValPhe     | 1580 |
| Db | 4681 | GAACACAGTATGCAGATGTGAATATGTACTACCAATTTGTACAGCATAAATCGGTGTC       | 4740 |
| OY | 1581 | IleValIleuPheThrGlyGlyCysValLeuLysLeuIleSerLeuArgHisTrpTrpPhe    | 1600 |
| Db | 4741 | ATTGTGCTATTACTGAGAGGTGGTGAACGTAACTCATCTCTACAGCCATTAATATTTT       | 4800 |
| OY | 1601 | ThrIleGlyTrpAsnIlePheAspPheValValValIleLeuSerIleValGlyMetPhe     | 1620 |
| Db | 4801 | ACCAATGTGATGAAATATTTTGAATTTTGGGTGTGCATTTCTCTCATTTGTAGGTATGTT     | 4860 |
| OY | 1621 | LeuAlaGluLeuIleGlyLysTrpPheValSerProThrIleuPheArgValIleArgLeu    | 1640 |
| Db | 4861 | CTTGCCAGCGATAGAAAGATATTCGTGTCCGTCCACCTGTTCCGAGTATCCGCTT          | 4920 |
| OY | 1641 | AlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLeuLeu     | 1660 |
| Db | 4921 | GCTGAGATTTGGCCAAATCTACCTGTGATCAACAAAGGCAAGAGGATCCGACGCTGTC       | 4980 |

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|----|------|---|------|
| QY | 1661 | PheAlaLeuMetKetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPheLeuVal    | 1660 |
| Db | 4981 | TTTTGCTTAAATGATGTCCTCTCTCGCTGTATTAACATGGCCCTCACTCTTCGTAGTC      | 5040 |
| QY | 1681 | MetPheIleValIleIlePheGlyMetSerAsnPheAlaTyrValLysArgGluValGly    | 1700 |
| Db | 5041 | ATGTTCAATCTAGCCCACTCTTTGGGAGTCCAACTTTCCTATGTGAAGAGGAAATTGGG     | 5100 |
| QY | 1701 | IleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPheGluIle    | 1720 |
| Db | 5101 | ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCATTCCAATTT      | 5160 |
| QY | 1721 | ThrThrSerAlaGlyTyrPaspGlyLeuLeuAlaProIleLeuAsnSerLysProProAsp   | 1740 |
| Db | 5161 | ACAAACCTCTGCTGGCGGGATGGATGGCTAGCAACCCATCTCAACACTAAGCCACCCGAC    | 5220 |
| QY | 1741 | CysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsnProSer    | 1760 |
| Db | 5221 | TGTGACCTCATATAAGTTAACTTGAAGCTTCAGTTAAGGAGAGACTGTGGAGCCCACTCT    | 5280 |
| QY | 1761 | ValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValValAsnMet       | 1780 |
| Db | 5281 | GTGTGAATTTTCTTTTGTGCAGTTACATCATCATATCCTTCCTCGTGTGGTGAACATG      | 5340 |
| QY | 1781 | TyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGluProLeu    | 1800 |
| Db | 5341 | TACATCTCGGGTCATCTGTGGAGAACTTCAGTGTGTCTACTAGAAAGTGCAGACCCCTGTG   | 5400 |
| QY | 1801 | SerGluAspAspPheGluMetPheTyrGluValTyrGluLysPheAspProAspAlaThr    | 1820 |
| Db | 5401 | ACTGAGGATGACTTGTAGATGTTCTATGAGGTTTGGGAGAAAGTTGATCCCGATGCAACT    | 5460 |
| QY | 1821 | GlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaAlaLeuGluProProLeuAsn    | 1840 |
| Db | 5461 | CAGTTCATGGAATTTGAAAAATTATCTCAAGTTTGCAGCTCGGCTTGAAACCGCCTCATAT   | 5520 |
| QY | 1841 | LeuProGlnProAsnLysLeuGluLeuIleAlaMetAspLeuProMetValSerGlyAsp    | 1860 |
| Db | 5521 | CTGGCCAAACCAACAAACTCCAGCTCAGCTCATGTCATGGCCAAAGTGAGTGGTAC        | 5580 |
| QY | 1861 | ArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGluSerGly    | 1880 |
| Db | 5581 | CGGATTCACATGCTTGTATATCTTATTTGCTTTTACAAAGCGGGTCTTAGAGAGAGTGGGA   | 5640 |
| QY | 1881 | GluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsnProSerLys    | 1900 |
| Db | 5641 | GAGATGGATGCTCTACGAATPACAGATGGAAGACCAATCATGGCTTCCATCTCTCAAG      | 5700 |
| QY | 1901 | ValSerTyrGlnProIleThrThrLysLysArgLysGlnGluValSerAlaVal          | 1920 |
| Db | 5701 | GTCTCTTAACACCACATCACTACTACTTTAAAAAGAAAAAGAAAGAAAGTATCTGCTGTC    | 5760 |
| QY | 1921 | IleIleGlnArgAlaTyrArgTyrArgHisLeuLeuLysArgThrValLysGlnAlaSerPhe | 1940 |
| Db | 5761 | ATTATTACGCGTCTTACGAGCGCACCTTTTAAAGCGAATCTTAAACAAAGCTTCTCTTT     | 5820 |
| QY | 1941 | ThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuIleLysGluAspMetIle    | 1960 |
| Db | 5821 | ACGTCACAAATAAAACAAATAACAAGSTGGGGCTAATCTTCTTATAAAGAAAGACATGATA   | 5880 |
| QY | 1961 | IleAspArgIleAsnGluAsnSerIleThrGluLysThrAspLeuThrMetSerThrAla    | 1980 |
| Db | 5881 | ATTGACAGATATAAATGAAAACTTATTACAGAAAAAATGATCTGACCAATGTCACCTGCA    | 5940 |
| QY | 1981 | AlaCysProProSerTyrAspArgValThrLysProIleValGluLysHisGluGlnGlu    | 2000 |
| Db | 5941 | GCTTGTCCACCTTCTCATACCGGGTGACAAAGCCAAATTGTGAAAAAACAATGAGCAAGAA   | 6000 |
| QY | 2001 | GlyLysAspGluLysAlaLysGlyLys 2009                                |      |
| Db | 6001 | GGCAAAAGATGAAAAAGCCAAAGGAAA 6027                                |      |

AX391142  
 LOCUS AX391142 5922 bp DNA linear PAT 19-MAR-2002  
 DEFINITION Sequence 13 from Patent WO0214498.  
 ACCESSION AX391142  
 VERSION AX391142.1 GI:19584238  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE  
 AUTHORS Turner, C.A., Mathur, B. and Mathur, D.  
 TITLE Novel human ion channel proteins and polynucleotides encoding the same  
 JOURNAL Patent: WO 0214498-A 13 21-FEB-2002;  
 Lexicon Genetics Incorporated (US)  
 FEATURES  
 source  
 1..5922  
 Location/Qualifiers  
 BASE COUNT 1746 a 1166 c 1320 g 1687 t 3 others  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 0 Length: 5922  
 Score: 1970.00 Matches: 1972  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 98.06% Indels: 0  
 Gaps: 0  
 US-09-930-871-12 (1-2009) x AX391142 (1-5922)

QY 1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20  
 DB 1 ATGGAGCAACAGTGGCTTACACACAGAGACCTGACAGCTTCAACTCTTCACACAGAA 60  
 QY 21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluAlaLysAsnProLysProAsp 40  
 DB 61 TCTCTGGCGGCTATTGAAAGACGCAATTCAGAGAAAGGCAAGAAATCCCAACAGAC 120  
 QY 41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60  
 DB 121 AAAAAAGATGAGACGAAATGGCCCAAGCCAAATAGAGCTTGGAAGTGAAGAAAC 180  
 QY 61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80  
 DB 181 CTTCCATTATTATTATGAGACATTCCTCCAGAGATGTGTCAAGAGCCCTGGAGGACTG 240  
 QY 81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100  
 DB 241 GACCCCTACTATATCAATAGAAACTTTTATATGATTAATAAAGGAGGAGCCATCTTC 300  
 QY 101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120  
 DB 301 CGGTCAGAGCCACCTCCGCTGACATTTTAACCTCCATCAACCTCTTGAGAAATA 360  
 QY 121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140  
 DB 361 GGTATTAAATTTGGTATCATTCATTCAGATGCTAATATATGACATATTTTGACA 420  
 QY 141 AsnGlyValPheMetThrMetSerAsnProProAspTyrThrLysAsnAlaGluArgLys 160  
 DB 421 AACCTGTGTTTATGACATATGATTAACCTCCGATGGAGCAAGAAATATAGAAATACCC 480  
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 SOURCE human.  
 ORGANISM Homo sapiens









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 DEFINITION Sequence 2 from Patent WO0138564.  
 ACCESSION AX164172  
 VERSION AX164172.1 GI:14545111  
 KEYWORDS human.  
 SOURCE

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 8378)  
REFERENCE  
AUTHORS  
Rouleau, G. A., Latremiere, R. G., Rochefort, D., Cossette, P. and  
Ragsdale, D.

TITLE  
Locf for idiopathic generalized epilepsy, mutations thereof and  
method using same to assess, diagnose, prognosis or treat epilepsy  
JOURNML  
Patent: WO 0138564-A 2 31-MAY-2001.

## FEATURES

Location/Qualifiers

1..8378

/organism="Homo sapiens"

/db\_xref="taxon:9606"

BASE COUNT 2498 a 1571 c 1775 g 2534 t

ORIGIN

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Score: 1447.00 Matches: 2002  
Percent Similarity: 99.40% Conservative: 0  
Best Local Similarity: 99.40% Mismatches: 7  
Query Match: 72.03% Indels: 12  
DB: 6 Gaps: 0

US-09-930-871-12 (1-2009) x AXI64172 (1-8378)

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| Db | 2782 | GGACGCTTACGCTGGTATGAACCTGGACATCGCCAAATGGCAAGATTAATCTTTCGCCGT  | 2841 |
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[illegible]

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RESULT 5  
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 DEFINITION Sequence 15 from Patent WO0214498.  
 ACCESSION AX391144  
 VERSION AX391144.1 GI:19584239  
 KEYWORDS

SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS Turner, C.A., Mathur, B. and Mathur, D.  
TITLE Novel human ion channel proteins and polynucleotides encoding the same  
JOURNAL Patent: WO 0214498-A 15 21-FEB-2002;  
LEXICON Lexicon Genetics Incorporated (US)  
FEATURES  
source 1. 4362  
Location/Qualifiers  
BASE COUNT 1300 a 845 c 995 g 1219 t 3 others  
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1 Turner,C.A., Mathur,B. and Mathur,D.
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REFERENCE  
 AUTHORS Turner, C.A., Mathur, B. and Mathur, D.  
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REFERENCE 1
AUTHORS Turner,C.A., Mathur,B. and Mathur,D.
TITLE Novel human ion channel proteins and polynucleotides encoding the

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JOURNAL Patent: WO 0214498-A 1 21-FEB-2002;
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Qy 41 LyslyAspAspAspGlyAsnGlyProIlyProAsnSerAspIleuAlaGlyIlyAsn 60
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Qy 61 LeuProPheIleIlyGlyAspIleProProGlyMetValSerGluProleuGluAspLeu 80
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Qy 81 AspProIlyrTyleuIleuIlyserPheIleValleuAsnIlyGlyIlyAlaIlePhe 100
Db 241 GAGCCCTATATATCAATTAAGAAAGAACTTTATAGATTAAGATTAAGAAAGAGAGAGAG 300
Qy 101 ArgPheSerAlaTrpSerAlaIleuIlyrIleleuThrProPheAsnProleuArgIlyIle 120
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Qy 121 AlaIleIlyIleleuValHisSerleuPheSerMetIleuIleMetCysThrIleleuThr 140
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Qy 141 AsnCysValPheMetThrMetSerAsnProProAspTrpPheIlyAsnValGluIlyrThr 160
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Db 481 TTCACAGAAATATATCTTTGAAATCACTTATTAATAATATATGCAAGAGGATTCGTTTA 540
Qy 181 GluAspPheThrPheleuArgAspProTrpAsnTrpPleuasPheThrValIleThrPhe 200
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Qy 201 AlaTyrValThrgluPheValAspIleuGlyAsnValSerAlaIleuArgThrPheArgVal 220
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Qy 221 leuArgAlaIleuIlystThrIleSerValIleProGlyleuIlystThrIleValAlaIleu 240
Db 661 CTCGAGCATTAAGAGAGATTCAGTCACTTCAGAGCGCGAAACATTTGTGGAGCCCTG 720
Qy 241 IleGlnSerValIlyIlyleuSerAspValMetIleleuThrValPheCysleuSerVal 260
Db 721 ATCCAGTGTGAGAGAGCTCTCAGATGATTAATGATTCGACTGTGTCTGTAGAGGTA 780
Qy 261 PheAlaIleuIleGlyleuGlnleuPheMetGlyAsnleuArgAsnIlyscysIleGluTrp 280

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Db 781 TTGCTCTAATGGGCTGACAGCTCTCATGGGCAACCTGAGAAATATATACAAATGG 840
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| OY | 1021 | LysGIValAlaIatyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg   | 1040 |
| Db | 3028 | AAGAGGTACTTAATGTGAAGAAGAAAATATATCAATTTATTCACAAGTCTCTTAATAGG     | 3087 |
| OY | 1041 | LysGlnLysIleLeuAspGlnIleLysProLeuAspAspLeuAsnLysLysAspSer       | 1060 |
| Db | 3088 | AAACAAAGATTTTATGATGAATTAACCACTTGATGATCTAAACAACAGAAAGAACAGT      | 3147 |
| OY | 1061 | CysMetSerAsnHisTrp***GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn    | 1080 |
| Db | 3148 | TGTATGTCCAAATATATACAGAAATTTGGGAAACATCTTCACTTAATTAAGATTAAT       | 3207 |
| OY | 1081 | GlyThrThrSergLysIleGlyThrGlySerSerValGluLysTyrIleIleAspGlnSer   | 1100 |
| Db | 3208 | GGAGACACAGAGTGTATAGAGACTGCCAGAGTGTAAAAATATCATTATTGATGAAGAAT     | 3267 |
| OY | 1101 | AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly    | 1120 |
| Db | 3268 | GATTACATGCATTCATTAACAACCAGCTTACTGTGACTGACATGAACAAATGGCTGATGA    | 3327 |
| OY | 1121 | GluSerAspPheGlnLysAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGlnL   | 1140 |
| Db | 3328 | GAATGTGACTTTAAAAATTTTAAACAGGAAGACTTATGATGTGATCGATCGGAAGAA       | 3387 |
| OY | 1141 | SerLysGlnLysLeuAsnGlnSerSerSerSerGluLysSerThrValAspIleGly       | 1160 |
| Db | 3388 | AGCAAAGAGAACTGATGAATGAAGAGATGCTCATCAGAAAGTAGACACTGTGGACATGGC    | 3447 |
| OY | 1161 | AlaProValGluGlnGlnProValValGluProGluThrLeuGluProGluAlaCys       | 1180 |
| Db | 3448 | GCACCGTAGMAAACAACGCCCGAGTGAACCTGAMAAACTCTTGAAACCAAGAAAGCTTGT    | 3507 |
| OY | 1181 | PheThrGlnGlyCysValGlnArgPheLysCysGlnIleAsnValGluGlnGlyArg       | 1200 |
| Db | 3508 | TTTCACGGAAGCGCTGTGACAAAGATTCAGTGTGTCAAAATCAATGTGGAGAAAGGACAGA   | 3567 |
| OY | 1201 | GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe    | 1220 |
| Db | 3568 | GGAAAAAATATGGGAAACCGAGAAAGACGCTGTTCCGAATAGTTGAACATTAATGCTTT     | 3627 |
| OY | 1221 | GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle    | 1240 |
| Db | 3628 | GGACCTTCATTTTTCATGATTCCTCTTAAGTAGTGCTCTGGCATTTGAAGATATA         | 3687 |
| OY | 1241 | TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr    | 1260 |
| Db | 3688 | TATATGTAGACAGGAAAGACGATTAAGACATGTGTGAATATGCTGCAAGGTTTTCACT      | 3747 |
| OY | 1261 | TyrIlePheIleLeuGlnMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPhe    | 1280 |
| Db | 3748 | TTCATTTTCAATCTTGAAATATGCTTCAAAATGGGTGGCAATATGCTTCAAAATATATTC    | 3807 |
| OY | 1281 | ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr    | 1300 |
| Db | 3808 | ACCAATGCTGTGGTGGCTGGCTGCTTATATGTGATGTTCATATGGTCAGATTAAACA       | 3867 |
| OY | 1301 | AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgTrpLeuArgAla    | 1320 |
| Db | 3868 | GCAAAATGCTGGGTATACACAGAACTTGAGCATCAAAATCTCCAGGACACATRAAGGCT     | 3927 |
| OY | 1321 | LeuArgProLeuArgAlaLeuSerArgPheGlnGlyMetArgValValAlaAsnAlaLeu    | 1340 |
| Db | 3928 | CTGAGACCTCTAAGACCTTATCTCATTTGAAAGGATGAGGGGTGGTTGTGAATGCCCTT     | 3987 |
| OY | 1341 | IleuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIle   | 1360 |
| Db | 3988 | TTTAGAGCAATTCATCCATCCATGAATATGCTTCTGCTTTATATTTCTGGCTAATTT       | 4047 |
| OY | 1361 | PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThr    | 1380 |
| Db | 4048 | TTTCAGCATCATGGCGTAAATTTGTTTGCCTGGCAAAATTCACCATGATTAACACCACA     | 4107 |
| OY | 1381 | ThrGlyAspArgPheAspIleGluAspValAsnAsnHisTrpAspCysLeuLysLeuIle    | 1400 |
| Db | 4108 | ACTGGTAGACGGTTTGACATCGAAGACGTGAATATATCACTACTGATGCTCAAAACTATA    | 4167 |
| OY | 1401 | GluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyPhe    | 1420 |
| Db | 4168 | GAAGAATATGACATGCTGCCATGGAAAAATGTGAAGATTAACCTTGATTAATGAGATTT     | 4227 |
| OY | 1421 | GlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTyrPheAspIleMetTyrAla    | 1440 |
| Db | 4228 | GGGATCTCTCTTGTTCCTCAAGTTGCCACATTCAAAGATGATGATATATATATGCA        | 4287 |
| OY | 1441 | AlaValAspSerArgAsnValGlnLeuGlnProLysTyrGlnLysSerLeuTyrMetTyr    | 1460 |
| Db | 4288 | GCACTGATTTCCAAATATGTGAACTCACAGCTTAAGTATGAAGAAGCTGTACATATGAT     | 4347 |
| OY | 1461 | LeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIleGly    | 1480 |
| Db | 4348 | CTTACCTTGTATTTTCATCATCTTTGGGCTCTTCCTCACTTGAACCTGTTATATGCT       | 4407 |
| OY | 1481 | ValIleIleAspAsnPheAsnGlnGlnLysLysLysPheGlyGlyGlnAspIlePheMet    | 1500 |
| Db | 4408 | GTCATCATATGATTAATTTCAACACACACAAAAAGAAATTTGGAGGTCAAGACATCTTATAG  | 4467 |
| OY | 1501 | ThrGluGlnGlnLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLysProGln    | 1520 |
| Db | 4468 | ACAGAAABAACGAAGAAATATCTATTAATGCAATGAAAAATTAAGATGCAAAAAACCCGA    | 4527 |
| OY | 1521 | LysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheValThrArg    | 1540 |
| Db | 4528 | AAGCTTATACCTGCACGAGAAACAAATTTCAAGAAATGCTTGTGACTTCGTAAACAGA      | 4587 |
| OY | 1541 | GlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMetMetVal    | 1560 |
| Db | 4588 | CAAGTTTTCATATGACATCATCATATCTCATCTGCTTAAACATGCTCACATATATGGTG     | 4647 |
| OY | 1561 | GluThrAspAspGlnSerGluTyrValThrThrIleLeuSerArgIleAsnLeuValPhe    | 1580 |
| Db | 4648 | GAACACATGACACGAGAGATATATGTACATCACTTTTGTACACCATCAATCTGGTGTCC     | 4707 |
| OY | 1581 | IleValLeuPheThrArgLysGlnCysValLeuLysLeuIleSerLeuArgHisTyrTyrPhe | 1600 |
| Db | 4708 | ATTTGCTATTTACTGTGAGAGGTGTACTGAATCTATCTCTACACCCATATATATTTT       | 4767 |
| OY | 1601 | ThrIleGlyTrpAsnIlePheAspPheValValIleLeuSerIleValGlyMetPhe       | 1620 |
| Db | 4768 | ACCATTTGATGGAATATTTTGTGATTTTGTGTGTCTCATCTCCATTTGATGATATTTT      | 4827 |
| OY | 1621 | LeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPheArgValIleArgLeu    | 1640 |
| Db | 4828 | CTTGCCGAGCTGATAGAAAGAT  |      |

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VERSION AX391132.1 GI:19584233
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE
1 Turner,C.A., Mathur,B. and Mathur,D.
AUTHORS Novel human ion channel proteins and polynucleotides encoding the
TITLE

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same
JOURNAL Patent: WO 0214498-A 3 21-FEB-2002;
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/db_xref="taxon:9606"
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Best Local Similarity: 99.14% Mismatches: 17
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| QY         | 1881   | GluMetAspAlaLeuArgIleGluMetGluIleArgPheMetAlaSerAsnProSerLys   | 1900   |
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| Db         | 5788   | ACGTCAATTAATAAACAATAATCAAAAGGTGGGCTATCTTCTTATAAAGAAGACTGATA    | 5847   |
| QY         | 1961   | IleAspArgIleAsnGluAsnSerIleThrGlyLys                           | 1972   |
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| SOURCE     | Homo sapiens.  |  |        |
| ORGANISM   | Homo sapiens.  |  |        |
| REFERENCE  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.                  |  |        |
| AUTHORS    | 1 (bases 1 to 6046)<br>Sugawara, T., Mazaki-Miyazaki, E., Fukushima, K., Shimomura, J., Fujisawa, T., Hamano, S., Inoue, Y. and Yamakawa, K. |  |        |
| TITLE      | Frequent mutations of SCN1A in severe myoclonic epilepsy in infancy  |  |        |
| JOURNAL    | Neurology 58 (7), 1122-1124 (2002)   |  |        |
| MEDLINE    | 21938587   |  |        |
| PUBMED     | 11940708   |  |        |
| REFERENCE  | 2 (bases 1 to 6046)<br>Sugawara, T., Mazaki, E.M. and Yamakawa, K.   |  |        |
| AUTHORS    | Homo sapiens neuronal voltage-gated sodium channel type I (Nav1.1)   |  |        |
| TITLE      |  |  |        |

JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Unpublished  
3 (bases 1 to 6046)  
Sugawara, T., Mazaki, E. M. and Yamakawa, K.  
Direct Submission  
Submitted (03-JUN-2001) Neurogenetics, BSL, RIKEN, 2-1 Hirotsawa,  
Wako, Saitama 351-0198, Japan

FEATURES  
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SDVSPINNSLTVYPIVYAGSDPEFNILDEDSRSSDLEEKREKLNESSESGTV  
DIAGPVEQPVPEPTELEAFCPTBECVORRCCOINVEGRKOMNLRICRTIV  
EHNPEFTVIFMLLSGALAFEDYITIDRKTKIMLEYADVFYITFLEMLKMYA  
YGYQTEYNAWCWIDFLVDVSLVSLTANALGSEGLAKISRTALRPLALSRFE  
GMRYVVALIGALPISIMNVLVCLIFMLFESINGVLAFGKRYHCINTTQGRPIED  
VNNHTDCKLIERNETARMKRVNVNFDNGYFGLSLOYATFRKMGDIYAVDSRY  
ELDQPESESLYMTIEFYVIFVIRIGSEPTNLFGYIILDNNOCKRFGGDDIYTEBOK  
KYINAMKLSKSKPQKPIRPCKRFGQMTDYTVROVEDISIMILCLMVTWMEYED  
DQSEVYTTILSRINLVEITLGECEVAKILSLRHYEFTGMNIPFVVYILSIVMLF  
AELEIKTFSPTELVIRIARIGIRILIRLKGAKGJITFLPALMSIPALFNIGLFL  
VMDLVAIFGMSNFAFYKREVGIDMPEFGMSMLCLQVITTSAGVODLAPLANSK  
PPQDDPAPKGVSSVKGDCGSPVGIFFEVSYIISFLVYNNATIMVILANESVATE  
SABIESDEDEMEFYWEKRPDPAQPMFEKLSQRAALEPLMLPQNRKQILAMD  
LPRVSGRCHICDILYAFTRKYVIGSEGDYALRIQHEERFANSNKSYQDTITTLK  
RKQEBVSATIIQYARHRLIKRTVYKQASTPYNLRKKGAGANLILKEDMIDRINENSI  
YTEYDILMSTAACPSPYDRTVYKRIYVKEHODEKDEKANK"

BASE COUNT 1808 a 1188 c 1345 g 1704 t 1 others

ORIGIN

Alignment Scores:

Score: No: 0 Length: 6046  
Predict: 1126.00 Matches: 1990  
Percent Similarity: 98.96% Conservative: 19  
Best local Similarity: 98.96% Mismatches: 19  
Query Match: 56.05% Indels: 21  
DB: 9 Gaps: 0

US-09-930-871-12 (1-2009) x AY043484 (1-6046)

OY 1 MetGIunThrValIleuValIProAspSerPheAsnPhenhetrArgGlu 20  
|||||  
DB 1 ATGAGCAACAGAGCTGTGTCACACGAGACCTGACAGCTTCAACTTCCACCAAGAA 60  
|||||  
21 SerLeuAlaAlaIleGluArgGArgIleAlaGluLysAlaIlysAsnProLysProAsp 40  
|||||



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Db 61 FCTCTGGGGCTATTGAAAGACGATGAGAGAAAGGCAAGAACATCCCAACAGACAG 120
Oy 41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
Db 121 AAAAAAGATGACGAGAGAAATGGCCCAAGCCAAATAGACCTTGAGAGCTGGAAGAAC 180
Oy 61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAsnLeu 80
Db 181 CTTCCATTTATTTATGAGACATTCCTCCAGAGATGAGTGTGACAGCCCTGGAGAGACCTG 240
Oy 81 AspProTyrTyrIleAsnLysLysThrPheIleValIleAsnLysGlyLysAlaIlePhe 100
Db 241 GACCCCTACTATATCAATAATAGAAAACCTTTATATGATTAATGAATGAAGGAGGACCTCTTC 300
Oy 101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
Db 301 CGGTCAGGCGCACCTGCTGCTGACATTTTAACTCCCTCAATCCCTTACGAGAAATTA 360
Oy 121 AlaIleLysIleLeuValHisSerLeuPheSerMetIleuIleMetCysThrIleLeuThr 140
Db 361 GCTATTATAGATTTGGTACATTCATTTATTCACATGCTAATATTATGCACTATTTTGACA 420
Oy 141 AsnCysValPheMetThrMetSerAsnProProAspTyrThrLysAsnValGluTyrThr 160
Db 421 AACTGTGTGTTATGACAAATGAGTAACCTCCTGATGAGACAAAGATGTAATGATACAC 480
Oy 161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
Db 481 TTCACAGCAATATATACCTTTGAACTGATTAATAAATATATGCAAGGGGATTCGTTTA 540
Oy 181 GluAspPheThrPheLeuArgAspProThrPasnThrPleuAspPheThrValIleThrPhe 200
Db 541 GAGATTTTACTTCTTCCTGGGATCCATGAGAACTGGCTGATTCACGTCTATTCATTT 600
Oy 201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
Db 601 GCGTACGTCACAGAGATGTTGGACCTGGCAATGTCCTGGCATGAGAAACATTCAGAGTT 660
Oy 221 LeuAlaGlyAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
Db 661 CTCACAGCAATGAAACAGATTCCTGACATTCACGACCTGAAACCATTCGTGGACCTCTG 720
Oy 241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
Db 721 ATCCAGTCTGTGAAGAGCTCTCAATGTATGATCTGACTGTCTGTCTGTGAGCGTA 780
Oy 261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTyr 280
Db 781 TTGCTCTAATTTGGGCTGAGCTGTTTCATGGGCAACCTGAGAAATTAATGATACAAATGG 840
Oy 281 ProProThrAsnAlaSerLeuGlnGluLysSerIleGlyLysAsnIleThrValAsnTyr 300
Db 841 CCTCCACCAAAAGCTTCTCTGGAGAGACATATATGAAGAAATTAACCTGTAATTAAT 900
Oy 301 AsnGlyThrIleuIleAsnGlnThrValPheGluPheAspTyrPlySerTyrIleGlnAsp 320
Db 901 AATGCTACCTTATATAAGAAACCTCTCTTGAGTTTGACTGGAAATCAATATTTCAAGAT 960
Oy 321 SerArgTyrHisTyrPheLeuGlnGluPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
Db 961 TCAAGATATCATTAATTTCTCTGGAGGCTTTTGGATGCACTATGTAAGAAATAGCTCT 1020
Oy 341 AspAlaGlyGlnCysProGlnGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360
Db 1021 GATGACAGGCGCAATGTCAGAGAGATATATGTGTGAAGAGCTGAGAAATCCCAATTAAT 1080
Oy 361 GlyTyrThrSerPheAspThrPheSerThrPalaPheLeuSerLeuPheArgLeuMetThr 380
Db 1081 GCGTACACAGAGCTTGAATACCTTCAGTGGGCTTTTGTCTCTTTCGACTAATAGACT 1140
Oy 381 GlnAspPheThrGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400

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Db 1141 CAGACTTCTGGGAAATCTTTATCAACTGATACGTGCTGCGGAAACGTAACAG 1200
Oy 401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420
Db 1201 AATATTTTGTATGTGCTATTTCTTGGGCTCACTTCTACCTATTAATTTGATCCCTGGCT 1260
Oy 421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGlnGluValIleGluGlnLys 440
Db 1261 GTGTGGCCATGCGCTTACAGAGAACAAATCAAGGCACTTGGAAACGACAGAAAGAAA 1320
Oy 441 GluAlaGluPheGlnGlnMetIleGlnGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460
Db 1321 GAGGCGGAATTCAGAGATGATGAAACGCTTAATAAACCAACAGGAGGAGCTCACGAC 1380
Oy 461 AlaIleThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480
Db 1381 GCAGCAACGCGCAATGCTCCAGAACATTCAGAGAGCCAGTGCACAGGAGGCTCTCA 1440
Oy 481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500
Db 1441 GACAGCTCATCTGAAACCTCTAAGTTGAGCTCCAAAGAGCTTAAGGAAAGAAATTCGG 1500
Oy 501 ArgLysLysArgLysGlnLysGlnLysGlnSerGlyGlyGluLysAspGluAspGluPhe 520
Db 1501 AGGAAGAAAGAAAGAAACAGAAAGACGAGCTCGTGGGGGAAAGAGAAATGAGATGATTC 1560
Oy 521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
Db 1561 CAAATATCTGAATCTGAGACAGACATCAGAGAGAAAGGTTTCGCTTCATTCATGAAAGG 1620
Oy 541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
Db 1621 AACCGATTACATATGAAAGAGATCTCTCCACACACAGCTTGTGTGACATCCGT 1680
Oy 561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580
Db 1681 GGCTCCCTATTTTACCAAGGCGGAATATAGACAAACAGCTTTTTCAGCTTTGAGAGGCA 1740
Oy 581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600
Db 1741 GCAAAGAGTGGGACTGAGAACGACTTCGCAAGAGAGAGACACGCACTTTGAGGAT 1800
Oy 601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620
Db 1801 AACGAGAGCCGTAAGATTCCTTGTGTGCCCCGACGACAGAGAGAGACGACACAGC 1860
Oy 621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValPheProAlaAsnGlyLys 640
Db 1861 AACCTGAGTCAGACCAAGTATGTCATCCGAGAGCTGGAGTGTTCACAGCAATGGAGAG 1920
Oy 641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660
Db 1921 ATGCACAGCAGCTGTGATGCAATGTGTGCTTCCTGTGGTGGAGACTTCAGTTCTCT 1980
Oy 661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680
Db 1981 ACATGCTGCTGTTG--G--A--C--A--G--C--T--F--C--T--G--C--A--G-- 2008
Oy 681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerPheHisValSer 700
Db 2009 AC--GGAACAAACACAGAACTGAATGAAGAAAGAGAGAGTCAAGTTCTTCCACGTTTC 2067
Oy 701 MetAspPheLeuGlnAspProSerGlnArgGlnAlaGlnMetSerIleAlaSerIleLeu 720
Db 2068 ATGGACTTTCTGAAGATCTTCCCAAAAGCAACGAGCAATAGATATACAGCATTTCTA 2127
Oy 721 ThrAsnThrValGluGluLeuGlnGluSerArgGlnLysCysProProCysTyrPyrLys 740
Db 2128 ACATTAATACAGTGAAGAACTTAAGAAATCAAGACGAGAAATGCCCACCTGTGGATTA 2187
Oy 741 PheSerAsnIlePheLeuIleThrAspCysSerProTyrTyrPheLysValLysHisVal 760
Db 2188 TTTTCCACATATCTTATATCTGGGACGTCTCCATATGTTAAAGTGAACATGTT 2247

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QY 761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780  
DB 2248 GTCAACTGCGTCGATGAGACCCATTTGTTACCTGGCCATCCACATCTGATTTGCTTA 2307  
QY 781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800  
DB 2308 AATACCTCTTTTCATGGCCATGAGACACTATTCATATGAGCAGCATTTCAATATATGCTT 2367  
QY 801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820  
DB 2368 ACAGTAGAAGAACTGGTTTTCACAGGGATCTTACAGAGAAATGTTCTGAAAATATAT 2427  
QY 821 AlaMetAspProTyrTyrTyrPheGluGluGlyIleTyrAsnIlePheAspGlyPheAlaIleVal 840  
DB 2428 GCCATGATCTTACTATTTATTTCCAGAGAGGCTGGAATATCTTGTGAGGGTTTATGTG 2487  
QY 841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860  
DB 2488 ACGCTTAGCCTGATAGAACTTGGACTCGCCAAATGTGGAGATTTATCTGTTCTCGTTCA 2547  
QY 861 PheArgLeuLeuValGlyPheLysLeuAlaLysSerTyrProThrLeuAsnMetLeuIle 880  
DB 2548 TTTTGATTTGCTGCGAGTTTTCAGTTGGCAAAATCTTGGCCAAAGTTAAATATGCTATA 2607  
QY 881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValIleAlaIleIle 900  
DB 2608 AAGATCATCGGCATTTCCGTGGGGGCTCTGGAAATTTAAACCTCGCTTGGCCATCATC 2667  
QY 901 ValPheIlePheAlaValAlaGlyMetGluLeuPheGlyLysSerTyrLysAspCysVal 920  
DB 2668 GTCTTCATTTTTCGCGTGGCGCATGCTCTTGTGTAAACCTCAAAAGATTTGCTG 2727  
QY 921 CysLysIleLeuAspCysGluLeuProArgTyrHisMetAsnAspPheHisSer 940  
DB 2728 TGCAGAGTCGCGATGATGCACTCCACGCTGSCAAGATGATCTTCCACTCC 2787  
QY 941 PheLeuIleValPheArgValLeuCysGlyGlyIleTyrPheIleGluThrMetTyrPAspCysMet 960  
DB 2788 TTCTCGATGCTGTTCCGCGTCTGTGGGAGATGAGATGAGACATGCGACTGTATG 2847  
QY 961 GluValAlaGlyAlaMetCysLeuThrValPheMetLeuValMetValIleGlyAsn 980  
DB 2848 GAGGTGCTGCTGATCAGCAGCTGCTTACTGTTTCATGATGATGATGATGATGAAAC 2907  
QY 981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu\*\*\*-SerSerPheSerLeuAspAsnLe 1000  
DB 2908 CTAGTGTCTGATCTCTTCTGCGCTTCTCTCT- GAGCTCATTTAGTGCAGCAACCT 2966  
QY 1000 ValAlaThrAspAspAspAsnGluMetAsnAsnLeuGluIleAlaValAspArgMetHis 1020  
DB 2967 TGCAGCCATCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3026  
QY 1020 slyGlyValAlaIleTyrValLysArgLysIleTyrGluPheIleGluIleSerPheIleArg 1040  
DB 3027 CAAGGAGTGTATGTGAAAGAAAATATGATTTATTCACAGCTCTCATATAG 3086  
QY 1040 GlyGluIleLysIleLeuAspGluIleLysProLeuAspAspLeuAsnLysLysAspSe 1060  
DB 3087 GAACCAAAATATTTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3146  
QY 1060 rCysMetSerAsnHisThr\*\*\*-GluIleGlyAspLeuAspTyrLeuLysAspValAla 1080  
DB 3147 TTGTATGTCCAAATCATCAAC- AGAAATGTGGAAGATCTTGACTATCTTAAAGATGATA 3205  
QY 1080 snGlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluS 1100  
DB 3206 ATGCAACTACAAAGTGTATGGAAGTGGAGCTGTGTAATAATCATATTTGATGATAA 3265  
QY 1100 eAspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValG 1120  
DB 3266 GTGATTAATGCTATCATATAAACACCCAGCTTACTGTGACTGTACCAATTTGCTGTAG 3325  
QY 1120 LysIleSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluG 1140  
DB 3326 GAGATCTGACTTTGAAAATTTTAAACGGAAGACTTATGATGAAATCGATCTGGAG 3385  
QY 1140 LysTyrGlyLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleG 1160  
DB 3386 AAACCAAAAGAACTGATGATGAAAGCAGTACTCATGAAAGATGAGCAGTGTGACATCG 3445  
QY 1160 LysIleProValGluGluIleProValValGluProGluGluThrLeuGluProGluIle 1180  
DB 3446 GCGCAGCTGTGAAAGAACAGCCCTAGTGGAACTGGAAGAAACCTTGAACCAAGACTT 3505  
QY 1180 LysPheThrGluGlyCysValGluIleArgPheLysCysGluIleAsnValGluGluGly 1200  
DB 3506 GTTTCAGTGAAGCTGTGTACAAAGATTCAGATTTGTCAAATCAATGTGAAAGAGCA 3565  
QY 1200 rGlyLysGluTyrTyrPAsnLeuArgTyrCysPheArgIleValGluIleAsnTyrP 1220  
DB 3566 GAGGAAAACAAATGTTGAGAACTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3625  
QY 1220 heGluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAsp 1240  
DB 3626 TTGAGACCTTCATTTGTTTCATGATTCCTTATGATGAGTGTGCTGCAATTTGAAGATA 3685  
QY 1240 LysTyrIleAspGluArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPhe 1260  
DB 3686 TATATATTTGATCAGCAGAAAGCATTAAGACGATGGAATATGATGACAAAGGTTTCA 3745  
QY 1260 hrTyrIlePheIleLeuGluMetLeuLeuLysTyrValAlaTyrGlyIleThrTyrP 1280  
DB 3746 CTTCATTTTCATCTGGAATGCTTCTAAATGGTGGCATATGCTATCAAAACATAT 3805  
QY 1280 heThrAsnAlaTyrCysTyrPheLysPheLeuIleValAspValSerLeuValSerLeu 1300  
DB 3806 TCACCAATGCTGTGTGTGGCTGATCTTAAATGTTGATGATGATGATGATGATGATG 3865  
QY 1300 hrAlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArg 1320  
DB 3866 CAGCAAAATGCTGTGGTATCAGAACTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3925  
QY 1320 LysLeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValAlaValAsnAla 1340  
DB 3926 CTCTGAGACCTCTGAAGAGCTTATCTGATTTGAAGAGAGAGAGAGAGAGAGAGAG 3985  
QY 1340 euleuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheThrLeu 1360  
DB 3986 TTTTATGAGGCAATTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 4045  
QY 1360 LysPheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThr 1380  
DB 4046 TTTTCACATCATGAGGCTGATTAATTTGTTGCTGCGCAATTTCTACCTGTATTAACCA 4105  
QY 1380 hrThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeu 1400  
DB 4106 CAACGTGTGACAGGTTTGAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4165  
QY 1400 LysGluArgAsnGluThrAlaArgTyrLysAsnValLysValAsnPheAspAsnValGly 1420  
DB 4166 TTAGAAAGAAATGAGACTGCTGATGAGAAATATGAAAGATTAATGATGATGATGATG 4225  
QY 1420 heGlyTyrLeuSerLeuLeuGluValAlaThrPheLysGlyTyrPheAspIleMetTyr 1440  
DB 4226 TTGGGTATCTCTCTTCTCTCAAGTTCCCATTTCAAGAGATGATGATGATGATGATG 4285  
QY 1440 LysAlaValAspSerArgAsnValGluLeuGluProLysTyrGluGluSerLeuTyrMet 1460  
DB 4286 CAGCAGTGTATTCAGAAAGTGAAGTCCAGCTTAAGATGAAAGAGAGAGAGAGAGAGAG 4345  
QY 1460 LysLeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIle 1480  
DB 4346 ATCTTACCTTGTATTTATCATCATCTTGTGGCTTCTTCCACTTGAACCTTGTATTTG 4405  
QY 1480 LysValIleLeuAspAsnPheAsnGluIleLysLysLysPheGlyGluAspIlePheMet 1500

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Db 4406 GTGTATCTATATATTTTCAACGACGAGAAAAGAGTTTGAGGTTCAGACATCTTAA 4465
Oy 1500 eethrGlunGlunlYslyTyrrYasnAlmetLysLysLeuGlYserLysLysProg 1520
Db 4466 TCACAGAGAGACAGAGAAATACATTAATGCAATGAAAAAATAGATCGAAAAACCCG 4525
Oy 1520 lnlYsPrOlePrOlePrOglYasnLysPhneGlYmetValPhneAspPheValThra 1540
Db 4536 AAAACCCATATACCTGACGACGAGAAACAAATTCAGAGAAAGTCTTGAATCGTAACA 4585
Oy 1540 rglInValPheAspLysSerLleMetLleLeuLleCysLeuAsnMetValThrMetMetY 1560
Db 4586 GACAACTTTTACATTAACATACATGATCTCATCTGTTTAACTAGGTCACATGATATG 4645
Oy 1560 aGlunThraspAspLysSerLglYurValThrThrlleuSerArglleAsnLeuValP 1580
Db 4646 TGGAAACAGATGACCAAGATGATATGATACCATTTTTCAGACGATCAATCTGTGT 4705
Oy 1580 heIlleValleuPheThrGlYglYcysValleuLysleuLleSerLeuAqHlStYrTyP 1600
Db 4706 TCATTGTGCTATTTACTGAGAGGTGTACTGAAACCTCACTCTACCCATTAATAT 4765
Oy 1600 heThrlleGlYTrpAsnLlePheAspPheValValleuSerLleValGlYmetP 1620
Db 4766 TTACCATTTGATGATATATTTTGTGATTTTGTGTTGTCTCTCCATTTGATGATGT 4825
Oy 1620 heLeuAlaGlYleuLleGlYlYsTyrrPheValSerProThrLeuPheArgValleuArgL 1640
Db 4826 TTCCTTGGCAGGTGATAGAAAAGTATTTGTGTCCCTTCCCTGATCCGAGATCCGTC 4885
Oy 1640 euAlaArglleGlYArglleLeuArglleLysGlYAlaLysGlYleuArgHlThra 1660
Db 4886 TTGCTAGAGATTTGCCGAAATCTACGCTGATCAAGGAGCAAAAGGAGTCCACGCTGC 4945
Oy 1660 euPhAlaLeuMetLleSerLeuProAlaLeuPheAsnLleGlYleuLeuPheLeuY 1680
Db 4946 TCTTTGCTTTGATGATGTCCTCTCTGCTGTTTAACTGCGCTTCTTCTTCTTCTG 5005
Oy 1680 alMetPheLleTyraAllePheGlYmetSerAsnPheAlaTyrrValLysArgGlValaG 1700
Db 5006 TCATGTTCATCTACGCCATCTTGGAGATGCCAACCTTCATGTGTAAAGAGAAATGTG 5065
Oy 1700 lYllleAspAspMetPheAsnPheGlYurThrPheGlYasnSerMetLleCysLeuPheGlIn 1720
Db 5066 GGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5125
Oy 1720 leThrThrSerAlaGlYTrpAspGlYleuLeuAlaProLleLeuAsnSerLysProPro 1740
Db 5126 TTACAACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5185
Oy 1740 sPCysAspProAsnLysValaAsnProGlYSerSerValLysGlYasPCysGlYasnPro 1760
Db 5186 ACTGAGACCTCTAATAAGATTAAACCTCGAAGCTCAGATTAAAGAGACCTGTGGAAACCAT 5245
Oy 1760 exValGlYllephePheValSerTyrrllelleSerPheLeuValValaAsnM 1780
Db 5246 CTGTTGGATTTCTTTTGTGCTGATCATCATCATCATCTCTCGGTGTGGTGAACA 5305
Oy 1780 eTyrrlleValleuAlleuGlYasnPheSerValaAlaThrGlYlYsLeuSerAlaGlYProL 1800
Db 5306 TGTACATGCGCGCTCAATCCGAGAACTTCAAGTGTGCTTCAAGAAAGTGCAGAGCCTC 5365
Oy 1800 euSerGlYasPhePheGlYmetPheTyrrGlYValaTyrrPglYlYsPheAspProAspAlaT 1820
Db 5366 TGAGTGAGAGATGATCTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 5425
Oy 1820 hrGlPheMetGlYubheGlYlYsleuSerGlYnPhaAlaAlaAlaLeuGlYurProProLeu 1840
Db 5426 CTCAGCTCAATGGAATTTGAAAAATTAATCATGATTTGACGCTGCTGGAACCGCTCTCA 5485
Oy 1840 snLeuProGlYnProAsnLysLeuGlYnLeuAlaMetAspLeuProMetValSerGlY 1860

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Db 5486 ATCTGCCACAAACAAACATCCAGCTCATCTCCATGATTTGCCATGTGAGTGTG 5545
Oy 1860 spArglleHlscysLeuAspLlleuPheAlaPheThrLysArgValleuGlYlYsSerG 1880
Db 5546 ACCGATCCACATGCTGTGATCTTATTTGCTTTTCAAAAGCGGGTTCTAGAGAGAGTG 5605
Oy 1880 lYglMetAspAlaLeuArglleGlYmetGlYlYsArgPheMetAlaSerAsnProSerL 1900
Db 5606 GAGAGATGATGCTCTACCAATACAGATGGAAGAGGATTCATGGCTTCAATCTCTCA 5665
Oy 1900 ysValSerTyrrlInProLleThrThrlleuLysArgLysGlYlYsValSerAlaY 1920
Db 5666 AGGTCTCCATACAGCAATCACTACTTCTTAAACGAAACAAAGAGAAAGATTCGCTG 5725
Oy 1920 alllellelInArgAlaTyrrArgArgHlslleuLysArgThrValLysGlYnAlaSerP 1940
Db 5726 TCATTATCAGCGTGTCTACAGACCCACCTTTTAAAGCAAGTGAACAAAGCTTCT 5785
Oy 1940 heThrTyrrAsnLysAsnLysLleYsGlYlYAlaAsnLeuLleLysGlYAspMetI 1960
Db 5786 TTACGTACATATAAAACAAATCAAGGTGGGCTTAATCTTAAAGAAAGACATGA 5845
Oy 1960 lelleAspArglleAsnGlYasnSerLleThrGlYlYsThraspLeuThrMetSerThra 1980
Db 5846 TAAATTCAGAAATTAATGAAATCTTATTAACGAAAAAATCTATCTGACCATGCTCACTG 5905
Oy 1980 lAlaCysProProSerTyrrAspArgValThrLysProLleValGlYlYsHlslYlGlnG 2000
Db 5906 CAGCTTGCTCACCTTCCTTGTGACCGGTGACAAAGCAATGTGGAAAAACATGAGCAAG 5965
Oy 2000 lYglYlYsAspGlYlYsAlaLysGlYlYs 2009
Db 5966 AAGCAAAAGATGAAAAAGCCAAAGGAAA 5994

RESULT 11
AF225985 8131 bp mRNA linear PRI 01-FEB-2001
LOCUS AF225985 Homo sapiens voltage-gated sodium channel alpha subunit SCN1A
DEFINITION (SCN1A) mRNA, complete cds.
ACCESSION AF225985
VERSION AF225985.1 GI:12642269
KEYWORDS Homo sapiens.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 8131)
AUTHORS Jeong,S.-Y., Goto,J. and Kanazawa,I.
TITLE Cloning of cDNA for human voltage-gated sodium channel alpha
subunit, SCN1A
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 8131)
AUTHORS Jeong,S.-Y., Goto,J. and Kanazawa,I.
TITLE Direct Submission
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| QY | 939  | sSerPheLeuIleValPheargValLeuCysGIyIuTyrPIleGIuThrMetTyrAsPCy   | 959  |
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| Db | 3522 | AGCTTGTTCACGAAAGCGGTGTACAAAGATTCAAGTCTTGTCAAACTATGTGGAGA       | 3581 |
| QY | 1198 | uGIyArgGIyIySGIInTyrPyrAsnLeuArgATrThrCysPheArgIleValGIuHisAs  | 1218 |
| Db | 3582 | AGCGAAGAGAAACAATGTGTGGAACCTGGAAGAGACGTCTTTCCGAATATGTGAACATPA   | 3641 |
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| O | 1258 | 1phehTrrTrillephelelleuGluMetleuMetleuIysTrrValAlaTrrGlyTrrGlnTh | 1276 |
| D | 3762 | TTTCCTCATCTTCATTTTCATCTTCGGAAGAGCTTCTTAATGGTGGCCATATGGCTATCAAC   | 3822 |
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| D | 3942 | AAGAGCTCTGGAGCTCTTAAGAGCTTATCTTCATTTGGAAGGGATAGGGTGGTGTGTA       | 4003 |
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| D | 4002 | TGCCCTTTTAGAGACCATTTCCATCCATCAATGAATGTGCTTCGTGGTTTGCTTAATTCG     | 4066 |
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| O | 1378 | rNtrThrThhGlyaspArgPheasp1leGluaspValAsnAsn1sthrAspCysleuIy      | 1396 |
| D | 4122 | CACCAACAACGTGTACAGGTTTGACATCGAAGACGTGAATATCATACATCGAATGGCTTAA    | 4181 |
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| D | 4182 | ACTAATATGAAAGAAATATAGACTGCTGCATGCAAAAAATGTGAAGTAACTTTGATTAAGT    | 4241 |
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| D | 4302 | GTAATGACAGCAAGTTGATTCAGAAATGTGGAAATCCAGCTTAATGTAAGAAAGCTCTGA     | 4361 |
| O | 1458 | rMetTrrleuTrrPheVal1lePhe1le1lePheGlySerPhePheThleuAsnLeuP       | 1478 |
| D | 4362 | CATGATACCTTACTTCTTGTATTATTTTCATCATCTTTGGGTCTCTTCATCCCTTAACCTGT   | 4421 |
| O | 1478 | e1leGlyVal1le1leAspAsnPheAsnGluIeuIysIysPheGlyGlyGlnAsp1l        | 1498 |
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| O | 1558 | tMetValGluThrAspaspGlnSerGluTrrValThrThr1leuSerArg1leAsnLe       | 1578 |
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| O | 1578 | uValPhe1leValleuPhehThhGlyIuGlyValleuIysleu1leSerleuArgH1stY     | 1598 |

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| Qy | 1598 | ITTPhehnrILleGIlyrPasnILlePheaspPheValValILleLeuSerILleValGI      | 1618 |
| Db | 4782 | TTATTTTACATGTGAGAGAAATATTTTGTATTTTGTGGTTGTTCATCTCTCCATGTGTAG      | 4842 |
| Qy | 1618 | ymcPheLeuValaGluLeuILleGluYSYrPheValSerProthPheLeuPheArgValII     | 1633 |
| Db | 4842 | TATGTTCCTTCCAGAGCTGATAGAAAGTATTTTCGTGCCCTTACCTCTTCCGAGTGAT        | 4901 |
| Qy | 1638 | eArgLeuValaArgILleGIlyrArgILleLeuArgLeuIIeYSgILValaLYsGIILleArgTh | 1651 |
| Db | 4902 | CCGCTTCCTGTAAGGATGTGGCCGAATCTCTACTGTGATCTCAAGAGCAAGGAGGATCCGCAC   | 4961 |
| Qy | 1658 | ILleuLeuPheValaLeuMetMetSerLeuProaILleuPheAsnILleGIlyLeuLeuLeuPhe | 1678 |
| Db | 4962 | GCTGCTCTTCTCTTGTATGATGTCCCTCTCTGGGTTGTTAACTATGGGCTCTTACTCT        | 5021 |
| Qy | 1678 | eLeuValaMetPheILleArgValaIIlePheGIlyMetSerAsnPheValaArgValaYsGI   | 1699 |
| Db | 5022 | CTTGTGTATGTTCATCTCAAGCCATCTTTGGAGATGTCCAACTTGTGCTATGTAAAGAGGA     | 5081 |
| Qy | 1698 | uValGILleLeaspPhePheLeuAsnPheGIlyuThrPheGIlyAsnSerMetILleCYsLeuPh | 1718 |
| Db | 5082 | AGTTGGATTCGATGATGATGATGTCACCTTGTGAGACTTGTGGCAACGATGATGTGCTATT     | 5141 |
| Qy | 1718 | eGluILleThrThrSerILleagILyTrPaspGIlyLeuLeuValaProILleAsnSerIAsPr  | 1738 |
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| Qy | 1738 | oProAsPcYsAspProAsnLYsValAsnProGIlySerSerValLYsGIlyAsPcYsGIlyAs   | 1758 |
| Db | 5202 | ACCCGATGTGACCCCTTAATTAACCTGAGAACCTGATTAAGGAGACTGTGGGA             | 5261 |
| Qy | 1758 | nProSerValGIlyrILlePhePhePheValSerTrILleILleIleSerPheLeuValaVala  | 1778 |
| Db | 5262 | CCCATCTGTGGAAATTTCTTTTGTTCAGATTACATCAATCAATCTCTCTGTTGTGTGT        | 5321 |
| Qy | 1778 | ILasMetTrILleValaValILleLeuGluAsnPheSerValaIaThrGluGluSerIaGI     | 1798 |
| Db | 5322 | GAACTATGTACTGGCGGCTATCTCTGGAGAACTTCATGTGTCTACTGAAGAAAGTCGAGA      | 5381 |
| Qy | 1798 | uProLeuSerGluAspAspPheGluMetPheTrGIlyValaITrPGIlyLYsPheAspProAs   | 1818 |
| Db | 5382 | GCCCTGAGTGAAGGATGATCTTGAAGATGTCTATGAGGTTGGGAGAAAGTTGATCCCGA       | 5441 |
| Qy | 1818 | PaLaThrGluPheMetGluPheGluLYsLeuSerGluPheValaIaIaLeuGluProPr       | 1838 |
| Db | 5442 | TGCAACTCAGTCAATGAATTAATAAAATTAATCTCAGTTTGGAGCTGGCTTGAACGCC        | 5501 |
| Qy | 1838 | OLeAsILleuProGluInProAsnLYsLeuGluILleuValaIaMetAspLeuProMetValSe  | 1858 |
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| Qy | 1898 | oSerLYsValaSerTrGluInProILleThrThrPheLYsArgLYsGluGluGluValSe      | 1918 |
| Db | 5682 | TTCCAAAGTCTCTATCAGCAATCTCTACTTATTAAGCAAAACAAACAGAGATATC           | 5741 |
| Qy | 1918 | rAlaValaILleGluILleArgValaArgArgHisLeuLeuLYsArgThrValaLYsGluI     | 1938 |
| Db | 5742 | TGCTGTATATATCAGGCTCTTACAGAGCCACCTTTAAAGCAACTGTAAACAAGC            | 5801 |
| Qy | 1938 | aSerPheThrTrYAsnLYsAsnLYsILleYsGILyGluLYsAsnLeuLeuILleYsGILyAs    | 1958 |
| Db | 5802 | TTCCCTTACGTCAATTAATAAAACAAATCAAAAGTGGGGCTATCTTCTTAATAAAGAGA       | 5861 |



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 REFERENCE 1 Turner C.A., Mathur B. and Mathur D.  
 AUTHORS Novel human ion channel proteins and polynucleotides encoding the  
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LOCUS AX391136 Sequence 7 from Patent WO0214498.
DEFINITION AX391136
ACCESSION AX391136
VERSION AX391136.1 GI:19584235
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 Turner,C.A., Mathur,B. and Mathur,D.
AUTHORS Novel human ion channel proteins and polynucleotides encoding the
TITLE Patent: WO 0214498-A 7 21-FEB-2002;
JOURNAL Lexicon Genetics Incorporated (US)
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1  
 AUTHORS Turner, C.A., Mathur, B. and Mathur, D.  
 TITLE Novel human ion channel proteins and polynucleotides encoding the same  
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 LEXICON Genetics Incorporated (US)  
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REFERENCE 1 (bases 1 to 1269)
AUTHORS Lu, C.-M., Han, J., Rado, T. A. and Brown, G. B.
TITLE Differential expression of two sodium channel subtypes in human
brain
JOURNAL FEBS Lett. 303 (1), 53-58 (1992)
MEDLINE 92275082
PUBMED 1317301
COMMENT The authors changed locus name to 'SCN1A' according to the consensus
nomenclature. This gene is abbreviated as HSC I for human brain
sodium channel I in reference [3] (FEBS Lett., 303:53-58 1992).
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DB 541 GAAGTGTGAATCGATGACATGTCACCTTGAGACCTTGGCAACAGCATGATCTGCCTA 600  
QY 1718 PheGlnIleThrThrSerAlaGlyTyrPAspGlyLeuLeuAlaProIleLeuAsnSerLys 1737  
DB 601 TTCCAATTTACACCTCTGCTGCTGGATGATGATGCTACGACCATTCATCAACAGTAA 660  
QY 1738 ProProAspCysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGly 1757  
DB 661 CCACCCGACGTGACCTTAATAAGTTAACCCGAGCTCAGTTAAGGGGACTGTGG 720  
QY 1758 AsnProSerValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValVal 1777  
DB 721 AACCCATCTGTGAAATTTCTTTTGTGCTACATCATCATATCTTCCTGCTGTGTG 780  
QY 1778 ValAsnMetTyrIleAlaValIleLeuGlnAsnPheSerValAlaThrGlnGlnSerAla 1797  
DB 781 GTGACATGTACATCGGGGATCATCTCGAGAACTTCAAGTGTGCTACTGAGAAAGTGA 840  
QY 1798 GluProLeuSerGlnAspAspPheGlnMetPheTyrGlnValTyrGlnLysPheAspPro 1817  
DB 841 GAGCCCTGTGAGTGAAGTACTTGTGATGATGTCTATGAGGTTGGAGAGTTGATCCC 900  
QY 1818 AspAlaThrGlnPheMetGlnPheGlnLysLeuSerGlnPheAlaAlaIleLeuGlnPro 1837  
DB 901 GATGCACTAGTTCATGAGATTTGAAATTTATCTCAGTTGTCAGCTGCGCTTGAACCG 960  
QY 1838 ProLeuAsnLeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetVal 1857  
DB 961 CTTCTCATATGTCACACAAACAACTCAGCTCATTTGCCATGATTTGCCCATGCTG 1020  
QY 1858 SerGlyAspArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGly 1877  
DB 1021 AGTGTGACCGGATCCACTGTGATATCTTATTTGCTTTTACAAAGCGGGTTTACGA 1080  
QY 1878 GluSerGlyGlnMetAspAlaLeuArgIleGlnMetGlnGlnLysArgPheMetAlaSerAsn 1897  
DB 1081 GAGAGTGTGAGATGTGCTTACGATACATGAGAGATGCAATTCATGCTTCCAAAT 1140

QY 1898 ProSerLysValSerTyrGlnProIleThrThrPheLeuLysArgLysGlnGlnGlnVal 1917  
DB 1141 CCTTCCAGAGTCTCTCTATACGCCAATCATCTTCTTAAACGAAACAAAGAGAGTA 1200  
QY 1918 SerAlaValIleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGln 1937  
DB 1201 TCTGCTCATTAATTCAGCGGTTCACAGAGCCACCTTTAAAGCCAACTGTAAACAA 1260  
QY 1938 AlaSerPhe 1940  
DB 1261 GCTTCCCTTT 1269

Search completed: April 23, 2003, 07:14:02  
Job time : 7936 secs

GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 23, 2003, 04:37:36 ; Search time 3698 Seconds

(without alignments)  
8798.468 Million cell updates/sec

Title: US-09-930-871-12

Perfect score: 2009

Sequence: 1 MEQTVIVPQGDSENFRTRE.....TKPIVENHGEQKDEKAKG 2009

Scoring table:

OLIGO  
Xgapop 60.0, Xgapext 60.0  
Ygapop 60.0, Ygapext 60.0  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 16154066 segs, 8097743376 residues

Word size: 1

Total number of hits satisfying chosen parameters: 32308016

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL-frame+ p2n model -DEV-xlh  
-O/-cgn2.1/USPPO.spool/US09930871/runat\_16042003\_114925\_8998/app\_query.fasta.1.2183  
-DB-BST -OFMT-fastap -SUFFIX-oligop2n.rst -MINMATCH-0.1 -ICOPCI-0 -LOOPEXT-0  
-UNITS-bits -START-1 -END-1 -MATRIX-oligo -TRANS-human40.cdi -LIST-45  
-DOCALLIGN-200 -THR SCORE-quality -THR MIN-1 -ALIGN-15 -MODE-LOCAL -OUTFMT-pto  
-NOR-ext -HEARSIZE-500 -MINLEN-0 -MAXLEN-2000000000  
-USER-US09930871.ecgn.1.1.2346-ctunac.16042003.114925.8998 -NCPD-6 -ICPD-3  
-NO\_XLPY -NO\_MMAP -LARGEQUERY -NEG\_SCORES-0 -WAIT -LONGLOG -DEV.TIMEOUT-120  
-WARN.TIMEOUT-30 -THREADS-1 -XGAPOP-60 -XGAPEXT-60 -Fgapop-6 -Fgapext-7  
-YGAPOP-60 -YGAPEXT-60 -DELop-6 -DELEXT-7

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_idv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vit:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_oth:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rtd:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 185   | 9.2         | 579    | 14    | BM718214    |
| 2          | 182   | 9.1         | 562    | 14    | BM682680    |
| 3          | 163   | 8.1         | 674    | 12    | BC342331    |
| 4          | 161   | 8.0         | 547    | 12    | BF470392    |
| 5          | 147   | 7.3         | 443    | 12    | BE864903    |
| 6          | 142   | 7.1         | 618    | 13    | BI667397    |
| 7          | 123   | 6.1         | 683    | 10    | BB622500    |
| 8          | 106   | 5.3         | 392    | 10    | AM046964    |
| 9          | 104   | 5.2         | 951    | 9     | AL533359    |
| 10         | 103   | 5.1         | 1777   | 11    | BC029489    |
| 11         | 102   | 5.1         | 509    | 11    | BC034643    |
| 12         | 102   | 5.1         | 510    | 11    | BC023034    |
| 13         | 98    | 4.9         | 577    | 9     | AD067361    |
| 14         | 97    | 4.8         | 495    | 12    | BF563427    |
| 15         | 91    | 4.5         | 800    | 9     | AU066802    |
| 16         | 90    | 4.5         | 540    | 10    | BE121161    |
| 17         | 88    | 4.4         | 581    | 10    | BB644560    |
| 18         | 87    | 4.4         | 710    | 9     | AL707423    |
| 19         | 88    | 4.3         | 928    | 14    | BO715936    |
| 20         | 82    | 4.1         | 508    | 13    | BI731882    |
| 21         | 76    | 3.8         | 370    | 10    | AM123974    |
| 22         | 76    | 3.7         | 494    | 12    | BE955837    |
| 23         | 75    | 3.7         | 735    | 13    | BI488967    |
| 24         | 72    | 3.6         | 513    | 13    | BI731739    |
| 25         | 70    | 3.5         | 455    | 9     | AA912739    |
| 26         | 70    | 3.5         | 717    | 12    | BF724147    |
| 27         | 69    | 3.4         | 902    | 12    | BE761119    |
| 28         | 68    | 3.4         | 437    | 10    | AA945598    |
| 29         | 68    | 3.4         | 778    | 9     | AU035605    |
| 30         | 66    | 3.3         | 662    | 12    | BE253038    |
| 31         | 66    | 3.3         | 665    | 10    | BB653500    |
| 32         | 66    | 3.3         | 774    | 13    | BI488790    |
| 33         | 65    | 3.2         | 480    | 13    | BM494034    |
| 34         | 65    | 3.2         | 908    | 14    | BO946179    |
| 35         | 63    | 3.1         | 325    | 12    | BE471558    |
| 36         | 63    | 3.1         | 379    | 12    | BE947431    |
| 37         | 63    | 3.1         | 386    | 12    | BE944106    |
| 38         | 63    | 3.1         | 706    | 9     | AA984063    |
| 39         | 62    | 3.1         | 547    | 12    | BE724185    |
| 40         | 62    | 3.1         | 561    | 12    | BF076296    |
| 41         | 60    | 3.0         | 373    | 10    | AA456773    |
| 42         | 60    | 3.0         | 633    | 10    | BB644172    |
| 43         | 60    | 3.0         | 700    | 10    | BB631922    |
| 44         | 60    | 3.0         | 1024   | 11    | AK020721    |
| 45         | 59    | 2.9         | 354    | 10    | AA431606    |

#### ALIGNMENTS

| RESULT 1 | LOCUS    | DEFINITION   | ACCESSION | VERSION | KEYWORDS                                  | SOURCE | ORGANISM     | REFERENCE   | AUTHORS                                 | TITLE  |
|----------|----------|--|-----------|---------|---|--------|--------------|---|---|--|
| BM718214 | BM718214 | UI-E-EJ1-ajf-a-09-0-01.r1 UI-E-EJ1 Homo sapiens cDNA clone | BM718214  | 1       | UI-E-EJ1-ajf-a-09-0-01 5', mRNA sequence. | human. | Homo sapiens | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | Bonaldi,M.F., Lennon,G. and Soares,M.B. | Normalization and subtraction: two approaches to facilitate gene |

JOURNAL  
MEDLINE  
COMMENT

discovery  
Genome Res. 6 (9), 791-806 (1996)  
97044477  
Contact: Soares, MB  
Program for Rat Gene Discovery and Mapping  
University of Iowa  
451 Eckstein Medical Research Building Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: msoares@blue.weeg.uiowa.edu  
Tissue Procurement: Dr. Gregg Hageman  
CDNA library preparation: Dr. M. Bento Soares, University of Iowa  
CDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).  
Seq primer: M13 Reverse.

# FEATURES

Location/Qualifiers

1..579  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="UI-E-EJ1-ajf-a-09-0-UI"  
/clone\_lib="UI-E-EJ1"  
/tissue\_type="fetal eyes, lens, eye anterior segment, optic nerve, retina, Retina Foveal and Macular, RPE and Choroid"  
/dev\_stage="fetal and adult"  
/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site\_1: EcoR I; Site\_2: Not I; UI-E-EJ1 is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGATCAGCA; lens, CGATTACCGA; eye anterior segment, AATCCCAT; optic nerve, CCATTACG; retina, CCGCG; Retina Foveal and Macular, GTCC; RPE and Choroid, ACCGA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."  
BASE COUNT 168 a 123 c 125 g 163 t  
ORIGIN

## Alignment Scores:

Pred. No.: 4.19e-188 Length: 579  
Score: 185.00 Matches: 185  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 9.21% Indels: 0  
DB: 14 Gaps: 0

US-09-930-871-12 (1-2009) x BM718214 (1-579)

OY 1758 AasnProSerValGlyIlePhePheValSerTyrIleIleIleSerPheLeuValVal 1777  
DB 3 AACCAATCGTGGAAATTTCTTTTGTCAATTCATCATCAATCCCTCCGCTGGTG 62  
OY 1778 ValAsnMetYrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAla 1797  
DB 63 GAGACATGATACATCGCGTCTATCTCGAGAACTTCAGTCTGCTGAGAAATGCA 122  
OY 1798 GluProLeuSerGluAspPheGluMetPheTyrGluValTyrPgiuLysPheAspPro 1817  
DB 123 GAGCTCTGAGTGGAGATGATTTGAGATGCTTGAAGTTGGAGAAATTTGATCC 182  
OY 1818 AspAlaThrGluPheMetGluPheGluLysLeuSerGluPheAlaAlaLeuGluPro 1837  
DB 183 GATGCACTGATCATGAAATTTGAAAAATATCTCACTTGCACGCTGCTTGAACCG 242

OY 1838 ProteusnLeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuPrometVal 1857  
DB 243 CCTCTCATCTGCGACACCAACCAAACTCCAGCTCATTCGACGATTTGCCATGGGTG 302  
OY 1858 SerGlyAspArgIleHisCysLeuAspIleLeuPheAlaPheTyrArgValLeuGly 1877  
DB 303 AGTGTGACCGGATCCACTGCTTGATATCTTATTTGCTTTACAAAGCGGCTTGGA 362  
OY 1878 GluSerGlyLumetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsn 1897  
DB 363 GAGATGAGAGATGATGCTCTGATGATATGATGATGATGATGATGATGATGATGAT 422  
OY 1898 ProSerLysValSerTyrGlnProIleThrThrThrLeuLysArgLysGluGluVal 1917  
DB 423 CCTTCAAGGTCTCTCATGACCAATCATCTACTTTAAACGAAACAGAGAAAGTA 482  
OY 1918 SerAlaValIleIleGlnAlaGlyAlaTyrArgThrHisLeuLysArgThrValValGln 1937  
DB 483 TCTCTCATATTCAGCGCTTACAGACGACCTTTAAAGCGAACTGTAAACAA 542  
OY 1938 AlaSerPheThrTyr 1942  
DB 543 GCTTCCTTACGTAC 557

## RESULT 2

BM682680/c 562 bp mRNA linear EST 27-FEB-2002  
LOCUS  
DEFINITION UI-E-EJ1-ajf-a-09-0-UI.s1 UI-E-EJ1 Homo sapiens cDNA clone

ACCESSION BM682680  
VERSION BM682680.1 GI:18992576  
KEYWORDS EST.

SOURCE  
ORGANISM Homo sapiens  
human.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
1 (Bases 1 to 562)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.  
TITLE Normalization and subtraction: two approaches to facilitate gene discovery  
JOURNAL Genome Res. 6 (9), 791-806 (1996)  
MEDLINE 97044477  
COMMENT

Contact: Soares, MB  
Program for Rat Gene Discovery and Mapping  
University of Iowa  
451 Eckstein Medical Research Building Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: msoares@blue.weeg.uiowa.edu  
Tissue Procurement: Dr. Gregg Hageman  
CDNA library preparation: Dr. M. Bento Soares, University of Iowa  
CDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).  
Seq primer: M13 Forward  
POLYA-Yes.

## FEATURES

Location/Qualifiers

1..562  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="UI-E-EJ1-ajf-a-09-0-UI"  
/clone\_lib="UI-E-EJ1"  
/tissue\_type="fetal eyes, lens, eye anterior segment, optic nerve, retina, Retina Foveal and Macular, RPE and Choroid"  
/dev\_stage="fetal and adult"  
/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site\_1: EcoR I; Site\_2: Not I; UI-E-EJ1 is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research,

6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (drr)18 tail. The sequence tags for this library are: fetal eyes, AGAATCACA; lens, CGATTAGCGA; eye anterior segment, ATGCCGCTAT; optic nerve, CCATTAGGTC; retina, CCAGCG; Retina foveal and Macular, GTCC; RPE and Choroid, ACCCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).

TAG-LIB-UI-E-EJ1  
TAG-TISSUE-Foveal and Macular Retina  
TAG-SEQ-GTCC

BASE COUNT 161 a 121 c 118 g 162 t  
ORIGIN

## Alignment Scores:

Pred. No.: 6 97e-185 Length: 562  
Score: 182.00 Matches: 182  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 9.06% Indels: 0  
DB: 14 Gaps: 0

US-09-930-871-12 (1-2009) x BM62680 (1-562)

QY 1761 ValGlyIlePhePheValSerTyrIleIleSerPheLeuValValAsnMet 1780

DB 562 GTGGAAATTTCTTTTGTGAGTACATCATATCTTCTGTTGTGTGAACATG 503

QY 1781 TyrIleValIleLeuGlnAsnPheserValAthrGlnGluSerAlaGluProLeu 1800

DB 502 TACATCCGGGTCATCTGAGAGAACTTCAGTCTCTACTAAGAAGAGCAGAGCTGTG 443

QY 1801 SerGlnAspPheGluMetPheTyrGlnValTyrGlnGluSerPheAspProAspAlaThr 1820

DB 442 AGTAGAGATGCTTGTGATGTCTATGAGGTTGGAGAAAGTTGATCCGATGCAACT 383

QY 1821 GlnPheMetGlnPheGlnGluSerGlnPheAlaAlaLeuGluProProLeuAsn 1840

DB 382 CAGTTCAATGGAATTTGAAATTTATCTCAGTTTCAGAGTCCCTTGAACCCCTCTCAT 323

QY 1841 LeuProGlnProAsnGlnGluGlnLeuIleAlaMetAspLeuProMetValSerGlyAsp 1860

DB 322 CTGCCACACCAACCAACTCCAGCTCATGTCATGATGATGCCATGAGTGTGAGTGCAC 263

QY 1861 ArgIleHisCysLeuAspIleLeuPheAlaPheThrIleAspValIleGluGluSerGly 1880

DB 262 CGGATTCACATCTTGTATATCTTATTTGCTTTTACAAAGCGGGTTCTAGAGAGAGTGA 203

QY 1881 GluMetAspAlaLeuArgIleGlnMetGlnGluArgPheMetAlaSerAspProSerLys 1900

DB 202 GAGATGATGATGCTACAGATACAGATGAGAGGATTCATGCTTCCATCTTCCAG 143

QY 1901 ValSerTyrGlnProIleThrThrLeuLysArgLysGlnGluValSerAlaVal 1920

DB 142 GTCTCCATACAGCCAACTACTACTTAAACGAAACAGAGGATTCGCTGCTC 83

QY 1921 IleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGlnAlaSerPhe 1940

DB 82 ATTTATTCAGGCTGTACAGAGCCACTTTTAAAGCAACTGTAAACAAAGCTTCTTT 23

QY 1941 ThrTyr 1942

DB 22 ACGTAC 17

RESULT 3 BG342331 674 bp mRNA linear EST 27-FEB-2001  
LOCUS BG342331  
DEFINITION 602374246F1 NIH\_MGC\_94 Mus musculus cDNA clone IMAGE:4481819 5',

## Accession

Accession BG342331  
Version BG342331.1  
KeyWords GI:13148769  
Source

## Organism

Organism Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## Reference

Reference 1 (bases 1 to 674)  
Authors NIH-MGC  
Title National Institutes of Health, Mammalian Gene Collection (MGC)  
Journal Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov

## Comment

Comment Tissue Procurement: The Cepko Laboratory  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LML at:  
http://image.llnl.gov  
Plate: LLM0317 row: 1 column: 12  
High quality sequence stop: 672.

## Features

Location/Qualifiers  
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/db\_xref="taxon:10090"  
/clone="IMAGE:4481819"  
/clone\_lib="NIH\_MGC\_94"  
/tissue\_type="retina"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: eye; Vector: pCMV-SPORT6; Site: 1; NCI; Site: 2; Sali; Cloned unidirectionally; oligo-dT primed; Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH\_MGC library."

## Base Count

BASE COUNT 146 a 167 c 161 g 200 t  
ORIGIN

## Alignment Scores:

Pred. No.: 2 6e-164 Length: 674  
Score: 163.00 Matches: 163  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 8.11% Indels: 0  
DB: 12 Gaps: 0

US-09-930-871-12 (1-2009) x BG342331 (1-674)

QY 1572 IleLeuSerArgIleAsnLeuValPheIleValLeuPheThrGlyGluCysValLeuLys 1591

DB 121 ATTTTGTACAGCAACCACTGCTGTATCTGCTGTTACCCGCGAGTGTGCTCAAG 180

QY 1592 LeuIleSerLeuArgHisTyrTyrPheThrIleGlyTyrAsnIlePheAspPheValVal 1611

DB 181 CTGATCTCGCTCCGCCATTTATTTTACCAATGAGAGAACTTTCGATTTGTGGTG 240

QY 1612 ValIleLeuSerIleValIleGlyMetPheLeuAlaGluLeuIleGluLysTyrPheValSer 1631

DB 241 GTGATCTCTCCATTCAGAGGATGTTCTTCGCGAGCTATATAGAAAGATTTTGTGCT 300

QY 1632 ProThrLeuPheArgValIleArgLeuAlaArgIleGlyArgIleLeuArgLeuLys 1651

DB 301 CTTACCTCTGTTCCGAGTCATCCGCTGCGCAGATTGAGAAATCCATACGCTGATCATA 360

QY 1652 GlyAlaLysGlyIleArgThrLeuLeuPheAlaLeuMetSerLeuProAlaLeuPhe 1671

DB 361 GGTGCCAAGGAGATCCGACAGCTGCTCTGTAGATGATGATCTTCTGCGCTGTTT 420

QY 1672 AsnIleGlyLeuLeuLeuPheLeuValMetPheIleTyrAlaIlePheGlyMetSerAsn 1691

DB 421 AACATGGGCTCTGCTTTTTCATCATCTTATCATCATCATCATCATCATCATCATCATCAT 480

QY 1692 PheAlaIyValIysArgIuValIyIleAspMetPheAsnPhgIuThrPheGly 1711  
 DB 481 TTTGCCATATGTTAAGAGGAGTTGGATGATGACATGTTCACTTGAGACCTTGCGC 540  
 QY 1712 AsnSerMetIleCysLeuPheGlnIleThrSerAlaGlyTyrPaspGlyLeuAla 1731  
 DB 541 AACGAGTGTATGCTGCTGTCATCAATCACCACCTGCGGCTGGATGATGATCTGCGC 600  
 QY 1732 ProIleLeu 1734  
 DB 601 CCCATCTC 609  
 RESULT 4  
 LOCUS BF470392 547 bp mRNA linear EST 04-DEC-2000  
 DEFINITION UI-M-BH3-avc-c-07-0-UI.r1 NIH\_BMAP\_M.S4 Mus musculus cDNA clone  
 VERSION BF470392  
 KEYWORDS UI-M-BH3-avc-c-07-0-UI 5', mRNA sequence.  
 ACCESSION BF470392.1 GI:11539575  
 SOURCE EST.  
 ORGANISM house mouse.  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE  
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.  
 TITLE Normalization and subtraction: two approaches to facilitate gene  
 JOURNAL discovery  
 MEDLINE Genome Res. 6 (9), 791-806 (1996)  
 COMMENT 97044477  
 Contact: Chih, H  
 National Institute of Mental Health  
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD  
 20892-9643, USA  
 Tel: 301 443 1706  
 Fax: 301 443 9890  
 Email: MEST@mail.nih.gov  
 CDNA Library Preparation: M.B. Soares Lab Clone distribution:  
 Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It  
 should be noted that Bento Soares is generating a small number of  
 additional specialized non-redundant arrays of BMAP cDNAs whose  
 availability will be considered under appropriate and limited  
 collaborative arrangements.  
 Seg primer: M13 Reverse.  
 Location/Qualifiers  
 1..547  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UI-M-BH3-avc-c-07-0-UI"  
 /clone\_1lb="NIH\_BMAP\_M.S4"  
 /rev\_start="27-32 days"  
 /lab\_host="DH10B (Life Technologies)"  
 /note="Vector: pT73D-Pac (Pharmacia) with a modified  
 polylinker. Site 1: Not I; Site 2: Eco RI; The  
 NIH\_BMAP\_M.S4 library is a subtracted library of a series,  
 ultimately derived from a mixture of individually tagged  
 normalized libraries from ten regions of the mouse brain  
 (cerebellum, brain stems, olfactory bulbs, hypothalamus,  
 cortex, amygdala, basal ganglia, pineal gland, striatum,  
 hippocampus) after a series of subtractions to reduce the  
 representation of cDNAs from which 3' ESTs had already been  
 generated. The following serially subtracted libraries  
 were generated in this process: NIH\_BMAP\_M.S4,  
 NIH\_BMAP\_M.S3.3, NIH\_BMAP\_M.S3.2, NIH\_BMAP\_M.S3.1,  
 NIH\_BMAP\_M.S2, NIH\_BMAP\_M.S1. The subtracted library  
 (NIH\_BMAP\_M.S4) was constructed as follows: PCR-amplified  
 cDNA inserts from NIH\_BMAP\_M.S3.3, NIH\_BMAP\_M.S3.2, and  
 NIH\_BMAP\_M.S3.1 clones from which 3' ESTs had been derived  
 was used as a driver in a hybridization with a pool of  
 the NIH\_BMAP\_M.S3.3, NIH\_BMAP\_M.S3.2, and NIH\_BMAP\_M.S3.1  
 libraries in the form of single-stranded circles. The  
 remaining single-stranded circles (subtracted library)

BASE COUNT 110 a 143 c 128 g 166 t  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 2,98e-162 Length: 547  
 Score: 161.00 Matches: 161  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 8.01% Indels: 0  
 DB: 12 Gaps: 0  
 US-09-930-871-12 (1-2009) x BF470392 (1-547)  
 QY 1576 IleAsnLeuValPheIleValIleuPheThrGlyCysValIleuIleuSerIleu 1595  
 DB 22 ATCAACCTGATGTTTCACGCTGTTCCACCGGAGTGTGCTCAAGCTTATCTCCTC 81  
 QY 1596 ArgHisTyrTyrPheThrIleGlyTyrPaspIlePheAspPheValIleuSer 1615  
 DB 82 CGCATTTATTTTTCACCATGATGATGACATTTTGTGTTGCTGATCTCTCC 141  
 QY 1616 IleValIleuPheLeuAlaIleuIleuIleuIleuIleuIleuIleuIleu 1635  
 DB 142 ATGTAGGAGATGTTTCGCGGAGCTGATAGAGATATTTGTTGCTTACCTGTTTC 201  
 QY 1636 ArgValIleuArgIleuAlaArgIleuAlaArgIleuAlaArgIleuAlaArg 1655  
 DB 202 CGAGTCATCCGCTGCGGAGATGAGACGATCTGATCAAGGCGCAAGGGG 261  
 QY 1656 IleArgThrLeuPheLeuPheAlaLeuMetSerLeuProAlaLeuPheAsnIleGly 1675  
 DB 262 ATCCGACGCTGCTCTTGTGCTGATGATGATGATGATGATGATGATGATGATG 321  
 QY 1676 LeuLeuPheLeuValMetPheIleThrIleAlaIlePheGlyMetSerAsnPheAla 1695  
 DB 322 CTCTCTTCTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 381  
 QY 1696 LysArgIleuValIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 1715  
 DB 382 AACAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 441  
 QY 1716 CysLeuPheGlnIleThrThrSerAlaGlyTyrPaspGlyLeuAlaProIleLeuAsn 1735  
 DB 442 TGCCTGTTCCAAATCACCACCTTGTGGGCTGGATGATGATGATGATGATGAT 501  
 QY 1736 Ser 1736  
 DB 502 AGT 504  
 RESULT 5  
 LOCUS BE864903 443 bp mRNA linear EST 29-SEP-2000  
 DEFINITION UI-M-BH1-alw-d-11-0-UI.r1 NIH\_BMAP\_M.S2 Mus musculus cDNA clone  
 VERSION BE864903  
 KEYWORDS UI-M-BH1-alw-d-11-0-UI 5', mRNA sequence.  
 ACCESSION BE864903.1 GI:10386411  
 SOURCE EST.  
 ORGANISM house mouse.  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE  
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.  
 TITLE Normalization and subtraction: two approaches to facilitate gene  
 JOURNAL discovery  
 MEDLINE Genome Res. 6 (9), 791-806 (1996)  
 COMMENT 97044477

was purified by hydroxyapatite column chromatography,  
 converted to double-stranded circles and electroporated  
 into DH10B bacteria (Life Technologies) to generate the  
 NIH\_BMAP\_M.S4 library. This procedure has been previously  
 described (Bonaldo, Lennon and Soares, Genome Research  
 6:791-806, 1996).





|            |  |   |      |
|------------|--|---|------|
| Oy         | 1903   | TyrGlnProIlePheThrThreonLeuysArglyssIngluValSerAlaValIlelle   | 1922 |
| Db         | 126  | TATCGCCCATACACTAGTCTTAATAAAGAAACAAGAAGGAATGTGCCTCATTATTT      | 185  |
| Oy         | 1923   | GlnAtgAlatYrArPARHISLeuleuysArqThrVallysGlalaserPhetHTyr      | 1942 |
| Db         | 186  | CAGCGGGCTTAGAGAGGCCACCCTTTAAAGCAACTGTAAAAACAAGCTTCCTTAGCAC    | 245  |
| Oy         | 1943   | AshLysAsnLysIllelsgLyGLVlaAsnleullelllyslguAspmettileasp      | 1962 |
| Db         | 246  | AATAAACCAAATCAAAAGTGEGGCTATATCTTCTTAFAAAAAGACATGATTAATGAC     | 305  |
| Oy         | 1963   | ArglieasnGuasSeriIephrcLylusmTrAplicuethrmeserThralalaacy     | 1982 |
| Db         | 306  | AGAAATPAANTGAACACTATTAACAGAAAAAATGATATCGACANVTCCAAGTCACACTTGT | 365  |
| Oy         | 1983   | ProposerTyASPdRVALthrlysprolieVLlgulysHSIaglugluclylys        | 2002 |
| Db         | 366  | CCACCTTCCTAAGACCGGCTCACAAAGCCAAATTGTGCAAAAAACATGACCAAGGACAA   | 425  |
| Oy         | 2003   | Aspglu 2004<br>     <br>Db 426 GATGAA 431                     |      |
| RESULT 7   |  |   |      |
| BEB622500  |  |   |      |
| LOCUS      | BEB622500  | 618 bp mRNA linear EST 31-AUG-2001                            |      |
| DEFINITION | BEB622500 RIKEN full-length enriched, adult male olfactory brain Mus   |   |      |
| ACCESSION  | BEB622500  | musculus cdna clone 643040BL01 5', mRNA sequence.             |      |
| VERSION    | BEB622500.1  | GI:15397780   |      |
| KEYWORDS   | EST.   |   |      |
| SOURCE     | house mouse.<br>Mus musculus   |   |      |
| ORGANISM   | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelestomi;<br>Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.   |   |      |
| REFERENCE  | 1 (bases 1 to 618)   |   |      |
| AUTHORS    | Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,<br>Hiimoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,T., Konno,H., Kouda,<br>K., Koya,S., Matsuyama,T., Miyasaki,A., Nomura,K., Ohno,M.,<br>Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasakib,<br>D., Shibata,K., Shingawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,<br>Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,<br>Muramatsu,M. and Hayashizaki,Y.  |   |      |
| TITLE      | RIKEN Mouse ESTs (Arakawa,T., et al. 2001)<br>Unpublished (2001)   |   |      |
| JOURNAL    | Contact: Yoshihide Hayashizaki<br>Laboratory for Genome Exploration Research Group, RIKEN Genomic<br>Sciences Center(GSC), Yokohama Institute<br>The Institute of Physical and Chemical Research (RIKEN)<br>1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan<br>Tel.: 81-45-503-9222<br>Fax: 81-45-503-9216<br>Email: genome-res@sc.riken.go.jp,   |   |      |
| COMMENT    | URI:http://genome.gsc.riken.go.jp/<br>Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itch<br>, M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.<br>. Normalization and subtraction of cap-trapper-selected cDNAs to<br>prepare full-length cDNA libraries for rapid discovery of new<br>genes. Genome Res. 10 (10), 1617-1630 (2000)<br>Wagil,K., Fujikake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,<br>Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsunra<br>, S., Kawai,T., Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and<br>Hayashizaki,Y.<br>RIKEN Integrated sequence analysis (RISA) system--384-format<br>sequencing pipeline with 384 multicapillary sequencer. Genome Res.<br>10 (11), 1757-1771 (2000)<br>Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara<br>, Y. and Hayashizaki,Y.<br>Computer-based methods for the mouse full-length cDNA<br>encyclopedia: real-time sequence clustering for construction of a<br>nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)<br>Yamanaka,I., Kiyosawa,H., Kondo,S., Saito,T., Shingawa,A., Aizawa |   |      |

|  |   |
|--|---|
|  | K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K., Arakawa,T., Ishii,Y. and Hayashizaki,Y.  |
|  | Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct. Func. Genomics 2 pre, 172-186 (2001   |
|  | Please visit our web site ( <a href="http://genome.gsc.riken.go.jp">http://genome.gsc.riken.go.jp</a> ) for further details.  |
|  | e mouse tissues.  |
| FEATURES   |   |
| source   | Location/Qualifiers   |
|  | 1..618  |
|  | /organism="Mus musculus"  |
|  | /db_xref="taxon:10090"  |
|  | /clone="643040BL10"   |
|  | /clone_lib="RIKEN full-length enriched, adult male olfactory brain"   |
|  | /sex="male"   |
|  | /tissue_type="olfactory brain"  |
|  | /dev_stage="adult"  |
|  | /lab_host="DH10B"   |
|  | /note="Site_1: SalI; Site_2: BamHI; CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGAGAGAGACGGCCGCACACTCGATTTTCTTTTTTTTNN 3'], cDNA was prepared by using trihalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTTCGATTAATAATATCCCCCCCCCCC 3']. cDNA was cleaved with BamHl and XhoI. Vector: a modified pluescript KS(+) after bulk excision from LambdaFLC I." |
| BASE COUNT   | 133 a 155 c 157 g 173 t   |
| ORIGIN   |   |
| Alignment Scores:  |   |
| Pred. No.:   | 3..21e-121 Length: 618  |
| Score:   | 123.00 Matches: 123   |
| Percent Similarity:  | 100.00% Conservative: 0   |
| Best Local Similarity:   | 100.00% Mismatch: 0   |
| Query Match:   | 6..12# Indels: 0  |
| DB:  | Gaps: 0   |
| US-09-930-871-12 (1-2009) x BB622500 (1-618)                             |   |
| OY 1614 LeusSerileValIGlyMetPheLeuAlaGluLeuIlleGlyLysTyrPheValSerProThr  | 1633  |
| Dd 1 CTCTCCATGTATGGAGTGTCTTCGCCGAGCGCATGAGAAGAAATTTCTGTCGCCCTAAC         | 60  |
| OY 1634 LeuPheAaGrVallleArgLeuAlaArgrlleGlargrlleLeuAargLeuIlleLysGlYala | 1653  |
| Dd 61 CTTGTCGCGATCATCCGCTTGCGCAGAGATGGACAACATCTCAACGCTGATCAAAGCGCC       | 120   |
| OY 1654 LysGglyleArgTrhleuLeuPheAlaleuMetMtsrleuProAlleuPheAsnille       | 1673  |
| Dd 121 AAGGGATCCGCACCCTGCTCTTGTCTGATGAATGTCCTTCGCGCTGTTTAACATC           | 180   |
| OY 1674 GlyLeuLeuLeuPheLeuValMetPheIlleTyrAlaIllePheGlyMetSerAsnPheAla   | 1693  |
| Dd 181 GGCCCTCGCTTTCCTGGTGCATGTTCATCTACGCCATCTTGGGATGCCAACATTGCC         | 240   |
| OY 1694 TyrVallysAArggluValAGlyllleAspsAsmetPheAsnPhegluThPheglyAsnSer   | 1713  |
| Dd 241 TACGTTAAGAGGAGGAGTTGGGATTTATGACATGTTCAACTTGGACACCTTGGCAACAGC      | 300   |
| OY 1714 MetliecylsleuPheGlnlleThrThrserAlaglyTTPAspglyLeuLeuAlaprolle    | 1733  |
| Dd 301 ATGATCTGCTCTTCCAATATCACCACTTCTGCGGCGCTGGATGGAGTCTGCGCCCTATA       | 360   |
| OY 1734 LeuAsnSer  | 1736  |

DB 361 CTAATAGT 369

|||||||

RESULT 8  
AM046964 392 bp mRNA linear EST 18-SEP-1999  
LOCUS UI-M-BH1-alp-c-08-0-UI-S1 NIH BMAP M.S2 Mus musculus cDNA clone  
DEFINITION UI-M-BH1-alp-c-08-0-UI 3', mRNA sequence.

ACCESSION  
AM046964  
AM046964.1 GI:5907493

VERSION  
EST.

KEYWORDS  
house mouse.

SOURCE  
Mus musculus

ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE  
1 (bases 1 to 392)  
Bonaldi, M.F., Lennon, G. and Soares, M.B.  
Normalization and subtraction: two approaches to facilitate gene  
discovery

AUTHORS  
TITLE

JOURNAL  
MEDLINE  
COMMENT  
Genome Res. 6 (9), 791-806 (1996)  
97044477

Contact: Chin, H  
National Institute of Mental Health  
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD  
20892-9643, USA  
Tel: 301 443 1706  
Fax: 301 443 9890  
Email: mestremail.nih.gov

The sequence contained an oligo-dT track that was present in the  
oligonucleotide that was used to prime the synthesis of first  
strand cDNA and therefore this may represent a bonafide poly A  
tail. The sequence tag present in the cDNA between the NotI site  
and the oligo-dT track served to identify it as a clone from the  
normalized corpus striatum library cDNA library Preparation: M.B.  
Soares lab Clone distribution: NIH BMAP cDNA clones will be made  
available by the means that is soon to be determined. When NIH  
determines the means for distribution of the BMAP cDNA clones, this  
record will be updated accordingly when that means is determined.  
Seq primer: M13 Forward  
PolyA-Tes.

FEATURES  
source  
1..392  
Location/Qualifiers  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UI-M-BH1-alp-c-08-0-UI"  
/clone\_1lb="NIH BMAP M.S2"  
/dev\_stage="27-32 days"  
/lab\_host="DH10B (Life Technologies)"  
/note="vector: pUT73D-Pac (Pharmacia) with a modified  
polylinker; Site\_1: Not I; Site\_2: Eco RI; The  
NIH BMAP M.S2 library is a subtracted library derived from  
NIH BMAP M.S1, which in turn is a subtracted library  
derived from a mixture of normalized libraries from ten  
regions of the mouse brain (cerebellum, brain stems,  
olfactory bulbs, hypothalamus, cortex, amygdala, basal  
ganglia, pineal gland, striatum, hippocampus). The driver  
used for subtraction consisted of a pool of 5,000 clones  
from the NIH BMAP M.S1 library and a pool of 2,000 clones  
obtained from non-normalized and normalized mouse brain  
spinal cord libraries.  
TAG\_1lb=NIH BMAP M.S2  
TAG\_TISSUE=corpus-striatum  
TAG\_SEQ=ACGGC

BASE COUNT 95 a 92 c 93 g 112 t

ORIGIN

Alignment Scores:  
Pred. No.: 4.2e-103 Length: 392  
Score: 106.00 Matches: 119  
Percent Similarity: 99.17% Conservatave: 0  
Best Local Similarity: 99.17% Mismatches: 0  
Query Match: 5.28% Indels: 1

DB: 10 Gaps: 0

US-09-930-871-12 (1-2009) x AM046964 (1-392)

OY 1764 PhepPheValSerTrpIleIleIleSerPheLeuValValAaenMetTrIleAa 1783  
|||||  
DB 7 TTTTTCCTTCCTCCACATCATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 66  
|||||

OY 1784 ValIleLeuGluAaPheSerValAlaTrpGluGluSerAlaGluProLeuSerGluAaP 1803  
|||||  
DB 67 GTCATCTGGAGAACTTACACCTGTCACAGAAAGAAAGTCCAGAGCTTCAGAGAGAC 126  
|||||

OY 1804 AspPheGluMetThrTrpGluValTrpGluValPheAspProAspAlaTrpGluPheMet 1823  
|||||  
DB 127 GACTTTGAGATGTCTTACAGAGGCTGGAGAAATTCACCCCTCAGCCAGCTCATG 186  
|||||

OY 1824 GluPheGluValysLeuSerGluPheAlaAlaAlaLeuGluProProLeuAaenProG 1843  
|||||

DB 187 GAATTTGAAAATTAATTAATCTCACTTTCACCTGCTCTAGAACCCCTCTCAATTTGCCA 246  
|||||

OY 1843 nProAaenLysLeuGluLeuAlaMetAspLeuProMetValSerGlyAspArgIleH 1863  
|||||

DB 247 ACCAAACAAACTTCAGCTCATTCATGCATGCACCTGCGCATGTGAGTGGAGACCGCATCA 306  
|||||

OY 1863 scYsLeuAaPheIleuPheAlaPheThrLysArgValLeuGlyGluSerGlyGluMet 1882  
|||||

DB 307 CTGCTTGACATCCATTTCTTTTACAAAGCGGTGGGTGAGAGATG 364  
|||||

RESULT 9  
AL533359 951 bp mRNA linear EST 13-FEB-2001  
LOCUS AL533359 LTI\_FL015\_Bn1 Homo sapiens cDNA clone CS0DN004YF22 5  
DEFINITION prime, mRNA sequence.

ACCESSION  
AL533359  
AL533359.1 GI:12796852

VERSION  
EST.

KEYWORDS  
SOURCE  
ORGANISM  
human.

REFERENCE  
1 (bases 1 to 951)  
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 Evry cedex - France  
Email: seqrefgenoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES  
source  
1..951  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="CS0DN004YF22"  
/clone\_1lb="LTI\_FL015\_Bn1"  
/sex="male"  
/tissue\_type="Adult brain"  
/note="vector: pCMVSPORT 6; Site\_1: NotI; 1st strand cDNA  
was primed with a NotI-oligo(dT) primer. Five prime end  
enriched, double-stranded cDNA was digested with Not I and  
cloned into the Not I and Eco RV sites of the pCMVSPORT 6  
vector. Library was constructed by life technologies.  
Contact : Feng Liang Life Technologies, a division of  
Invitrogen 9800 Medical Center Drive Rockville, Maryland  
20850, USA Fax : (1) 301 610 8371 Email :  
filiang@lifetech.com URL :  
http://fulllength.invitrogen.com"

BASE COUNT 303 a 189 c 203 g 247 t 9 others

ORIGIN

Alignment Scores:  
Pred. No.: 1.57e-100 Length: 951  
Score: 104.00 Matches: 104  
Percent Similarity: 100.00% Conservatave: 0

Best Local Similarity: 100.00%  
Query Match: 5.18%

Mismatches: 0  
Indels: 0  
Gaps: 0

US-09-930-871-12 (1-2009) x AL533359 (1-951)

QY 1807 MetPheTYrGluValIrrpGluIysPheAspProAspAlaThrGlnPheMetGluPheGlu 1826  
DB 66 ATGTTTATGAGAGTTGGGAGAGTTGATCCGATGCAACTGATTCATGAAATTTGAA 125  
QY 1827 LysLeuSerGlnPheAlaAlaLeuGluProIleuAsnLeuProGlnProAsnLys 1846  
DB 126 AATATATCTCAGTTTCACCTGCGCTTGAAACCCCTCTCAATGTCACACCAACCAAA 185  
QY 1847 LeuGlnLeuIleAlaMetAspLeuProMetValSerGlyAspArgIleHisCysLeuAsp 1866  
DB 186 CTCACACTATGTCATGCAATGATTTGCCCAGTGTAGTGACCGATGCCACTGCTTGAT 245  
QY 1867 IleLeuPheAlaPheThrLysArgValIleuGlyGluSerGlyGluMetAspAlaLeuArg 1886  
DB 246 ATCTATATTCCTTTACAAAGCGGTTCTAGAGAGAGAGAGATGATGCTCTACGA 305  
QY 1887 IleGlnMetGluGluArgPheMetAlaSerAsnProSerLysValSerTyrglnProIle 1906  
DB 306 ATACAGATGCAAGAGCATTCATGCTTCCAAATCCTTCCAGGCTCTATCAGCCAAATC 365  
QY 1907 ThrThrThrLeu 1910  
DB 366 ACTACTACTTTA 377  
RESULT 10  
LOCUS BC029489 1777 bp mRNA linear HTC 16-MAY-2002  
DEFINITION Homo sapiens, clone IMAGE:5278436, mRNA.  
ACCESSION BC029489.1 GI:20809571  
VERSION BC029489.1  
KEYWORDS HTC.  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens.  
REFERENCE 1 (bases 1 to 1777)  
AUTHORS Strausberg, R.  
TITLE Direct Submission  
JOURNAL Submitted (01-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov  
COMMENT Contact: MGC help desk  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
CDNA Library Preparation: Michael J. Brownstein (MHGR) & Shiraki Toshiyuki and Piero Carninci (KIKEN)  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILML)  
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305  
Web site: http://www.shgc.stanford.edu  
Contact: (Dickson, Mark) mcdickpaxil.stanford.edu  
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILML at: http://image.llnl.gov  
Series: IRAX Plate: 48 Row: b Column: 9  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 10337596  
This clone has the following problem: frame shifted.

## FEATURES

location/Qualifiers

1..1777  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5278436"

/tissue\_type="Brain, hypothalamus"  
/clone\_lib="NIH\_MGC\_96"  
/lab\_host="DH10B"  
/note="Vector: pBluescript"

BASE COUNT 526 a 333 c 395 g 523 t

## ALIGNMENT SCORES:

Pred. No.: 3.7e-99 Length: 1777  
Score: 103.00 Matches: 145  
Percent Similarity: 98.64% Conservative: 0  
Best Local Similarity: 98.64% Mismatches: 1  
Query Match: 5.13% Indels: 2  
DB: 11 Gaps: 0

US-09-930-871-12 (1-2009) x BC029489 (1-1777)

QY 132 MetLeuIleMetCysThrIleLeuThrAsnCysValPheMetThrMetSerAsnProPro 151  
DB 644 ATGCTCATTTATGTGACAGATTTCTTACCAACTGTGATTTATGACCATGATACCTTCCA 703  
QY 152 AspTrpThrLysAsnValGluTrpThrPheThrGlyIleTyThrPheGluSerLeuIle 171  
DB 704 GACTGACAAAGCATGTGGAGATATACCTTTACAGCAATTTATACCTTTGAATCATTAT 763  
QY 172 LysIleIle-AlaArgGlyPheCysLeuGluAspPheThrPheLeuArgAspProTrpAs 191  
DB 764 AAAATATCT-TGCAGAGGGGCTTTTGTGTAGAGATTTCAATTTTACGGGATTCATGAA 822  
QY 191 nTrpLeuAspPheThrValIleThrPheAlaTrpValThrGluPheValAspLeuGlyAs 211  
DB 823 TTGGTTGGATTTACAGATTTACTTTTTCATATGTGACAGAGTTGTGGACCTGGGCA 882  
QY 211 nValSerAlaLeuArgTrpPheArgValLeuArgAlaLeuLysTrpIleSerValIlePr 231  
DB 883 TCTCTCAGCGTTGAGAACATTCAGAGTTCTCCAGACATTTGAATAACAATTCAGTATTC 942  
QY 231 nGlyLeuLysThrIleValGlyAlaLeuIleGlnSerValLysLysLeuSerAspValMe 251  
DB 943 AGGCTGGAAGACCATTTGGGGCCCTGATCCAGTCAGCAAGAGAAAGCTTCTGATGTCAT 1002  
QY 251 tIleLeuThrValPheCysLeuSerValPheAlaLeuIleGlyLeuGlnLeuPheMet1 271  
DB 1003 GATCTTGATGTTGTTCTGTCTAAGGCTGTTCGCGCTAATAGATTCAGTTTTCATGG 1062  
QY 271 yAsnLeuArgAsnLysCys 277  
DB 1063 CAACCTACGAAATAATATG 1081  
RESULT 11  
LOCUS BC034643 509 bp mRNA linear HTC 07-AUG-2002  
DEFINITION Mus musculus, similar to sodium channel, voltage-gated, type 1,  
ACCESSION BC034643  
VERSION BC034643.1 GI:21961658  
KEYWORDS HTC.  
SOURCE house mouse.  
ORGANISM Mus musculus.  
REFERENCE 1 (bases 1 to 509)  
AUTHORS Strausberg, R.  
TITLE Direct Submission  
JOURNAL Submitted (24-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov  
COMMENT Contact: MGC help desk  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: The Cepko Laboratory  
CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Baylor College of Medicine Human Genome  
Sequencing Center

Center code: BCM-HGSC  
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)  
Gunnarone, P.H., Garcia, A.M., Lu, X., Huliy, S.W., Hale, S.M.,  
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,  
Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>  
Series: IRAX Plate: 54 Row: 0 Column: 1  
This clone was selected for full length sequencing because it  
passed the following selection criteria: Hexamer frequency ORF  
analysis

This clone has the following problem: frame shifted.

FEATURES  
source  
1. 509  
Location/Qualifiers

/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/clone="IMAGE:5361050"  
/tissue\_type="Eye, retina, mouse strain C57Bl/6"  
/clone\_lib="NIH\_MGC\_94"  
/lab\_host="DH10B"  
/note="Vector: pCMV-SPORE6"  
BASE COUNT 155 a 105 c 128 g 121 t  
ORIGIN

#### Alignment Scores:

Pred. No.: 1.15e-98 Length: 509  
Score: 102.00 Matches: 509  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 5.08% Indels: 0  
DB: 11 Gaps: 0

US-09-930-871-12 (1-2009) x BC034643 (1-509)

OY 346 ProgluGlyTyrMetCysValIysAlaGlyArgAsnProAsnTyrGlyTyrThrSerPhe 365  
DB 26 CCAGAGGATATATGCTGTAAAGCTGTAGAAACCTTAATATGTTACACAACTTT 85  
OY 366 AspThrPheSerTrrAlaPheLeuSerLeuPheArgLeuMetThrGlnsPhePglu 385  
DB 86 GATACCTTCAGTTGGCATTGTCCTGCTTGCATGCTGATGCTGAGACTTCTGGGAA 145  
OY 386 AsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMetIlePhePheValLeu 405  
DB 146 AATCTATACCACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 205  
OY 406 ValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAlaValAlaMetAla 425  
DB 206 GTCATTTCTTGGGCTCATTTACCTGATAACTTGCATCTGCTGCTGCTGCTGCTG 265  
OY 426 TyrGlnGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLysGlnLysGlnLys 445  
DB 266 TATGAGGACCAATTCAGCCACACTGAGAGGAGCTGAAACAGAAAGAGCAGAAATTCAG 325  
OY 446 GlnMet 447  
DB 326 CAGATG 331

#### RESULT 12

LOCUS BC023034 510 bp mRNA linear HTC 07-AUG-2002  
DEFINITION Mus musculus, clone IMAGE:5361055, mRNA.  
ACCESSION BC023034  
VERSION BC023034.1 GI:18606017  
KEYWORDS HTC.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

#### REFERENCE

1 (bases 1 to 510)  
AUTHORS Strusberg, R.  
TITLE Direct Submission  
JOURNAL Submitted (04-FEB-2002) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA

REMARK  
COMMENT NIH-MGC Project URL: <http://mgc.ncl.nih.gov>  
Contact: [cgapbs-rt@mail.nih.gov](mailto:cgapbs-rt@mail.nih.gov)  
Email: [cgapbs-rt@mail.nih.gov](mailto:cgapbs-rt@mail.nih.gov)  
Tissue Procurement: The Cepko Laboratory  
CDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Baylor College of Medicine Human Genome  
Sequencing Center  
Center code: BCM-HGSC  
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)  
Gunnarone, P.H., Garcia, A.M., Lu, X., Huliy, S.W., Hale, S.M.,  
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,  
Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>  
Series: IRAX Plate: 54 Row: 0 Column: 3  
This clone was selected for full length sequencing because it  
passed the following selection criteria: Hexamer frequency ORF  
analysis

This clone has the following problem: frame shifted.

FEATURES  
source  
1. 510  
Location/Qualifiers

/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/clone="IMAGE:5361055"  
/tissue\_type="Eye, retina, mouse strain C57Bl/6"  
/clone\_lib="NIH\_MGC\_94"  
/lab\_host="DH10B"  
/note="Vector: pCMV-SPORE6"  
BASE COUNT 156 a 105 c 128 g 121 t  
ORIGIN

#### Alignment Scores:

Pred. No.: 1.15e-98 Length: 510  
Score: 102.00 Matches: 510  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 5.08% Indels: 0  
DB: 11 Gaps: 0

US-09-930-871-12 (1-2009) x BC023034 (1-510)

OY 346 ProgluGlyTyrMetCysValIysAlaGlyArgAsnProAsnTyrGlyTyrThrSerPhe 365  
DB 26 CCAGAGGATATATGCTGTAAAGCTGTAGAAACCTTAATATGTTACACAACTTT 85  
OY 366 AspThrPheSerTrrAlaPheLeuSerLeuPheArgLeuMetThrGlnsPhePglu 385  
DB 86 GATACCTTCAGTTGGCATTGTCCTGCTTGCATGCTGATGCTGAGACTTCTGGGAA 145  
OY 386 AsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMetIlePhePheValLeu 405  
DB 146 AATCTATACCACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 205  
OY 406 ValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAlaValAlaMetAla 425  
DB 206 GTCATTTCTTGGGCTCATTTACCTGATAACTTGCATCTGCTGCTGCTGCTGCTG 265  
OY 426 TyrGlnGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLysGlnLysGlnLys 445  
DB 266 TATGAGGACCAATTCAGCCACACTGAGAGGAGCTGAAACAGAAAGAGCAGAAATTCAG 325  
OY 446 GlnMet 447

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Db      326 CAGATG 331
|||||
RESULT 13
LOCUS   A0067361
DEFINITION A0067361 Sugano mouse brain mncb Mus musculus cDNA clone MNCB-3353
5', mRNA sequence.
ACCESSION A0067361
VERSION   A0067361.1 GI:4968098
KEYWORDS EST.
SOURCE   house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 577)
Hashimoto,K., Kusuda,J., Tanuma,R., Ito,A., Hirata,M., Toyoda,A.,
Suzuki,Y., Sasaki,M. and Sugano,S.
Isolation of full-length cDNA clones from a mouse brain cDNA
library made by oligo-capping method
Unpublished (1999)
JOURNAL Contact: Katsuyuki Hashimoto
Division of Genetic Resources
National Institute of Infectious Diseases
23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
Email: khashi@nih.go.jp
URL: http://www.nih.go.jp/yoiken/genbank/.
FEATURES
Source
1. 577
/organism="Mus musculus"
/strain="C57BL"
/db_xref="taxon:10090"
/clone_1lb="MNCB-3353"
/sex="female"
/dev_stage="adult"
/lab_host="TOP10"
/note="Organ: brain; Vector: pME18S-FL3; 1st strand cDNA
was primed with an oligo(dT) primer
ATGTGGCTTTTCTTTTCTTTTCTTTT; double-stranded cDNA was
ligated to a DraIII adaptor (TGTGGCTACTG), digested and
cloned into distinct DraIII sites of the pME18S-FL3. XhoI
sites just outside the DraIII sites can be used to isolate
the cDNA insert. Size selection was performed by Sugano et
al. (University of Tokyo, Institute of Medical Science).
Custom primer used for sequencing: 5' end primer
[CTGTGCTCTATAAGCTGCG], 3' end primer
[CGACTCGAGCTCGACACA]"
BASE COUNT 178 a 118 c 130 g 148 t 3 others
ORIGIN
Alignment Scores:
Pred. No.: 2.7e-94 Length: 577
Score: 98.00 Matches: 98
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.88% Indels: 0
Gaps: 0
DB: 9
US-09-930-871-12 (1-2009) x A0067361 (1-577)
OY 1 MetGluGlnThrValIleuValProProGlyProAspSerPheAsnPhenPheThrArgGlu 20
|||||
Db 191 ATGGAGCAACAGTCTGTGACACAGGACGTGACAGCTTCAACTTCCACAGAGAA 250
OY 21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
|||||
Db 251 TCCTTGACACTATGTGAAGGCGCAATGCAAGAGAGAGAGAACTAATCCCAAGCCAGAC 310
OY 41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuAlaGlyLysAsn 60
|||||
Db 311 AAAAAAGATGATGATGAAAAATGGCCCAAAACCAAGCAAGTGTGAAGCTGGAGAGAAC 370
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```

OY 61 LeuProPheIleTyrgIyAspIleProProGluMetAlaSerGluProLeuGluAspLeu 80
|||||
Db 371 CTTCCATTATTCATATGAGACATTCCTCCACAGATGGTGTGGAGCCCTGTGAGAGACTG 430
OY 81 AspProTyrrTyrlleAsnLysLysThrPheIleValIleuAsnLysGlyLysAla 98
|||||
Db 431 GACCCCTCATATCATATAGAGACCTTTATGATATTGATATTAAGGAGAGCA 484
|||||
RESULT 14
LOCUS   BF563427/c
DEFINITION BF563427 495 bp mRNA linear EST 12-DEC-2000
UI-R-BT1-akh-f-12-0-UI-R1 UI-R-BT1 Rattus norvegicus cDNA clone
BF563427
UI-R-BT1-akh-f-12-0-UI 5', mRNA sequence.
ACCESSION BF563427
VERSION   BF563427.1 GI:11673157
KEYWORDS EST.
SOURCE   Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 495)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL 97044477
MEDLINE Contact: Soares, MB
PROGRAM for Rat Gene Discovery and Mapping
UNIVERSITY of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone Distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at
LBNL (info@lmage.llnl.gov). IMAGE ID=1799538 The following
repetitive elements were found in this cDNA sequence: 31-100, >(CAG
)n(Simple,repeat
Seq primer: M13 Forward.
FEATURES
Source
1. 495
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone_1lb="UI-R-BT1-akh-f-12-0-UI"
/clone_1lb="UI-R-BT1"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7/3D-Pac (Pharmacia) with a modified
polylinker; Site.1: Not I; Site.2: Eco RI; The library
UI-R-BT1 is a subtracted library derived from a mixture of
the following tissues: hippocampus, thalamus, mid-brain,
medulla, corpus striatum, cerebral cortex and testis. For
a detailed description of the library from which this
clone was derived, please visit our web site at
rtest.eng.uiowa.edu. The subtraction has been previously
described in (Bonaldo, Lennon and Soares, Genome Research
6:791-806, 1996)."
BASE COUNT 120 a 135 c 110 g 130 t
ORIGIN
Alignment Scores:
Pred. No.: 2.74e-93 Length: 495
Score: 97.00 Matches: 97
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.83% Indels: 0
Gaps: 12
DB: 12
US-09-930-871-12 (1-2009) x BF563427 (1-495)

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|            |            |  |                 |
|------------|------------|--|-----------------|
| QY         | 351        | Cysallysalaaglyatargasnprcasnpyrcltytrthsrphesapthphesertrp      | 370             |
| QY         | 371        | AlapheusSerLeuPhaArgLeuMethrhcInaspheTrpGluAsnLeuTyrGlnLeu       | 390             |
| Db         | 382        | TGTGTGAAGGCTGGGAGAAACCCAACTACAGGCTACACAAATTTTGACACCTTACGCTGG     | 323             |
| QY         | 322        | GCCTTCCTTGCTTATTTCCGTCATGACGTCAAGACTTCGGGAAAACCTTTATTCAGCTG      | 263             |
| QY         | 391        | ThrLeuArgAlaIaaglyLysTrhTyrMetIlePhePheValIleValIlePheLeuGly     | 410             |
| Db         | 262        | ACCTTGCGCTGCTGCCGGGAAAACATACATGATATTTTTTTCGTCGTCATTTCTTGAGC      | 203             |
| QY         | 411        | SerPheTyrLeuIleasnLeuIleleuAlaValIleAlaMetAlaTyrGlnGlnInsn       | 430             |
| Db         | 202        | TCATTCACCTGATTAATTAATTAATTCCTGCTGCTGTGGTGGCAAGGCTTACAGGACACGAAAC | 143             |
| QY         | 431        | GlnAlaThrLeuGluGluAlaGluGlnLysGlnIleValIaGluPheGlnInmet          | 447             |
| Db         | 142        | CAGGCCACACGTGAGAGAGGCTGACACAGAAAGGACGAGGTTTCAGCAGATG             | 92              |
| RESULT 15  |            |  |                 |
| AU066802   |            |  |                 |
| LOCUS      |            |  |                 |
| DEFINITION | AU066802   | 800 bp   | MRNA            |
| VERSION    | AU066802   |  | linear          |
| KEYWORDS   | AU066802.1 | GI:4967539   | EST 12-JUL-2000 |
| SOURCE     |            |  |                 |
| ORGANISM   |            |  |                 |
| REFERENCE  |            |  |                 |
| AUTHORS    |            |  |                 |
| TITLE      |            |  |                 |
| JOURNAL    |            |  |                 |
| COMMENT    |            |  |                 |
| FEATURES   |            |  |                 |
| Source     |            |  |                 |

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Best Similarity: 100.00%
Percent Similarity: 100.00%
Best local Similarity: 100.00%
Query Match: 4.53%
DB: 9
gaps: 0
Conservative: 0
Mismatch: 0
Indels: 0
gaps: 0

US-09-930-871-12 (1-2009) x AU066802 (1-800)

QY 1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhenethrArgIleu 20
Db 189 ATGGGCAAAAGAGCTGTGTACCAACAGGACCTCAGCTTCACTTCCACAGGAA 248
QY 21 SerLeuAlaAlaIleGluArgPheIleIaGluGluLysAlaIysAsnProLysProAsp 40
Db 249 TCCCTTGAGCTATTGGAAGGCGCATTTGCACAAAGAAAGGCTTAAGAAATCCCAAGCCAGAC 308
QY 41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
Db 309 AAAAAAGATGATGATGAAATAATGGGCCCAAGCCAAACGATGACTTGGAGAGCTGGGAATAAC 368
QY 61 LeuProPheIleArgGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
Db 369 CTTCATATTATCTATGGAGACATCTCCACAAAGATGGTGTGGAGGCTCTGGAGAGACCTG 428
QY 81 AspProTyrrTyrrIleAsnLysLysThrPheIle 91
Db 429 GACCCCTACTATATCAAAATAAACAACCTTTTATA 461

Search completed: April 23, 2003, 08:09:47
Job time : 3717 secs

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GenCore version 5.1.4 p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 23, 2003, 04:55:12 ; Search time 98 Seconds  
(without alignments)  
6286.874 Million cell updates/sec

Title: US-09-930-871-12

Perfect score: 2009

Sequence: 1 MEQRTLVPPGDSFNFTRRE.....TKPIYKHEGSKDEKAKGK 2009

Scoring table:

OLIGO  
Xgapop 60.0, Xgapext 60.0  
Ygapop 60.0, Ygapext 60.0  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 441362 seqs, 153338381 residues

Word size: 1

Total number of hits satisfying chosen parameters: 878600

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL-frame+g2n.model -DEV-xlh  
-O-/cgn2\_1/USPTO.spool/US09930871/runat\_16042003\_114926\_9013/app\_query.fasta\_1.2183  
-DB-issued.patents.NA -QEMT-fastlap -SUFFIX-oligop2n.rni -MINMATCH-0.1  
-LOOCL-0 -LOOEXT-0 -UNITS-bits -START-1 -END-1 -MATRIX-oligo  
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR SCORE-quality -THR\_MIN-1  
-ALIGN-15 -MODE-LOCAL -OUTFMT-PRO -NORM-ext -HEAPSIZE-500 -MINLEN-0  
-MAXLEN-2000000000 -USER-US09930871.ecgn\_1\_1\_55\_etrunat\_16042003\_114926\_9013  
-NCP-6 -ICPU-3 -NO\_XLPHY -NO\_MAP -LARGEQUERY -NEG\_SCORES-0 -WAIT -LONGLOG  
-DEV.TIMEOUT-120 -WARN\_TIMEOUT-30 -THREADS-1 -XGAPOP-60 -XGAPEXT-60 -FGAPOP-6  
-FGAPEXT-7 -YGAPOP-60 -YGAPEXT-60 -DELOP-6 -DELEXT-7

Database :

Issued Patents.NA:\*  
1: /cgn2\_6/ptodata/1/ina/5A.COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq:\*  
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4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PCBUS.COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description       |
|------------|-------|-------------|--------|-------|-------------------|
| 1          | 77    | 3.8         | 5977   | 3     | US-09-024-020B-1  |
| 2          | 77    | 3.8         | 5977   | 4     | US-09-425-043-1   |
| 3          | 77    | 3.8         | 6007   | 4     | US-09-024-020B-2  |
| 4          | 77    | 3.8         | 6007   | 4     | US-09-425-043-2   |
| 5          | 77    | 3.8         | 6556   | 4     | US-09-024-020B-7  |
| 6          | 77    | 3.8         | 6556   | 4     | US-09-425-043-7   |
| 7          | 77    | 3.8         | 6586   | 4     | US-09-024-020B-43 |
| 8          | 77    | 3.8         | 6586   | 4     | US-09-425-043-43  |
| 9          | 72    | 3.6         | 930    | 3     | US-08-605-284B-1  |
| 10         | 72    | 3.6         | 930    | 3     | US-08-605-284B-2  |
| 11         | 72    | 3.6         | 930    | 3     | US-08-605-284B-21 |
| 12         | 72    | 3.6         | 3033   | 3     | US-08-836-325-1   |

|    |    |     |      |   |                   |
|----|----|-----|------|---|-------------------|
| 13 | 72 | 3.6 | 6452 | 3 | US-08-836-325-9   |
| 14 | 69 | 3.4 | 6826 | 3 | US-09-024-020B-8  |
| 15 | 69 | 3.4 | 6826 | 4 | US-09-425-043-8   |
| 16 | 66 | 3.3 | 6371 | 3 | US-08-836-325-13  |
| 17 | 66 | 3.3 | 6404 | 3 | US-08-836-325-14  |
| 18 | 47 | 2.3 | 930  | 3 | US-08-605-284B-3  |
| 19 | 37 | 1.8 | 696  | 3 | US-09-024-020B-5  |
| 20 | 37 | 1.8 | 696  | 4 | US-09-425-043-5   |
| 21 | 36 | 1.8 | 6048 | 4 | US-09-634-920-3   |
| 22 | 33 | 1.6 | 2573 | 4 | US-08-669-656A-3  |
| 23 | 33 | 1.6 | 5874 | 4 | US-08-843-417-9   |
| 24 | 33 | 1.6 | 6344 | 4 | US-08-843-417-1   |
| 25 | 33 | 1.6 | 6524 | 4 | US-08-669-656A-1  |
| 26 | 33 | 1.6 | 6527 | 4 | US-08-669-656A-7  |
| 27 | 33 | 1.6 | 7052 | 4 | US-08-669-656A-5  |
| 28 | 32 | 1.6 | 702  | 4 | US-08-843-417-3   |
| 29 | 24 | 1.2 | 5461 | 3 | US-07-998-289B-7  |
| 30 | 24 | 1.2 | 6315 | 2 | US-08-808-793-2   |
| 31 | 24 | 1.2 | 6315 | 3 | US-08-808-793-7   |
| 32 | 24 | 1.2 | 6315 | 2 | US-08-772-512A-2  |
| 33 | 24 | 1.2 | 6318 | 3 | US-08-808-793-1   |
| 34 | 24 | 1.2 | 6318 | 3 | US-08-772-512A-1  |
| 35 | 24 | 1.2 | 6513 | 1 | US-08-337-339-7   |
| 36 | 24 | 1.2 | 6513 | 1 | US-08-724-095-7   |
| 37 | 24 | 1.2 | 6513 | 5 | PCT-US95-14262-7  |
| 38 | 24 | 1.2 | 6513 | 5 | PCT-US95-14378-7  |
| 39 | 24 | 1.2 | 6519 | 2 | US-08-808-793-24  |
| 40 | 22 | 1.1 | 1237 | 2 | US-08-808-793-26  |
| 41 | 22 | 1.1 | 2279 | 3 | US-07-998-289B-3  |
| 42 | 13 | 0.6 | 568  | 3 | US-07-998-289B-10 |
| 43 | 11 | 0.5 | 2416 | 3 | US-07-998-289B-1  |
| 44 | 9  | 0.4 | 29   | 1 | US-08-401-512-58  |
| 45 | 9  | 0.4 | 987  | 6 | 5240847-19        |

#### ALIGNMENTS

Sequence 9, Appl  
Sequence 8, Appl  
Sequence 13, Appl  
Sequence 14, Appl  
Sequence 5, Appl  
Sequence 5, Appl  
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Sequence 5, Appl  
Sequence 3, Appl  
Sequence 7, Appl  
Sequence 2, Appl  
Sequence 1, Appl  
Sequence 1, Appl  
Sequence 26, Appl  
Sequence 3, Appl  
Sequence 10, Appl  
Sequence 1, Appl  
Sequence 58, Appl  
Patent No. 5240847

RESULT 1  
US-09-024-020B-1  
; Sequence 1, Application US/09024020B  
; Patent No. 6030810  
; GENERAL INFORMATION:  
; APPLICANT: DELGADO, STEPHEN G.  
; APPLICANT: DIETRICH, PAUL S.  
; APPLICANT: FISH, LINDA M.  
; APPLICANT: HERMAN, RONALD C.  
; APPLICANT: SANGAMESWARAN, LAKSHMI  
; TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: JANET PAULINE CLARK  
; STREET: 3401 HILLVIEW AVENUE, MS A2-250  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: U.S.A.  
; ZIP: 94304-1397  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/024,020B  
; FILING DATE: 16-FEB-1998  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/039,447  
; FILING DATE: 26-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CLARK, JANET P.  
; REGISTRATION NUMBER: 34,799  
; REFERENCE/DOCKET NUMBER: R0020B-REG

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 852-3097  
TELEFAX: (650) 855-5322  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5977 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-024-0208-1

## Alignment Scores:

| Pred. No.:             | 2,78e-63 | Length:       | 5977 |
|------------------------|----------|---------------|------|
| Score:                 | 77.00    | Matches:      | 77   |
| Percent Similarity:    | 100.00%  | Conservative: | 0    |
| Best Local Similarity: | 100.00%  | Mismatches:   | 0    |
| Query Match:           | 3.83%    | Indels:       | 0    |
| DB:                    | 3        | Gaps:         | 0    |

US-09-930-871-12 (1-2009) x US-09-024-0208-1 (1-5977)

OY 201 AlAtyYValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220  
|||||  
Db 634 GCATATGTGACAGAGTTGTGGACCTGGGCAATGCTCAGCGCTGAGAACATTCAGGTT 693  
OY 221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240  
|||||  
Db 694 CTCGAGCTTGAAGAACTATCTGTATATCCAGGCTGGAAGACATCGTGGCGCCCTTA 753  
OY 241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260  
|||||  
Db 754 ATCCAGTCCGGAAGAACCTCTCGACGTGATGATCCGACAGAGTGTTCGCTGAGTGT 813  
OY 261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCys 277  
|||||  
Db 814 TTCGCCCTGATGGCTGCACCTCTTCATGGGGAACCTTCGAAACAAGTGT 864

## RESULT 2

US-09-425-043-1

Sequence 1, Application US/09425043

Patent No. 6335172

## GENERAL INFORMATION:

APPLICANT: DELGADO, STEPHEN G.  
APPLICANT: DIETRICH, PAUL S.  
APPLICANT: FISH, LINDA M.  
APPLICANT: HERRAN, RONALD C.  
APPLICANT: SANGAMESWARAN, LAKSHMI  
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE  
TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICED VARIANT THEREOF  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: JANET PAULINE CLARK  
STREET: 3401 HILLVIEW AVENUE, MS A2-250  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94304-1397  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/425,043  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/024,020  
FILING DATE: 16-FEB-1998  
APPLICATION NUMBER: US 60/039,447  
FILING DATE: 26-FEB-1997  
ATTORNEY/AGENT INFORMATION:

NAME: CLARK, JANET P.

REGISTRATION NUMBER: 34,799

REFERENCE/DOCKET NUMBER: R0020B-REG

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 852-3097  
TELEFAX: (650) 855-5322  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5977 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-425-043-1

## Alignment Scores:

| Pred. No.:             | 2,78e-63 | Length:       | 5977 |
|------------------------|----------|---------------|------|
| Score:                 | 77.00    | Matches:      | 77   |
| Percent Similarity:    | 100.00%  | Conservative: | 0    |
| Best Local Similarity: | 100.00%  | Mismatches:   | 0    |
| Query Match:           | 3.83%    | Indels:       | 0    |
| DB:                    | 4        | Gaps:         | 0    |

US-09-930-871-12 (1-2009) x US-09-425-043-1 (1-5977)

OY 201 AlAtyYValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220  
|||||  
Db 634 GCATATGTGACAGAGTTGTGGACCTGGGCAATGCTCAGCGCTGAGAACATTCAGGTT 693  
OY 221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240  
|||||  
Db 694 CTCGAGCTTGAAGAACTATCTGTATATCCAGGCTGGAAGACATCGTGGCGCCCTTA 753  
OY 241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260  
|||||  
Db 754 ATCCAGTCCGGAAGAACCTCTCGACGTGATGATCCGACAGAGTGTTCGCTGAGTGT 813  
OY 261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCys 277  
|||||  
Db 814 TTCGCCCTGATGGCTGCACCTCTTCATGGGGAACCTTCGAAACAAGTGT 864

## RESULT 3

US-09-024-0208-2

Sequence 2, Application US/090240208

Patent No. 6030810

## GENERAL INFORMATION:

APPLICANT: DELGADO, STEPHEN G.  
APPLICANT: DIETRICH, PAUL S.  
APPLICANT: FISH, LINDA M.  
APPLICANT: HERRAN, RONALD C.  
APPLICANT: SANGAMESWARAN, LAKSHMI  
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE  
TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICED VARIANT THEREOF  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: JANET PAULINE CLARK  
STREET: 3401 HILLVIEW AVENUE, MS A2-250  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94304-1397  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/024,020B  
FILING DATE: 16-FEB-1998  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/039,447  
FILING DATE: 26-FEB-1997



CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/039,447  
FILING DATE: 26-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: CLARK, JANET P.  
REGISTRATION NUMBER: 34,799  
REFERENCE/DOCKET NUMBER: R0020B-REG  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 852-3097  
TELEFAX: (650) 855-5322  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6556 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-024-020B-7

Alignment Scores:  
Pred. No.: 3,04e-63 Length: 6556  
Score: 77.00 Matches: 77  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.83% Indels: 0  
DB: 3 Gaps: 0

US-09-930-871-12 (1-2009) x US-09-024-020B-7 (1-6556)

QY 201 AATATGATGCTGACAGAGTTGGACCTGGCAATGCTCAGCGCTGGAACATTCAGGCTT 220  
DB 781 GCATATGTCAGACAGTTGGACCTGGCAATGCTCAGCGCTGGAACATTCAGGCTT 840  
QY 221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240  
DB 841 CTCGAGCTTTGAAACATATCTCTGTAATTCAGGCTGGAACATTCGCGGCGCCCTA 900  
QY 241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260  
DB 901 ATCCAGTCCGTGAAGAGCTGTCGAGCGTATGATCTCGACAGTGTCTGCGCTGAGTGT 960  
QY 261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCys 277  
DB 961 TTCGCCCTGATGTGCGCTGCAAGCTCTTCATGCGGGAACCTTGGAACAAGTGT 1011

RESULT 6  
US-09-425-043-7  
Sequence 7, Application US/09425043  
Patent No. 6335172

GENERAL INFORMATION:  
APPLICANT: DELGADO, STEPHEN G.  
APPLICANT: DIETRICH, PAUL S.  
APPLICANT: FISH, LINDA M.  
APPLICANT: HERMAN, RONALD C.  
APPLICANT: SANGAMESWARAN, LAKSHMI  
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: JANET PAULINE CLARK  
STREET: 3401 HILLVIEW AVENUE, MS A2-250  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94304-1397  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/425,043

FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/024,020  
FILING DATE: 16-FEB-1998  
APPLICATION NUMBER: US 60/039,447  
FILING DATE: 26-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: CLARK, JANET P.  
REGISTRATION NUMBER: 34,799  
REFERENCE/DOCKET NUMBER: R0020B-REG  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 852-3097  
TELEFAX: (650) 855-5322  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6556 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-425-043-7

Alignment Scores:  
Pred. No.: 3,04e-63 Length: 6556  
Score: 77.00 Matches: 77  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.83% Indels: 0  
DB: 4 Gaps: 0

US-09-930-871-12 (1-2009) x US-09-425-043-7 (1-6556)

QY 201 AATATGATGCTGACAGAGTTGGACCTGGCAATGCTCAGCGCTGGAACATTCAGGCTT 220  
DB 781 GCATATGTCAGACAGTTGGACCTGGCAATGCTCAGCGCTGGAACATTCAGGCTT 840  
QY 221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240  
DB 841 CTCGAGCTTTGAAACATATCTCTGTAATTCAGGCTGGAACATTCGCGGCGCCCTA 900  
QY 241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260  
DB 901 ATCCAGTCCGTGAAGAGCTGTCGAGCGTATGATCTCGACAGTGTCTGCGCTGAGTGT 960  
QY 261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCys 277  
DB 961 TTCGCCCTGATGTGCGCTGCAAGCTCTTCATGCGGGAACCTTGGAACAAGTGT 1011

RESULT 7  
US-09-024-020B-43

Sequence 43, Application US/09024020B  
Patent No. 6030810  
GENERAL INFORMATION:  
APPLICANT: DELGADO, STEPHEN G.  
APPLICANT: DIETRICH, PAUL S.  
APPLICANT: FISH, LINDA M.  
APPLICANT: HERMAN, RONALD C.  
APPLICANT: SANGAMESWARAN, LAKSHMI  
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: JANET PAULINE CLARK  
STREET: 3401 HILLVIEW AVENUE, MS A2-250  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94304-1397  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/024,020B  
FILING DATE: 16-FEB-1998  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/039,447  
FILING DATE: 26-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: CLARK, JANET P.  
REGISTRATION NUMBER: 34,799  
REFERENCE/DOCKET NUMBER: R0020B-REG  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 852-3097  
TELEFAX: (650) 855-5322  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6586 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-024-020B-43

Alignment Scores:  
Pred. No.: 3,06e-63 Length: 6586  
Score: 77.00 Matches: 77  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.83% Indels: 0  
DB: 3 Gaps: 0

US-09-930-871-12 (1-2009) x US-09-024-020B-43 (1-6586)

QY 201 AlaTyrValThrcIuPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220  
DB 781 GCATATGTGACAGAGTTTGTGGACCTGGCAATGTCTCAGCGCTGAGAACATTGAGGGTT 840

QY 221 LeuArgAlaLeuysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240  
DB 841 CTCGCGCTTGAAGAACTATCTCTGTAATTCAGCGCTGAGAACAAATCGTGGCGCCCTA 900

QY 241 IleGlnSerValIysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260  
DB 901 ATCCAGTCCGTGAAGAGCTGTGCGACGTGATGATCTCTGACAGTGTCTGCTGAGTGT 960

QY 261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCys 277  
DB 961 TTCGCCCTGATGGCTGCGAGCTCTTCATGCGGGAACCTTCGAAACAAGTGT 1011

RESULT 8  
US-09-425-043-43  
Sequence 43, Application US/09425043  
GENERAL INFORMATION:  
PATENT No. 6335172  
APPLICANT: DELGADO, STEPHEN G.  
APPLICANT: DIETRICH, PAUL S.  
APPLICANT: FISH, LINDA M.  
APPLICANT: HERMAN, RONALD C.  
APPLICANT: SANGAMESWARAN, LAKSHMI  
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE  
TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICED VARIANT THEREOF  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: JANET PAULINE CLARK  
STREET: 3401 HILLVIEW AVENUE, MS A2-250  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94304-1397  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/425,043  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/024,020  
FILING DATE: 16-FEB-1998  
APPLICATION NUMBER: US 60/039,447  
FILING DATE: 26-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: CLARK, JANET P.  
REGISTRATION NUMBER: 34,799  
REFERENCE/DOCKET NUMBER: R0020B-REG  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 852-3097  
TELEFAX: (650) 855-5322  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6586 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-425-043-43

Alignment Scores:  
Pred. No.: 3,06e-63 Length: 6586  
Score: 77.00 Matches: 77  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.83% Indels: 0  
DB: 4 Gaps: 0

US-09-930-871-12 (1-2009) x US-09-425-043-43 (1-6586)

QY 201 AlaTyrValThrcIuPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220  
DB 781 GCATATGTGACAGAGTTTGTGGACCTGGCAATGTCTCAGCGCTGAGAACATTGAGGGTT 840

QY 221 LeuArgAlaLeuysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240  
DB 841 CTCGCGCTTGAAGAACTATCTCTGTAATTCAGCGCTGAGAACAAATCGTGGCGCCCTA 900

QY 241 IleGlnSerValIysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260  
DB 901 ATCCAGTCCGTGAAGAGCTGTGCGACGTGATGATCTCTGACAGTGTCTGCTGAGTGT 960

QY 261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCys 277  
DB 961 TTCGCCCTGATGGCTGCGAGCTCTTCATGCGGGAACCTTCGAAACAAGTGT 1011

RESULT 9  
US-08-605-284B-1  
Sequence 1, Application US/08605284B  
GENERAL INFORMATION:  
PATENT No. 6060271  
APPLICANT: WALEWSKI, JOSE L.  
APPLICANT: RECIO-PINTO, ESPERANZA  
TITLE OF INVENTION: VOLTAGE GATED SODIUM CHANNELS FROM  
TITLE OF INVENTION: HUMAN PERIPHERAL NERVE  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP  
STREET: CLINTON SQUARE, P.O. BOX 1051  
CITY: ROCHESTER  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 14603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/605,284B  
FILING DATE: 09-FEB-1996  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: BRAMAN, SUSAN J.  
REGISTRATION NUMBER: 34,103  
REFERENCE/DOCKET NUMBER: 19603/800 (CRF D-1705)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 716-263-1636  
TELEFAX: 716-263-1600  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 930 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-605-284B-1

Alignment Scores:  
Pred. No.: 2,71e-59  
Score: 72.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 3.58%  
Matches: 930  
Conservative: 72  
Mismatches: 0  
Indels: 0  
Gaps: 0

US-09-930-871-12 (1-2009) x US-08-605-284B-1 (1-930)

QY 1625 IIGLILYSTRYPHEVALSERPROTHLEUPHARYALLIARGLAIAARGLILEGLY 1644  
DB 436 ATGAGAAAGATATTTGGTCCCTACCTTGTCCGAGTACCTCTTGCAGATTGCC 495  
QY 1645 ATGILEUARGLEUILLEYSGLYALALYSGLYILEARPHLEULEUPHEALALEUMET 1664  
DB 496 CGATCTAGCTGATGACCAAGAGCAAGGAGATCCGACGCTGCTTGTTCATG 555  
QY 1665 METSERLEUPROALALEUPHEANILLEGYLEULEUPHEULEVALMETPHEILETYR 1664  
DB 556 ATGCCCCCTCTGCTGCTTTACATCGCGCTCTGCTCTCCGTCATGTTATCTAT 615  
QY 1685 ALAILEPHEGLMETSERANPHEALATYRVALYS 1696  
DB 616 GCCATCTTGGATGTCACACTTGCCTATGTAATAA 651

RESULT 10  
US-08-605-284B-2  
Sequence 2, Application US/08605284B.  
Patent No. 6060271  
GENERAL INFORMATION:  
APPLICANT: WALEMSKI, JOSE L.  
APPLICANT: RECIO-PINTO, ESPERANZA  
TITLE OF INVENTION: VOLTAGE GATED SODIUM CHANNELS FROM  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP  
STREET: CLINTON SQUARE, P.O. BOX 1051  
CITY: ROCHESTER  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 14603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/605,284B  
FILING DATE: 09-FEB-1996

CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: BRAMAN, SUSAN J.  
REGISTRATION NUMBER: 34,103  
REFERENCE/DOCKET NUMBER: 19603/800 (CRF D-1705)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 716-263-1636  
TELEFAX: 716-263-1600  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 930 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-605-284B-2

Alignment Scores:  
Pred. No.: 2,71e-59  
Score: 72.00  
Percent Similarity: 98.08%  
Best Local Similarity: 98.08%  
Query Match: 3.58%  
Matches: 930  
Conservative: 102  
Mismatches: 1  
Indels: 2  
Gaps: 0

US-09-930-871-12 (1-2009) x US-08-605-284B-2 (1-930)

QY 1594 SERLEUARGHLSYTRYRPHRILILEGLYTRPANSILPHEASPPHEVALVALILE 1613  
DB 343 TCCCTCAGACACTACTACTACTACTATAGCGCTGACATCTTGTGCTGCTAT 402  
QY 1614 LEUSERILEVALIGLYMETPHELEUALAGULEU-ILIGLILYSTYRPHYVALSERPROTH 1633  
DB 403 CTCACATGTCAGTATGTTCTGCTGAGAT-GATGAGAAAGATATTTGTCCTCTAC 461  
QY 1633 RLEUPHARVALIILEARGLEUALARGILEGLYARGLILEUARGLEUILLEYSGLYAL 1653  
DB 462 CTCTTCCGAGTATCCGCTCTGCGCAGATTGCCGAACTCTACGTGATCAAGAGAC 521  
QY 1653 ALYSGLYILEARGTHLEULEUPHEALALEUMETSERLEUPROALALEUPHEANIL 1673  
DB 522 AAAGGGGATCCGACGCTGCTTTCCTTGATGATGCTCCCTGCTGTTTACAT 581  
QY 1673 EGYLEULEUPHEULEVALMETPHEILETYRALAILEPHEGLYMETSERANPHEAL 1693  
DB 582 CGGCTCTCTCTCTCTGCTGATGTTATGATGATGATGATGATGATGATGATGAT 641  
QY 1693 ATYRVALYS 1696  
DB 642 CTATGTTAA 651

RESULT 11  
US-08-605-284B-21  
Sequence 21, Application US/08605284B  
Patent No. 6060271  
GENERAL INFORMATION:  
APPLICANT: WALEMSKI, JOSE L.  
APPLICANT: RECIO-PINTO, ESPERANZA  
TITLE OF INVENTION: VOLTAGE GATED SODIUM CHANNELS FROM  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP  
STREET: CLINTON SQUARE, P.O. BOX 1051  
CITY: ROCHESTER  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 14603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30



CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/605,284B  
FILING DATE: 09-FEB-1996  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: BRAMAN, SUSAN J.  
REGISTRATION NUMBER: 34,103  
REFERENCE/DOCKET NUMBER: 19603/800 (CRF D-1705)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 716-263-1636  
TELEFAX: 716-263-1600  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 930 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-605-284B-21

Alignment Scores:  
Pred. No.: 2,71e-59 Length: 930  
Score: 72.00 Matches: 102  
Percent Similarity: 98.08% Conservative: 0  
Best Local Similarity: 98.08% Mismatches: 1  
Query Match: 3.58% Indels: 2  
DB: 3 Gaps: 0

US-09-930-871-12 (1-2009) x US-08-605-284B-21 (1-930)

QY 1594 SerLeuArgHisTyrPheThrIleGlyTyrPheValIlePheAspPheValValIle 1613  
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DB 343 TCCCTAGACACTACTACTACTACTAGGCTGGAACATCTTGACCTTGCGGCGATT 402  
|||||  
QY 1614 LeuSerIleValIleGlyMetPheLeuAlaGluLeu-IleGlyLysTyrPheValSerProth 1633  
|||||  
DB 403 CTCTCATGTTGAGTATGTTCTGCGCTGAGAT-GATAGAAAGTATTGTTGCTCCCTAC 461  
|||||  
QY 1633 rleuPheArgValIleArgLeuAlaArgIleGlyArgIleLeuArgLeuIleGlyAl 1653  
|||||  
DB 462 CTGTGTCAGAGTATCCGCTTGGCAGATGGCCGAATCTAGCTGATCAAGAGAGC 521  
|||||  
QY 1653 alysgIleArgThrLeuLeuPheAlaLeuMetSerLeuProAlaLeuPheAsnI 1673  
|||||  
DB 522 AAAGGGAGATCCGACGCTGCTCTTGTGATGATGTCCTTCGCTGCTGTTTAACT 561  
|||||  
QY 1673 eGlyLeuLeuLeuPheLeuValMetPheIleTyrAlaIlePheGlyMetSerAsnPheAl 1693  
|||||  
DB 582 CGGCTCTGCTCTCTCTGTCATGTTTATCATGCCATCTTGGGATGCCAACTTGC 641  
|||||  
QY 1693 aTyrrValLys 1696  
|||||  
DB 642 CTATGTTTAA 651  
|||||

RESULT 12  
US-08-836-325-1  
Sequence 1, Application US/08836325  
Patent No. 6110672  
GENERAL INFORMATION:  
APPLICANT: Mandel, Gail  
APPLICANT: Halegoua, Simon  
APPLICANT: Borden, Laurence A.  
TITLE OF INVENTION: Peripheral Nervous System Specific  
TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,  
TITLE OF INVENTION: X-Ray Diffraction, Computer Molecular Modeling, Rational  
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 New York Ave., N. W., Suite 600  
CITY: Washington  
STATE: DC

COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/836,325  
FILING DATE: 2-MAY-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/14251  
FILING DATE: 02-NOV-1995  
PRIOR APPLICATION DATA: 08/482,401  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/334,029  
FILING DATE: 02-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ludwig, Steven R.  
REGISTRATION NUMBER: 36,203  
REFERENCE/DOCKET NUMBER: 0917.0240002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3033 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..3033  
US-08-836-325-1

Alignment Scores:  
Pred. No.: 8.56e-59 Length: 3033  
Score: 72.00 Matches: 72  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.58% Indels: 0  
DB: 3 Gaps: 0

US-09-930-871-12 (1-2009) x US-08-836-325-1 (1-3033)

QY 1625 IleGlyLysTyrPheValSerProThrLeuPheArgValIleArgLeuAlaArgIleGly 1644  
|||||  
DB 1930 ATAGAGAGATTTGCTGCTCCCTACCTGTCGAGTCAATCCGCTGCGCAGAGATTGA 1989  
|||||  
QY 1645 ArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLeuLeuPheAlaLeuMet 1664  
|||||  
DB 1990 CGAATCTAGCCTGATCAAGGCGCAAGGAGATCGCACTGCTGCTTGTGATG 2049  
|||||  
QY 1665 MetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPheValMetPheIleTyr 1684  
|||||  
DB 2050 ATGTCCCTTCTGCTGCTCAACATCGGCTGCTGCTTCTGCTGATGATCATCTAC 2109  
|||||  
QY 1685 AlaIlePheGlyMetSerAsnPheAlaTyrValLys 1696  
|||||  
DB 2110 GCCATCTTGGGATGTCCAACTTGGCTACGTTTAA 2145  
|||||

RESULT 13  
US-08-836-325-9  
Sequence 9, Application US/08836325  
Patent No. 6110672  
GENERAL INFORMATION:  
APPLICANT: Mandel, Gail  
APPLICANT: Halegoua, Simon  
APPLICANT: Borden, Laurence A.

|||||  
TITLE OF INVENTION: Peripheral Nervous System Specific  
TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,  
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational  
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using  
TITLE OF INVENTION: Thereof  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 New York Ave., N. W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/836,325  
FILING DATE: 2-MAY-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/14251  
FILING DATE: 02-NOV-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/482,401  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/334,029  
FILING DATE: 02-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ludwig, Steven R.  
REGISTRATION NUMBER: 36,203  
REFERENCE/DOCKET NUMBER: 0917.0240002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ. ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6452 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: both  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 326..6277  
US-08-836-325-9

Alignment Scores:  
Pred. No.: 1,78e-58 Length: 6452  
Score: 72.00 Matches: 72  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.58% Indels: 0  
Gaps: 0  
DB: 3

US-09-930-871-12 (1-2009) x US-08-836-325-9 (1-6452)

QY 1625 ILEGLIUTSTYRPhEVALSERProthrlleuPhaArgValIleArgleuAlaArgIleGly 1644  
DB 5114 ATGAGAGATTTCCTGTCCTACCTGTCGAGTCATCCGCTGGCCAGGATTGGA 5173  
QY 1645 ArgIleleuArgleuIleuysglYAlaIlysglyIleArgThrleuIleuPhaIleuMet 1664  
DB 5174 CGAATCTACGCTGATCAAGGCGCAAGGGATCGGACCTGCTTGTGTTGATG 5233  
QY 1665 MetSerleuProAlaIleuPhaIleuIleuIleuIleuIleuIleuIleuIleuIleu 1684  
DB 5234 ATGTCCTTCCTGCTGCTTCAACATCGGCTCTGCTTCTGCTGATGATTCATCTAC 5293  
QY 1685 AlaIlePhelGlyMetSerAaPhaIleuIleuValIleuValIleuValIleuValIleuVal 1696

|||||  
DB 5294 GCCATCTTGGATGTCACACTTGGCTTACGTTAAA 5329  
RESULT 14  
US-09-024-020B-8  
Sequence 8, Application US/09024020B  
Patent No. 6030810  
GENERAL INFORMATION:  
APPLICANT: DELGADO, STEPHEN G.  
APPLICANT: DIETRICH, PAUL S.  
APPLICANT: FISH, LINDA M.  
APPLICANT: HERMAN, RONALD C.  
APPLICANT: SANGAMESWARAN, LAKSHMI  
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE  
TITLE OF INVENTION: SODIUM CHANNEL 1-SUBUNIT AND A SPLICE VARIANT THEREOF  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: JANET PAULINE CLARK  
STREET: 3401 HILLVIEW AVENUE, MS A2-250  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94304-1397  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/024,020B  
FILING DATE: 16-FEB-1998  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/039,447  
FILING DATE: 26-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: CLARK, JANET P.  
REGISTRATION NUMBER: 34,799  
REFERENCE/DOCKET NUMBER: R0020B-REG  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 852-3097  
TELEFAX: (650) 855-5322  
INFORMATION FOR SEQ. ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6826 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-024-020B-8

Alignment Scores:  
Pred. No.: 1,38e-55 Length: 6826  
Score: 69.00 Matches: 69  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.43% Indels: 0  
Gaps: 0  
DB: 3

US-09-930-871-12 (1-2009) x US-09-024-020B-8 (1-6826)

QY 201 AlaIleuValIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 220  
DB 619 GATATGTACAGAGATTTCGTGACCTGGGCAATGCTCAGACCTGAGAACATTCAGGGGT 678  
QY 221 LeuArgAlaIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 240  
DB 679 CTCGAGCTTGAAGACTATCTGTAAATTCAGGCTGAGAACATTCGAGGCGCTTA 738  
QY 241 ILEGLISerValIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 260  
DB 739 ATCAGATCCGTGAAGAGCTGTGCGAGCTGATGATCTTCAAGATGTTGCTGAGATGTT 798

OY 261 pheAlaLeuIleGlyLeuGlnLeuphe 269  
|||||  
DB 799 TTCGCCCTGATGGCCTGCAGCCTCTT 825

## RESULT 15

US-09-425-043-8  
; Sequence 8, Application US/09425043

; Patent No. 6335172

## GENERAL INFORMATION:

APPLICANT: DELGADO, STEPHEN G.

APPLICANT: DIETRICH, PAUL S.

APPLICANT: FISH, LINDA M.

APPLICANT: HERMAN, RONALD C.

APPLICANT: SANGAMESWARAN, LAKSHMI

TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE

TITLE OF INVENTION: SODIUM CHANNEL 1-SUBUNIT AND A SPLICE VARIANT THEREOF

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: JANET PAULINE CLARK

STREET: 3401 HILLYVIEW AVENUE, MS A2-250

CITY: PALO ALTO

STATE: CA

COUNTRY: U.S.A.

ZIP: 94304-1397

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/425,043

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/024,020

FILING DATE: 16-FEB-1998

APPLICATION NUMBER: US 60/039,447

FILING DATE: 26-FEB-1997

ATTORNEY/AGENT INFORMATION:

NAME: CLARK, JANET P.

REGISTRATION NUMBER: 34,799

REFERENCE/DOCKET NUMBER: R00208-REG

TELEPHONE: (650) 852-3097

TELEFAX: (650) 855-5322

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 6826 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-09-425-043-8

Alignment Scores:

pred. No.: 1.38e-55

Score: 69.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 3.43%

DB: 4

US-09-930-871-12 (1-2009) x US-09-425-043-8 (1-6826)

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DB 619 GCATATGTGACAGAGTTGTGACCTGGGCAATGCTCAAGCGCTGAGAACATTCAGGGTT 678

OY 221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240

DB 679 CTCGAGCTTGAAGAACTATCTCTGTAAATCCAGGCTGAAAGCAATCGTGGGCGCCCTA 738

OY 241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260

DB 739 ATCCAGTCCGTGAAGAAGCTGTGCGAGCATGATCCTGACAGTGTTCGCGTGAAGTGT 798

OY 261 pheAlaLeuIleGlyLeuGlnLeuphe 269

DB 799 TTCGCCCTGATGGCCTGCAGCCTCTT 825

Search completed: April 23, 2003, 08:13:03  
JOB Time : 197 secs

GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_p2n model

Run on: April 23, 2003, 07:14:12 ; Search time 449 Seconds

(without alignments)  
4668.710 Million cell updates/sec

Title: US-09-930-871-12

Perfect score: 2009  
Sequence: 1 MEGTALVPPSPDSENFRTRE.....TKPIVEKHEDGCKDKAKGR 2009

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|       | Ygapop 60.0 | Ygapext 60.0 |
|       | Fgapop 6.0  | Fgapext 7.0  |
|       | Delop 6.0   | Delext 7.0   |

Searched: 709820 segs, 544064369 residues

Word size: 1

Total number of hits satisfying chosen parameters: 1417911

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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-LOOPEXT-0 -LOOPEXT-0 -UNITS-bits -START-1 -MATRIX-oligo  
-TRANS-human40.csi -LIST-45 -DOCCALIGN-200 -THR SCORE-quality -THR MIN-1  
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-NCPD-6 -ICPD-3 -NO\_XLPHY -NO\_MMAP -LARGEQUERY -NEG\_SCORES-0 -WAIT -LONGLOG  
-DEV TIMEOUT-120 -WARN TIMEOUT-30 -THREADS-1 -XGAPOP-60 -XGAPEXT-60 -FCGAPOP-6  
-FCGAPEXT-7 -YGAPOP-60 -YGAPEXT-60 -DELOP-6 -DELEXT-7

Database :

Published Applications\_NA:  
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2: /cgn2\_6/ptodata/2/pubpna/PTCT\_NEM\_PUB.seq:  
3: /cgn2\_6/ptodata/2/pubpna/US06\_NEM\_PUB.seq:  
4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:  
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10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:  
11: /cgn2\_6/ptodata/2/pubpna/US10\_NEM\_PUB.seq:  
12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:  
13: /cgn2\_6/ptodata/2/pubpna/US60\_NEM\_PUB.seq:  
14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Length | DB ID | Description      |
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| 2          | 1970  | 98.1         | 5922  | US-09-930-871-13 |
| 3          | 1444  | 71.9         | 4362  | US-09-930-871-15 |
| 4          | 1382  | 68.8         | 4179  | US-09-930-871-17 |

|    |      |      |      |    |                     |                   |
|----|------|------|------|----|---------------------|-------------------|
| 5  | 1332 | 66.3 | 4197 | 10 | US-09-930-871-19    | Sequence 19, Appl |
| 6  | 1326 | 66.0 | 5997 | 10 | US-09-930-871-1     | Sequence 1, Appl1 |
| 7  | 1289 | 64.2 | 5889 | 10 | US-09-930-871-3     | Sequence 3, Appl1 |
| 8  | 763  | 38.0 | 4329 | 10 | US-09-930-871-5     | Sequence 5, Appl1 |
| 9  | 701  | 34.9 | 4146 | 10 | US-09-930-871-7     | Sequence 7, Appl1 |
| 10 | 670  | 33.3 | 4164 | 10 | US-09-930-871-9     | Sequence 9, Appl1 |
| 11 | 392  | 19.5 | 1992 | 10 | US-09-864-761-10189 | Sequence 10189, A |
| 12 | 385  | 19.2 | 1194 | 10 | US-09-864-761-18334 | Sequence 18334, A |
| 13 | 379  | 18.9 | 1178 | 10 | US-09-864-761-26829 | Sequence 26829, A |
| 14 | 322  | 16.0 | 969  | 10 | US-09-864-761-1576  | Sequence 1576, Ap |
| 15 | 99   | 4.9  | 6822 | 10 | US-09-917-800A-1604 | Sequence 1604, Ap |
| 16 | 88   | 4.4  | 490  | 10 | US-09-864-761-10615 | Sequence 10615, A |
| 17 | 87   | 4.3  | 487  | 10 | US-09-864-761-15573 | Sequence 15573, A |
| 18 | 83   | 4.1  | 249  | 10 | US-09-864-761-32083 | Sequence 32083, A |
| 19 | 83   | 4.1  | 264  | 10 | US-09-864-761-27235 | Sequence 27235, A |
| 20 | 80   | 4.0  | 249  | 10 | US-09-864-761-27066 | Sequence 27066, A |
| 21 | 77   | 3.8  | 465  | 10 | US-09-864-761-10437 | Sequence 10437, A |
| 22 | 74   | 3.7  | 347  | 10 | US-09-864-761-11970 | Sequence 11970, A |
| 23 | 74   | 3.7  | 467  | 10 | US-09-864-761-15456 | Sequence 15456, A |
| 24 | 49   | 2.4  | 343  | 10 | US-09-030-482B-17   | Sequence 17, Appl |
| 25 | 46   | 2.3  | 473  | 10 | US-09-864-761-3944  | Sequence 3944, Ap |
| 26 | 46   | 2.3  | 473  | 10 | US-09-864-761-13959 | Sequence 13959, A |
| 27 | 40   | 2.0  | 297  | 10 | US-09-864-761-22921 | Sequence 22921, A |
| 28 | 38   | 1.9  | 142  | 10 | US-09-864-761-20706 | Sequence 20706, A |
| 29 | 36   | 1.8  | 6048 | 9  | US-09-896-994-1     | Sequence 1, Appl1 |
| 30 | 36   | 1.8  | 6048 | 10 | US-09-840-125-3     | Sequence 3, Appl1 |
| 31 | 32   | 1.6  | 142  | 10 | US-09-864-761-30523 | Sequence 30523, A |
| 32 | 32   | 1.6  | 304  | 9  | US-10-040-739-1072  | Sequence 1072, Ap |
| 33 | 29   | 1.4  | 472  | 10 | US-09-864-761-6181  | Sequence 6181, Ap |
| 34 | 23   | 1.1  | 123  | 10 | US-09-030-482B-16   | Sequence 16, Appl |
| 35 | 10   | 0.5  | 31   | 10 | US-09-801-274-97    | Sequence 97, Appl |
| 36 | 10   | 0.5  | 31   | 10 | US-09-801-274-98    | Sequence 98, Appl |
| 37 | 10   | 0.5  | 31   | 10 | US-09-801-274-99    | Sequence 99, Appl |
| 38 | 10   | 0.5  | 31   | 10 | US-09-801-274-100   | Sequence 100, App |
| 39 | 10   | 0.5  | 31   | 10 | US-09-801-274-101   | Sequence 101, App |
| 40 | 10   | 0.5  | 31   | 10 | US-09-801-274-102   | Sequence 102, App |
| 41 | 10   | 0.5  | 31   | 10 | US-09-801-274-103   | Sequence 103, App |
| 42 | 10   | 0.5  | 31   | 10 | US-09-801-274-106   | Sequence 106, App |
| 43 | 10   | 0.5  | 31   | 10 | US-09-801-274-107   | Sequence 107, App |
| 44 | 10   | 0.5  | 31   | 10 | US-09-801-274-108   | Sequence 108, App |
| 45 | 10   | 0.5  | 31   | 10 | US-09-801-274-109   | Sequence 109, App |

## ALIGNMENTS

RESULT 1  
US-09-930-871-11  
: Sequence 11, Application US/09930871  
: Patent No. US20020076780A1  
: GENERAL INFORMATION:  
: APPLICANT: Turner, C. Alexander Jr.  
: APPLICANT: Mathur, Daniel  
: TITLE OF INVENTION: No. US20020076780A1 Human Ion Channel Proteins and Polynuc  
: TITLE OF INVENTION: Same  
: FILE REFERENCE: LEX-0216-USA  
: CURRENT APPLICATION NUMBER: US/09/930, 871  
: PRIOR FILING DATE: 2001-08-14  
: PRIOR APPLICATION NUMBER: US 60/225, 989  
: NUMBER OF SEQ ID NOS: 20  
: SOFTWARE: PASTSEQ for Windows Version 4.0  
: SEQ ID NO 11  
: LENGTH: 6030  
: TYPE: DNA  
: ORGANISM: homo sapiens  
US-09-930-871-11

Alignment Scores:  
Pred. No.: 0  
Score: 2007.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%

Length: 6030  
Matches: 2009  
Conservative: 0  
Mismatches: 0

Query Match: 99.90% Indels: 0  
DB: 10 Gaps: 0  
US-09-930-871-12 (1-2009) x US-09-930-871-11 (1-6030)

QY 1 MetGluGlnThrValLeuValProGluProAspSerPheAspPheThrArgGlu 20  
DB 1 ATGGAGCAAGAGCTGCTGACCAAGAGAGCTGACCTCACTTCTTCCAGAGAGA 60  
QY 21 SerLeuAlaAlaIleGluArgArgIleAlaGluIuLyAlaLysAsnProLysProAsp 40  
DB 61 TCTCTGGGGCTATGAAAGAGCATGTCAGAAAGAAAGCAAAAGCCCAACAGAGAC 120  
QY 41 LysLysAspAspAspGluAsnGluProLysProAsnSerAspLeuGluAlaGlyLysAsn 60  
DB 121 AAAAAGATGACGAGAAATGAGCCCAAGCAATAGTACTGAGAGCTGGAAGAGAC 180  
QY 61 LeuProPheIleTyrgLysPileProGluMetValSerGluProLysLysAsn 80  
DB 181 CTTCATTTATTTATGAGAGACTTCTCCAGAGATGCTGAGAGCCCTGAGAGAGCTG 240  
QY 81 AspProTyrrLysAsnLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100  
DB 241 GACCCCTACTATATCAATAGAAACCTTTATAGATTAATGAAAGAGAGAGCCATCTTC 300  
QY 101 ArgPheSerAlaThrSerAlaLeuTyrrIleLeuThrProPheAsnProLeuArgLysIle 120  
DB 301 CGGTTCAGTGGCCCTGCTGCTGACATTTTAACTCCCTCAACCTCTTGAAGAAATTA 360  
QY 121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140  
DB 361 GCTATTAAGATTTTGGTTCATTCATTAATGACAGCATTAATATGACATTTTGGACA 420  
QY 141 AsnGlyValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrrThr 160  
DB 421 AACTGTGCTTATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480  
QY 161 PheThrGlyIleTyrrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180  
DB 481 TTCACAGCAATATATATCTTTTCAATCACTTATTAATAATTTATGCAAGGAGATTCGTGTTA 540  
QY 181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200  
DB 541 GAAGATTTTACTTCTCTCGGATCCATGAGAACTGCTGATTCATGCTATTCATTT 600  
QY 201 AlaTyrrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220  
DB 601 GCGTACGTCACAGAGTGTGTGACCTGGGCAATGCTCGGCAATGAGAAATTCAGAGTT 660  
QY 221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240  
DB 661 CTCGACGATGAGAGACATTTTCACTTCATTCAGGCTCGAAACCATTTGTGGAGCCCTG 720  
QY 241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260  
DB 721 ATCCAGTCTGTGTAAGAACTCTCAGATGTAATGATCTGAGCTGTCTGCTGAGCGTA 780  
QY 261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleLeuTrp 280  
DB 781 TTTGCTCAATTTGGGCTCAGCTGTTCATGAGCAACCTGAGGAAATTAATGATTAAGG 840  
QY 281 ProProThrAsnAlaSerLeuGluGluLysSerIleGlyLysAsnIleThrValAsnTyrr 300  
DB 841 CCTCCACCAATGCTTCTCTGAGAGACATAGTATGAAAGAAATATATATCTGTAATAT 900  
QY 301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrrIleGlnAsp 320  
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QY 321 SerArgTyrrHisTyrrPheLeuGluGluGlyPheLeuAspAlaLeuLeuGlyLysAsnSer 340  
DB 961 TCAGATATATATATATCTCTGAGAGGTTTTTATGATGACATGATATGAGAAATAGCTCT 1020

QY 341 AspAlaGlyGlnCysProGluGluTyrrMetCysValLysAlaGlyArgAsnProAsnTyrr 360  
DB 1021 GATGAGGCGCAATGCTCCAGAGGATATATGTGTGAAAGCTGCTGAGAAATCCCAATATAT 1080  
QY 361 GlyTyrrThrSerPheAspTrpThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380  
DB 1081 GGCCTACACAGCTTGTATATCACTTCACTTGGGCTTTTGTCTTCTGTTGCTGATATGACT 1140  
QY 381 GluAspPheTrpGluAsnLeuTyrrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrrMet 400  
DB 1141 CAGGACTTCTGGGAAATCTTTATCACTGATCACTGCTGCTGGGAAATCCATCATATG 1200  
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DB 1201 ATATTTTGTGTGTGCTATTTTCTTGGGCTCATTTCTCAATTAATATTTATCTGCTGCT 1260  
QY 421 ValValAlaMetAlaTyrrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluLys 440  
DB 1261 GTGGTGGCCATGCTCAGAGAGACAGATGAGCCACCTTGGAAAGAGAGAGAGAGAGAG 1320  
QY 441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460  
DB 1321 GAGGCCAATTTTCAACAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380  
QY 461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480  
DB 1381 GAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1440  
QY 481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerSerAlaLysGluArgArgAsnArg 500  
DB 1441 GACAGCTCATGTCAGAACCTTAAGTTAGTTGATGCAAGATGCTGAAGAAAGAAATCGG 1500  
QY 501 ArgLysLysArgLysGlnLysGlnLysGlnLysGlnLysGlnLysGlnLysGlnLys 520  
DB 1501 AGGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAATTC 1560  
QY 521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540  
DB 1561 CAAATATGTAATCTGAGAGACATGACATGAGAGAGAAAGTTTCCCTTCCATTTGAAAGG 1620  
QY 541 AsnArgLeuThrTyrrGluLysArgTyrrSerSerProHisGlnSerLeuLeuSerIleArg 560  
DB 1621 AACCATTTGACATATGAAAGAGGATCTCTCCACAGCATGCTTGTGACATTCGCT 1680  
QY 561 GlySerLeuPheSerProArgArgAsnSerArgTrpThrSerLeuPheSerPheArgGlyArg 580  
DB 1681 GCTCTCTATTTTACCAAGGCGAAATGACAGAAACACCTTTTCACTTTAAGAGGCGGA 1740  
QY 581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600  
DB 1741 GCAAGAGATGTCGATCTGAGAGACATCTCCAGATGATGAGACAGACATCTTGGAGAT 1800  
QY 601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgAsnSer 620  
DB 1801 AACGAGAGCCGATGAGATCTCTTGTGTGCTGCGGACAGACAGGAGAGAGAGCAACAGC 1860  
QY 621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValPheProAlaAsnGlyLys 640  
DB 1861 AACCTGAGTTCAGACAGATGATCCCGAGATGCTGAGAGCTTTCAGCCAAATGGGAAG 1920  
QY 641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660  
DB 1921 ATGCACACACATGTCGATGTCGATGTCGATGTCGATGTCGATGTCGATGTCGATGTC 1980  
QY 661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680  
DB 1981 ACATGCGCTGTGGACACCTTCTGCGAGAGGTGATATATGATGATGATGATGATGATG 2040  
QY 681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerPheHisValSer 700  
DB 2041 AATGAGACACCACTGAAATCTGAATGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2100  
QY 701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720

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Db 2161 ACAAAATCAGTAGAAGAACTGGAAGAAATCCAGGCAAGAAATGCCACCCCTGTGTATATAA 2220  
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Qy 961 GluValAlaIleGlyAlaMetCysLeuThrValPheMetCysValMetValIleGlyAsn 980  
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Db 4261 GGGTATCTCTTGT 4320



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 QY 1681 MetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgIleValGly 1700  
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 QY 1781 TyrIleAlaValIleLeuGlnAsnPheSerValAlaThrGlnGlnSerAlaGluProLeu 1800  
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 DB 5761 ATTATTCAGCGTCTTACAGACGCGCACTTTTAAACGAAATGTAACAAAGTCTCTT 5820  
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 QY 1961 IleAspArgIleAsnGluAsnSerIleThrGlyLysThrAspLeuThrMetSerThrAla 1980  
 DB 5881 ATTGACAGATTAATGAAAACTTATTAACGAAAAAGATGATGATGATGATGATGATG 5940  
 QY 1981 AlaCysProSerSerTyrAspArgValThrLysProIleValGlnLysIleGlnGln 2000  
 DB 5941 GCTTGTCCACTCTTCTATGACCGGATGACAAAGCAATGTGAAACAAATGACGAA 6000  
 QY 2001 GlyLysAspGluLysAlaLysGlyLys 2009  
 DB 6001 GCCAAAGATGAAAAAGCCAAAGGAAA 6027

RESULT 2  
 US-09-930-871-13  
 : Sequence 13, Application US/09930871  
 : Patent No. US20020076780A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Turner, C. Alexander Jr.  
 : APPLICANT: Mathur, Daniel  
 : APPLICANT: Mathur, Brian  
 : TITLE OF INVENTION: No. US20020076780A1 Human Ion Channel Proteins and Polynuc  
 : FILE REFERENCE: Same  
 : FILE REFERENCE: LEX-0216-USA  
 : CURRENT APPLICATION NUMBER: US/09-930,871  
 : CURRENT FILING DATE: 2001-08-14  
 : PRIOR APPLICATION NUMBER: US 60/225,989  
 : PRIOR FILING DATE: 2000-08-16  
 : NUMBER OF SEQ ID NOS: 20  
 : SOFTWARE: FASTSQ for Windows Version 4.0  
 : SEQ ID NO 13  
 : LENGTH: 5922  
 : TYPE: DNA  
 : ORGANISM: homo sapiens  
 : US-09-930-871-13

Alignment Scores:  
 Pred. No.: 0  
 Score: 1970.00  
 Percent Similarity: 100.00%  
 Best Local Similarity: 100.00%  
 Query Match: 98.06%

Length: 5922  
 Matches: 1972  
 Conservative: 0  
 Mismatches: 0  
 Indels: 0

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DB: 10 Gaps: 0
US-09-930-871-12 (1-2009) * US-09-930-871-13 (1-5922)

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Oy 61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
Db 181 CTTCATTTATTTATGAGACATTCCTCCAGAGATGTGTCCAGAGCCCTGGAGGACCTG 240
Oy 81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
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Oy 101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
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Oy 121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
Db 361 GCTATTAGATTTTGGTACATTCATTTATTCACATGCTAATATATGACATTTTATGACA 420
Oy 141 AsnGlyValPheMetThrMetSerAsnProProAspTyrPheLysAsnValGluTyrThr 160
Db 421 AACCTGTGGTTATGACAAATGAGTAACCTCTGATGAGCAAGAGATGTAAATAACACC 480
Oy 161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgLysPheCysLeu 180
Db 481 TTCACAGCAATATATACCTTTTGAATACACTTATATAAATATATGCAAGGGATTCGTTA 540
Oy 181 GluAspPheThrPheLeuArgAspProTyrAsnTyrPheAspPheThrValIleThrPhe 200
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Oy 201 AlaTyrValThrGluPheValAspLeuGluAsnValSerAlaLeuArgThrPheArgVal 220
Db 601 GCGTACGTCACAGAGTGTGTGGAACCTGGCAATGTCTGGCAATGAGAACATTCAGAGTT 660
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Oy 261 PheAlaLeuIleGlyLeuGluLeuPheMetGlyAsnLeuArgAsnLysGlyIleGlnTyr 280
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Oy 441 GluAlaGluPheGluGluMetIleGluGluLeuLysLysGluGluGluAlaAlaGluGln 460
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 : Sequence 15, Application US/09930871  
 : Patent No. US20020076780A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Turner, C. Alexander Jr.  
 : APPLICANT: Mathur, Daniel  
 : APPLICANT: Mathur, Brian  
 : TITLE OF INVENTION: No. US20020076780A1el Human Ion Channel Proteins and Polynuc  
 : TITLE OF INVENTION: Same  
 : FILE REFERENCE: LEX-0216-USA  
 : CURRENT APPLICATION NUMBER: US/09/930, 871  
 : PRIOR FILING DATE: 2001-08-14  
 : PRIOR APPLICATION NUMBER: US 60/225, 989  
 : PRIOR FILING DATE: 2000-08-16  
 : NUMBER OF SEQ ID NOS: 20  
 : SOFTWARE: FastSeq for Windows Version 4.0  
 : SEQ ID NO 15  
 : LENGTH: 4362  
 : TYPE: DNA  
 : ORGANISM: homo sapiens  
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 Alignment Scores:  
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 Score: 1444.00 Matches: 1446  
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QY 181 GluAspPheThrPheLeuArgAspProTyrlAsnTyrlLeuAspPheThrValIleThrPhe 200  
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QY 201 AlaTyrlValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220  
Db 601 GCGTAGCTCAGACAGTTTGTGGACCTGGCAATGCTCCGCGCATTCGAGAAATTCAGAGTT 660  
QY 221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240  
Db 661 CTCGAGCATTTGAAAGCATTTTCAGTATTCAGGCTCGAAGAACATTCGAGGACCTGTG 720  
QY 241 IleGluSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260  
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QY 261 PheAlaLeuIleGlyLeuGluLeuPheMetGlyAsnLeuArgAsnLysCysIleGluThr 280  
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QY 281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyrl 300  
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QY 301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspThrLysSerTyrlIleGluAsp 320  
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QY 321 SerArgTyrlHisTyrlPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340  
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QY 341 AspAlaGlyLysLysProGluGlyTyrlMetCysValLysAlaGlyArgAsnProAsnTyrl 360  
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QY 361 GlyTyrlThrSerPheAspThrPheSerTyrlAlaPheLeuSerLeuPheArgLeuMetThr 380  
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QY 421 ValValAlaMetAlaTyrgLysGluGluAsnGluAlaThrLeuGluGluAlaGluGluLys 440  
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 Oy 1261 TyrIlePheIleLeuGluMetLeuLeuLysTyrValAlaTyrGlyThrTyrPhe 1280  
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RESULT 4  
 US-09-930-871-17  
 : Sequence 17, Application US/09930871  
 : Patent No. US20020076780A1  
 : GENERAL INFORMATION:



APPLICANT: Turner, C. Alexander Jr.  
 APPLICANT: Mathur, Daniel  
 APPLICANT: Mathur, Brian  
 TITLE OF INVENTION: No. US0020076780A1 Human Ion Channel Proteins and Polynucleot  
 TITLE OF INVENTION: Same  
 FILE REFERENCE: LEX-0216-USA  
 CURRENT APPLICATION NUMBER: US/09/930,871  
 CURRENT FILING DATE: 2001-08-14  
 PRIOR APPLICATION NUMBER: US 60/225,989  
 PRIOR FILING DATE: 2000-08-16  
 NUMBER OF SEQ ID NOS: 20  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 17  
 LENGTH: 4179  
 TYPE: DNA  
 ORGANISM: homo sapiens  
 US-09-930-871-17

Alignment Scores:  
 Pred. No.: 0 Length: 4179  
 Score: 1382.00 Matches: 1384  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 68.79% Indels: 0  
 DB: 10 Gaps: 0

US-09-930-871-12 (1-2009) x US-09-930-871-17 (1-4179)

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Db 2701 GCTTTATTTTTCCTGCTGCGGACATGACCTCTTGTGTAACATCTCAAAAGATTTGTCTC 2760  
OY CysLysIleLeuAspCysGlnLeuProArgTyrPheIleMetAsnAspPhePheHisSer 940  
Db 2761 TGGCAAGATGCGCAGTAGTTGTCAATCCACGGTGGCACAATGATGATCTTCCATCC 2820  
OY PheLeuIleValPheArgValLeuCysGlyGluTyrPheIleGluThrMetTyrPAspCysMet 960  
Db 2821 TTCCCTGATTTGTGTGCTGCTGTGTGGGAGATGAGACCAATGTGGGACTGTATG 2880

OY GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980  
Db 2881 GAGTTGCTGCTCAAGCCATGTGCTTACTGCTTCATGATGTGATGTGATTTGGAAC 2940  
OY LeuValValLeuAsnLeuPheLeuAlaLeuLeu\*\*\*SerSerPheSerAlaAspAsnLeu 1000  
Db 2941 CTAGTGCTGCTCAATCTCTTGTGGCTTGTGTAGTCTCTTTAGTGCACACACCTT 3000  
OY AlaAlaThrAspAspAspAsnGluMetAsnLeuGlnIleAlaValAspArgMetHis 1020  
Db 3001 GCAGCCACTGATGATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 3060  
OY LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040  
Db 3061 AAAGAGATGCTTATGTGAAAAAAGAAATATATGATTAATTAATCAACAGCTCTCAATTAG 3120  
OY LysGlnLysIleLeuAspGluIleLysProLeuAspPheAsnAsnLysAspSer 1060  
Db 3121 AAACAAAAGATTTTATGATTAATTAATCACTTGTGATGATTAATCAACACAGAAAGACAGT 3180  
OY CysMetSerAsnHisThr\*\*GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080  
Db 3181 TGTATGCTCAATCATACACAGAAATTTGGAAGATCTTGAATATCTTAATATTAAT 3240  
OY GlyThrThrSerGlyIleGlyThrGlySerValGluLysTyrIleLeuAspLeuSer 1100  
Db 3241 GGAATCAAGCTGTATGAGAACTGGCAGAGTGTGAAAAATATATGATTAATGATTAAT 3300  
OY AspTyrMetSerPheIleAsnAspProSerLeuThrValProIleAlaValGly 1120  
Db 3301 GATTCATGCTATTCATTAACACCCAGCTTACTGTGACGATGACCAATGTCTATGAGA 3360  
OY GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140  
Db 3361 GAATCTGACTTTGAAATTTTAAACACGAGACCTTACTAGATGATGATGATGATGAA 3420  
OY SerLysGlyLysLeuAsnGlnSerSerSerSerSerSerSerSerThrValAspIleGly 1160  
Db 3421 AGCAAAAGAAACCTGAATGAAGACGTAGCTCATCAGAGAGTAGACATGTCGACATCCG 3480  
OY AlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluLys 1180  
Db 3481 GCACCTGTAGAGAAACACCCGCTAGTGAACCTGAAAGAACTTGAACACCAAGCTTGT 3540  
OY PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluLysArg 1200  
Db 3541 TTCACGTGAAGGCTGTGTAACAAAGATTCAAAGTGTGTCAATCAATGTGGAAGAGCAGA 3600  
OY GlyLysGlnTyrPAsnLeuArgArgThrCysPheArgIleValGluHisAsnTyrPhe 1220  
Db 3601 GGAAGAACATGTGTGAACCTGAGAGAGCGTGTTCGAAATGTTGAACATAACGCGT 3660  
OY GluThrPheIleValPheMetIleLeuLeuSerSerGlyValAlaLeuAlaPheGluAspIle 1240  
Db 3661 GAGACCTCATGTGTTTCATATATCTCTTGTAGTGTGTGTGTGTGTGTGTGTGTGTGT 3720  
OY TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr 1260  
Db 3721 TATATGTATCAGCAAGACATTAAGACGATTTGGAATATGTCGACAAAGCTTTTCACT 3780  
OY TyrIlePheIleLeuGluMetLeuLeuLysTyrPheAlaTyrGlyTyrGlnThrTyrPhe 1280  
Db 3781 TACATTTTCATCTGGAATATCTTAAAGGCGGATGATGATGATGATGATGATGATGAT 3840  
OY ThrAsnAlaTyrCysTyrPheAspPheLeuIleValAspValSerLeuValSerLeuThr 1300  
Db 3841 ACAGATGCTGT 3900  
OY AlaAsnAlaLeuGluGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320  
Db 3901 GCAATATGCTGT 3960

|    |      |  |      |
|----|------|--|------|
| OY | 1321 | LeuArgProLeuArgAlaLeuSerArgPheGlnGlyMetArgValValAlaAsnAlaLeu   | 1340 |
| Db | 3961 | CTGAGACCTCTTAAGACCTTATCTCGATTTGAAGGAGTGAAGGTGTGTGATGCCCTT      | 4020 |
| OY | 1341 | LeuGlyAlaAlaProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIle   | 1360 |
| Db | 4021 | TTAGGAGCAATTCATCCATCATCAATGTCCTTCTGGTTTGCTATATATTCGGCTAATT     | 4080 |
| OY | 1361 | PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTrpHisCysIleAsnThr      | 1380 |
| Db | 4081 | TTTCAGCAACAAGGGCGTAAATTTGTTGCTGGCAAAATCTACCACTGATTTAAACACACACA | 4140 |
| OY | 1381 | ThrGlyAspArg   | 1384 |
| Db | 4141 | ACTGCTGACAGG   | 4152 |

RESULT 5

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: Sequence 19 Application US/09930871
: Patent No. US20020076780A1
: GENERAL INFORMATION:
: APPLICANT: Turner, C. Alexander Jr.
: APPLICANT: Mathur, Daniel
: APPLICANT: Mathur, Brian
: TITLE OF INVENTION: No. US20020076780A1 Human Ion Channel Proteins and Polynucleotides
: TITLE OF INVENTION: Same
: FILE REFERENCE: LEX-0216-US-A
: CURRENT APPLICATION NUMBER: US/09/930, 871
: CURRENT FILING DATE: 2001-08-14
: PRIOR APPLICATION NUMBER: US 60/225,989
: PRIOR FILING DATE: 2000-08-16
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 19
: LENGTH: 4197
: TYPE: DNA
: ORGANISM: homo sapiens
: US-09-930-871-19

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**Alignment Scores:**

|                        |         |               |      |
|------------------------|---------|---------------|------|
| Pred. No.:             | 0       | Length:       | 4197 |
| Score:                 | 1332.00 | Matches:      | 1334 |
| Percent Similarity:    | 100.00% | Conservative: | 0    |
| Best Local Similarity: | 100.00% | Mismatches:   | 0    |
| Query Match:           | 66.30%  | Indels:       | 0    |
| DB:                    | 10      | Gaps:         | 0    |

US-09-930-871-12 (1-2009) x US-09-930-871-19 (1-4197)

|    |     |  |     |
|----|-----|--|-----|
| QY | 1   | MetGluGlnThrValIleValProProGlyProAspSerPheAsnPhePheThrArgGlu   | 20  |
| Dp | 1   | ATGGAGCAAAACAGTGTCTGTACACAGAGACTGACAGCTTCAACTCTTCCACAGAGAA     | 60  |
| QY | 21  | SerLeuAlaAlaIleGluIuArgAlleAlaGluIuLysAlaIuAsnProLysProAsp     | 40  |
| Dp | 61  | TCTCTTGGGGTATTTGAAAGACGCAATGCAACAAAAAGGCCAAAGATCCCAACCGAGAC    | 120 |
| QY | 41  | LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuAlaGlyLysAsn      | 60  |
| Dp | 121 | AAAAAAGATGACGACGAAAAAGGGCCAAAGCCAAATAGTGACTTGGAAAGCTGGAAAAAGAC | 180 |
| QY | 61  | LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu   | 80  |
| Dp | 181 | CTTCATTATTATTATGGAGCAATTCCTCCACAAAGTGTGTACAGGCCCTGGAGGAGACTG   | 240 |
| QY | 81  | AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe   | 100 |
| Dp | 241 | GACCCCTCTATATCAATAAAGAAACTTTATATGATTTGAATAAAGGAGGACCACTTC      | 300 |
| QY | 101 | ArgPheSerAlaThrSerAlaIleuTyrIleLeuThrProPheAsnProLeuAlaGlyIle  | 120 |
| Dp | 301 | CGGTTCAGTCCACACTCTGCCCTGTACATTTTAACTCCCTTCAATCTCTTTAGAAAAATA   | 360 |

|    |      |   |      |
|----|------|---|------|
| OY | 121  | AlailelyslleleuValHisserleuPheSermetleuileMetCysThrIleleuThr      | 140  |
| Db | 361  | GGTATTAAAGATTGGTGCATTCATTATTCAGCATGCTAAATTAATGTCACATATTTGGACA     | 420  |
| OY | 141  | AsnCysValPheMetThrMetSerAsnProProAspTrpTrpLysAsnValGluYrThr       | 160  |
| Db | 421  | AACTGTGTGTTTATATACAAATGATGACACCTCTCTGTATGGACAAAGATGTAATACACC      | 480  |
| OY | 161  | PheThrGlyIleYrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu       | 180  |
| Db | 481  | TTCCACAGGAATATATACCTTTTGAATCACTTATAAAATTAATGGCAAGGGATTCGTGTTA     | 540  |
| OY | 181  | GluAspPheThrPheLeuAlaAspProTrpAsnTrpLeuAspPheThrValIleThrPhe      | 200  |
| Db | 541  | GAAAGATTTTACTTCTCTCTGGGATTCACAGAACTGGCTGCATTTCCACTGTCATTAACATTT   | 600  |
| OY | 201  | AlaYrValIleThrGluPheValAspLeuGlyAsnValSerIleAlaLeuArgThrPheArgVal | 220  |
| Db | 601  | GGCTACGTCACAGATTTGTGGACCTGGGCAATGCTCTGGCATTGAAGAACATTCAGAGTT      | 660  |
| OY | 221  | LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu      | 240  |
| Db | 661  | CTCCGAGCATTTGAAGACATTTTCAAGTATTCACAGCCTGAAGAACATTTGGGAGCCCTG      | 720  |
| OY | 241  | IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal      | 260  |
| Db | 721  | ATCCAGCTCTGTGAGAACCTCTCAGATGTAATGATCTGCACTGTCTCTCTGACGGTA         | 780  |
| OY | 261  | PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp      | 280  |
| Db | 781  | TTTGCTCTTAATTTGGGCTGCACCTGTTCATGGGCAACCTGGAGAAATTAATATPACATGG     | 840  |
| OY | 281  | ProProThrAsnAlaSerLeuGluGluHisSerIleGlyLysAsnIleThrValAsnYr       | 300  |
| Db | 841  | CTCCACCAATAGCTCTCTCTGGAGAACATATGTAATAAAAGATTAATCACTGCAATTAT       | 900  |
| OY | 301  | AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerYrIleGlnAsp       | 320  |
| Db | 901  | AATGCTACACTTAATAAAGAAACGTCTTTCAGTTTCACTGAGGAAGCATATATATCAAGAT     | 960  |
| OY | 321  | SerArgYrHisYrPheLeuGluGlyPheLeuAspIleLeuLeuGlyAsnSerSer           | 340  |
| Db | 961  | TCAAGATATTCATTTATTTCTGTGGAGGGTATTTAATCACTCACTACTGTAATGAAATACCTCT  | 1020 |
| OY | 341  | AspAlaGlyIleCysProGluGlyYrMetCysValLysAlaGlyArgAsnProAsnYr        | 360  |
| Db | 1021 | GATGAGGCCAATGTCCAGAGGAGTATATATGTGTGTGAACCTGTGAAATATCCCAATTAT      | 1080 |
| OY | 361  | GlyYrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr       | 380  |
| Db | 1081 | GGCTACACAACTTTGATACCTTCAGTTGGGCTTTTGTCTGTTTCACATTAATAGACT         | 1140 |
| OY | 381  | GlnAspPheTrpGluAsnLeuYrGlnLeuThrLeuArgAlaIleGlySerThrYrMet        | 400  |
| Db | 1141 | CAGGACTCTGGGAAATCTTTATCAACATGACATTAAGTCTCTGGGAAAGATGACATG         | 1200 |
| OY | 401  | IlePhePheValLeuValIlePheLeuGlySerPheYrLeuIleAsnLeuIleLeuAla       | 420  |
| Db | 1201 | ATATTTTTTGTGTGGTCATTTCTCTGGGCTCANTCTACTAATTAATTTGAATCCCGGCT       | 1260 |
| OY | 421  | ValValAlaMetAlaYrGluGluGlnAsnGlnAlaThrLeuGluGluValIleGluGlnLys    | 440  |
| Db | 1261 | GTGTGGCCCAATGGCTCTACAGAGAACAAATCAAGGCCACTTGGAAAGAACACAAACGAAA     | 1320 |
| OY | 441  | GluValGluPheGlnGlnMetIleGluGlnLeuLysGlyGlnGluValIleGlnGln         | 460  |
| Db | 1321 | GAGGCCGAATTTCCAGAGATGATTTGAACACCTTAAAGACAAACAGAGAGCAGCTCAGCAG     | 1380 |
| OY | 461  | AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer      | 480  |
| Db | 1381 | GCACCAACAGGCACACTGCTCAGAAACATTTCCAGAGAGGCCAGTCCACACAGGAGGCTCTA    | 1440 |
| OY | 481  | AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg      | 500  |

|    |      |   |      |
|----|------|---|------|
| Db | 1441 | GACAGCTCATCTGAAAGCCTCAAGTTAAGTCCAAAGTGTCTAAGGAAGAAAGAAATGCG     | 1500 |
| Qy | 501  | ArglylsyArglysGlnlysgLnSerGlyglYgluGlnlyAspGlnlyAspGlnlyPhe     | 520  |
| Db | 1501 | AGGAAGAAAGAAAGAAAGAAAGAGAGCTGCGTGGGGAAAGAAAGATGAGATGATATTC      | 1560 |
| Qy | 521  | GlnlysserGlnserGlnlyAspSerIleArgArgLyglyPheArgPheSerIleGluGly   | 540  |
| Db | 1561 | CAAAATATCTGAATCTGAGGAGCAGCATCAGAGGAGAAAGTTTTCGGTCTTCATTTGAAAGG  | 1620 |
| Qy | 541  | AsnArgLeuThrArgIlyAsArgTyIserSerProHisGlnSerLeuIleuSerIleArg    | 560  |
| Db | 1621 | AACCGATTGACATATGAAAAGAGGTACTCTCCCAACACAGCTCTTGTGTGACATCCGT      | 1680 |
| Qy | 561  | GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgIlyArg    | 580  |
| Db | 1681 | GGCTCCCATATTTTACCAAGGCGAAATAGAGAAACAAGCCTTTTCAGCTTTAGAGGGCGA    | 1740 |
| Qy | 581  | AlaIysAspValGlyserGlnAsnAspPheAlaAspAspGlnHisSerThrPheGlnAsp    | 600  |
| Db | 1741 | GCAAAAGGATGTGGGATCTGGAAGACAGCTTCGCGAGATGAGACACAGCACTTTGAGGAT    | 1800 |
| Qy | 601  | AsnGlySerArgArgAspSerLeuPheValProArgArgHisGlyGlnArgArgAsnSer    | 620  |
| Db | 1801 | AACGAGACCCGTAAAGATCTCTGTTGTGTGCCCCGACGACAGAGAGAGAGCAACAGC       | 1860 |
| Qy | 621  | AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaIValPheProAlaAsnGlylys   | 640  |
| Db | 1861 | AACGAGATGAGACCACTAGTGTATCCCGGATCTCTGCGAGTCTTTCCAGCAATGGGAAG     | 1920 |
| Qy | 641  | MethIserThrValAspCysAsnGlyValIValSerLeuValGlyIlyProSerValPro    | 660  |
| Db | 1921 | ATGCAACAGCACTGTGGATCTCAATGGTGGTGTTCTTGTTGGTGGAGCTTCAGTTCCT      | 1980 |
| Qy | 661  | ThiSerProValGlyGlnIleuLeuProGlnIValIleIleAspIlyProAlaThrAspAsp  | 680  |
| Db | 1981 | ACATCGCCTGTGGACAGCTCTGTGCCAGAGGTGATATATGATAACCCAGCTACGATGAC     | 2040 |
| Qy | 681  | AsnGlyThrThrPheGlnThrGlnMetArgIysArgArgSerSerPheHisValSer       | 700  |
| Db | 2041 | AATGGACAAACCACTGAAACTGAAATAGAGAAAGAGAGTCAAGTCTTTCCACGCTTCC      | 2100 |
| Qy | 701  | MetAspPheLeuGlnAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu    | 720  |
| Db | 2101 | ATGCACTTCTAGAAAGATCTCTCCCAAGGCAACGAGCAATGATATGATGACGACATCTA     | 2160 |
| Qy | 721  | ThiAsnThrValGlnGluIleuGlnGlnIserArgGlnIlyCysProProCysTrpTyrIlys | 740  |
| Db | 2161 | ACAAATACAGTAGAAGAACTTGAAGATCCAGGCAAAATGCCCCCTGTGGATATATA        | 2220 |
| Qy | 741  | PheSerAsnIlePheLeuIleTrpAspCysSerProTyITrpLeuIysValHisVal       | 760  |
| Db | 2221 | TTTTCCAAACATATCTTAACTGTGGAGCTGTCTCCATATGTGTTAAAGTGAACAAGTT      | 2280 |
| Qy | 761  | ValAsnLeuValIValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu   | 780  |
| Db | 2281 | GTCACACCTGGTGTGAGAGACCCATTTGTTGACTGGCCATCACCATCTGATATGTCTTA     | 2340 |
| Qy | 781  | AsnThrLeuPheMetIleMetGlnHisTyIrrPrometThrAspHisPheAsnAsnValLeu  | 800  |
| Db | 2341 | AATACTCTTTTCATGGCCATGAGGACACTATCCAAATGAGGACCAATTTAAATATGTCTT    | 2400 |
| Qy | 801  | ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGlnMetPheLeuIysIleIle    | 820  |
| Db | 2401 | ACATAGAGAAACTGTGTTTCACTGGGACCTTTACAGCAAGAAATTTTCTGAAAATATATT    | 2460 |
| Qy | 821  | AlaMetAspProTyIrrTyIrrPheGlnGlnGlyTyTPasnIlePheAspGlyPheIleVal  | 840  |
| Db | 2461 | GCCATGATCTCTACTTATTTATTCCAAGAGGCTGGAATATCTTGACGGTTTATATGTC      | 2520 |
| Qy | 841  | ThiLeuSerLeuValGlnIleuGlyLeuAlaAsnValGlnGlyLeuSerValIleuArgSer  | 860  |

[illegible]

[illegible]







3448 GCACCTGTAGAGACAGCCCGTAGTGAACCTGAGAAACCTCTGAAACCAAGACTTGT 3507  
1181 PheThrGlnGlnGlyValGlnArgPheGlyCysGlnIleAsnValGluGluGlyArg 1200  
3508 TTCACGAGAGGCTGTGACAAAGATTCAGTGTGTCAAATGAGGAGAGGAGA 3567  
1201 GlyGlnGlnTrpPheAsnLeuArgTrpCysPheArgIleValGluHisAsnTrpPhe 1220  
3568 GGAAGAACATAGTGGAGAACCTGAGAGAGAGCTGTTCCGAATAGTTGAACTAATCGTTT 3627  
1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240  
3628 GAGACCTCATTTGTTTCATGATTCCTTCAAGTAGTGCTGCTGGCATTTGAAGATATA 3687  
1241 TyrIleAspGlnArgGlyThrIleGlyThrMetLeuGlnGlyTrpAlaAspGlyValPheThr 1260  
3688 TAAATGATCAGGAGAAAGAGATTAAGACATGTGGAAATGCTGCAGAGGTTTTCATC 3747  
1261 TyrIlePheIleLeuGlnMetLeuLeuLysTrpValAlaArgGlyTrpGlnThrTrpPhe 1280  
3748 TACATTTTCATTTGGAATGCTTCAAAATGGGTGGCATATGGCTATTCAAACATATTTTC 3807  
1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300  
3808 ACCAATGCTGTGGTGTGGCTGACCTCTTAATGTTGATGTTTCATGTGTCAGTTTACA 3867  
1301 AlaAsnAlaLeuGlnGlyTrpSerGlnLeuGlyAlaIleLysSerLeuArgTrpThrLeuArgAla 1320  
3868 GGAAGAGCTTGGGTGACACAGAACTGGAGCATCAAACTCTCGAGGACACCAAGAGCT 3927  
1321 LeuArgProLeuArgAlaLeuSerArgPheGlnGlyMetArgValAlaValAsnAlaLeu 1340  
3928 CTGAGAGCTCTAAGACCTTATCTCATTTGGAAGGATGAGGTGGTGTGCAATGCCCTT 3987  
1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIle 1360  
3988 TTAGGAGCAATTCACATCCATGATGAAATGTGCTTGTGTTATCTGGCTAAT 4047  
1361 PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTrpThrIleAsnTrpThr 1380  
4048 TTCAGCATATGGGCTAAATTTGTTGCTGGCAAAATCTCACAGCTATTAACCCACA 4107  
1381 ThrGlyAspArgPheAspIleGlnAspValAsnAsnHisThrAspCysLeuLysLeuIle 1400  
4108 ACTGGGACAGGTTTGACATCGAAGACGTGAATATCATAGTATGCCAAAACATAATA 4167  
1401 GluArgAsnGlnThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyPhe 1420  
4168 GAAAGAAATGAGACTGCTGATGGAAATGTGAAAGTAACTTGTATATGATGATTTT 4227  
1421 GlyTrpLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetTrpAla 1440  
4228 GGGTATCTCTCTTGGCTTCAAGTGGCCATTCAAAGATGAGATTAATGAATGCA 4287  
1441 AlaValAspSerArgAsnValGluLeuGlnProLysTrpGlnGluSerLeuTrpMetTrp 1460  
4288 GCAGTTGATTCAGAAATGTGGAACCTCAGCTAAGTATGAAAGAAAGTGTATCATGTAT 4347  
1461 LeuTrpPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIleGly 1480  
4348 CTTTACTTGTATTTATTTCAATCTTTGGGTCTCTTCACTTGAACCTGTTATTTGGT 4407  
1481 ValIleIleAspAsnPheAsnGlnGlnLysLysPheGlyGlyGlnAspIlePheMet 1500  
4408 GTCATCATATGATTAATTTCAACAGCAAGAAAGAAAGTGGAGGTCAAGCATCTTTATG 4467  
1501 ThrGluGlnGlnLysLysTrpTrpAsnAlaMetLysLysLeuGlySerLysLysProGln 1520  
4468 ACAGAGAGAACAGAAATATCATATGATGAAATGAAATATGAGATCGAAAAACCGCAA 4527  
1521 LysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheValThrArg 1540  
4528 AAGCTTATACCTGACAGCAAGAAACAAATTTCAAGGAATGCTTTGACATTCGTAACCA 4587  
1541 GlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMetMetVal 1560  
4588 CAACTTTTTCACATTAACATCATCATGATTTCTCATGTGCTTAACATGTGCACAAATGATG 4647  
1561 GluThrAspAsnGlnSerGlnTrpValThrThrIleLeuSerArgIleAsnLeuValPhe 1580  
4648 GAAACATATGACAGATGATATGATGATCAATTTGTACAGCATCAATCTGGTGTTC 4707  
1581 IleValLeuPheThrGlnGlyCysValIleLysLeuIleSerLeuArgHisTrpTrpPhe 1600  
4708 ATTGCTATTTACTGGAGAGTGTGATCAACTCATCTCTACGCCATTTATTTT 4767  
1601 ThrIleGlyTrpAsnIlePheAspPheValValIleLeuSerIleValGlyMetPhe 1620  
4768 ACCATTTGATGAGATATTTTGTATTTGTGTGTCTCATTCATTTGATGATGTTT 4827  
1621 LeuAlaGluLeuIleGlyLysTrpPheValSerProThrLeuPheArgValIleArgLeu 1640  
4828 CTTCGAGAGCTGATGAAAGATATTTGTCCTTACCTTACCTGTCGAGATCCGCTT 4887  
1641 AlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgTrpLeuLeu 1660  
4888 GCTAGATTTGGCGAATCTCAGCTGATCAAGAGACCAAGGAGATCCGACGCTGCTC 4947  
1661 PheAlaLeuMetLeuSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPheLeuVal 1680  
4948 TTTGCTTTGATGATGATGCTTCTGCTGCTGTTTAACTGCGCTCACTTCCCTGATG 5007  
1681 MetPheIleTrpAlaIlePheGlyMetSerAspPheAlaTrpValLysArgGluValGly 1700  
5008 ATGTTATCTACGCATCTTGGATGTCCAACTTGTCCATGTAAAGAGGAAGTTGGG 5067  
1701 IleAspAspMetPheAsnPheGlnTrpPheGlyAsnSerMetIleCysLeuPheGlnIle 1720  
5068 ATCATGACATGTTCAACTTTGAGACCTTGGCAACAGATGATGCTATTCCTCAAT 5127  
1721 ThrThrSerIleGlyTrpAspGlyLeuLeuAlaProIleLeuAsnSerLysProProAsp 1740  
5128 ACAACCTCTGCTGGCTGGGATGATGCTAGCACCACTTCTCAACAGTAAAGCCACCCG 5187  
1741 CysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsnProSer 1760  
5188 TGTGACCATTAATAAGTTAACTCGGAAGCTCAGTTAAGGAGACGTGGGAACCATCT 5247  
1761 ValGlyIlePhePhePheValSerTrpIleIleIleSerPheLeuValValAsnMet 1780  
5248 GTTGAATTTTCTTTTGTGACATTCATCATCATATCTCTGCTGTTGGTGAACATG 5307  
1781 TyrIleAlaValIleLeuGlnAsnPheSerValAlaThrGlnGluSerAlaGluProLeu 1800  
5308 TACATGCGGTCACTCTGGAGAACTTCAGTGTGCACTGAAACAAAGTGCAGAGCCCTG 5367  
1801 SerGluAspAspPheGlnMetPheTrpGluValTrpGlnLysPheAspProAspAlaThr 1820  
5368 AGTGAAGATGACTTATGATGTTCTATGAGGTTTGGGAGAAAGTTATCCCATGCAACT 5427  
1821 GlnPheMetGluPheGlnLysLeuSerGlnPheAlaAlaAlaLeuGlnLysProLeuAsn 1840  
5428 CAGTTCATGGAATTTGAAATAATATCTCAGTTGACAGTGGCGCTTCAACCGCTTCAT 5487  
1841 LeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSerGlyAsp 1860  
5488 CTGCCCAACCAACCAACCTCCAGCTCATTTGCCATGATTTGCCCATGATGGTGTGAC 5547  
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5608 GAGATGATGCTCTACGATATACAGATGAGAAAGAGCATTCATGCTTCCATCTTCCAA 5667

QY 1901 ValSerTyrGluProIleThrThrLeuLysArgLysGluGluValSerAlaVal 1920  
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 QY 1921 IleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGlnAlaSerPhe 1940  
 DB 5728 ATTATTCACAGCGCTTACAGACGACCTTTAAAGCGAACTGTAAACAACTCTCTT 5787  
 QY 1941 ThrTyrAsnLysAsnLysIleLysGlyValAlaAsnLeuLeuIleLysGluAspMetIle 1960  
 DB 5788 AGGTACAAATAAAACAAATCAAGAGTGGCTAACTCTTATTAACAAAGACATGAGA 5847  
 QY 1961 IleAspArgIleAsnGluAsnSerIleThrGluLysThrAspLeuThrMetSerThrAla 1980  
 DB 5848 ATTGACAGATATAATGAAGCACTATACAGAAACAAAGATGACCTATGCTCATGCA 5907  
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 DB 5968 GGCAAGATGAAGAAAGCCAAAGGAAA 5994

## RESULT 7

US-09-930-871-3

Sequence 3, Application us/09930871

Patent No. US20020076780A1

GENERAL INFORMATION:

APPLICANT: Turner, C. Alexander Jr.

APPLICANT: Mathur, Daniel

APPLICANT: Mathur, Brian

TITLE OF INVENTION: No. US20020076780A1 Human Ion Channel Proteins and Polynucleot

FILE REFERENCE: Same

CURRENT APPLICATION NUMBER: US/09/930, 871

CURRENT FILING DATE: 2001-08-14

PRIOR APPLICATION NUMBER: US 60/225, 989

PRIOR FILING DATE: 2000-08-16

NUMBER OF SEQ ID NOS: 20

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3

LENGTH: 5889

TYPE: DNA

ORGANISM: homo sapiens

US-09-930-871-3

## Alignment Scores:

Pred. No.: 0 Length: 5889  
 Score: 1289.00 Matches: 1955  
 Percent Similarity: 99.14% Conservative: 0  
 Best Local Similarity: 99.14% Mismatches: 17  
 Query Match: 64.16% Indels: 17  
 Gaps: 0

US-09-930-871-12 (1-2009) x US-09-930-871-3 (1-5889)

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 QY 21 SerLeuAlaIleLeuArgArgIleLeuGluGluLysAlaLysAsnProLysProAsp 40  
 DB 61 TCTCTGGCGGCTATGAAAGACGCTTCACAGAGAAAGCAAAATCCCAACACAGAC 120  
 QY 41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60  
 DB 121 AAAAAGATGAGAGAAATGGCCCAAGCCAAATAGTGAAGCTGGAGAAAGAAC 180  
 QY 61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80  
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 DB 301 CGGTACAGTCCACACCTGCTGCTGACATTTTAACCTCCCTCAATCCTCTTAGGAAATA 360  
 QY 121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140  
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 QY 161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180  
 DB 481 TTCACAGGATATATATCTTTGATATCACTATATAAATATTTCAGAGGGGATTCGTGTTA 540  
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3808 ACCAATGCTGT 3867  
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3868 GCAATATGCTGT 3927  
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| Db | 2548 | TTTCATTGCTGGCAAGTTTCAAGTTGGCAAAATCTTGCGCCAAAGCTTAATATGCTAAT    | 2607 |
| QY | 881  | LysLleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIe    | 900  |
| Db | 2608 | AAGATCATCGGCATTTCCGTCGGGGGCGCTCTGGAAATTTAAACCTCGCTTGGCCATC     | 2667 |
| QY | 901  | ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTrpLysAspCysVal   | 920  |
| Db | 2668 | GTCCTCATTTTGGCGGCGGCGGATGACACCTCTTGGTAAAGCAACAAAGATTGTGTC      | 2727 |
| QY | 921  | CysLysLleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPheHisSer      | 940  |
| Db | 2728 | TGCAGAGTCGCAGTGTGATTCACACTCCACGCTGGCACATGATGACTCTTCCACATCC     | 2787 |
| QY | 941  | PheLeuIleValPheAargValLeuCysGlyGlnTrpIleGluThrMetTrpAspCysMet  | 960  |
| Db | 2788 | TTTCCTGATTGTGTTCCCGCTGCTGTGTGGGGAATGGATAGAGCCATGTGGGACGTGATG   | 2847 |
| QY | 961  | GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn   | 980  |
| Db | 2848 | GAGGTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCAATGGTATGGAAAC     | 2907 |
| QY | 981  | LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu   | 1000 |
| Db | 2908 | CTAATGTGCTCGAATTCCTTCTTGCGCTTGCTTMTAGCTCATTTAGTCAACAAACCTT     | 2967 |
| QY | 1001 | AlaAlaThrAspAspAspAsnGluMetCAsnAsnLeuGlnIleAlaValAspArgMetHis  | 1020 |
| Db | 2968 | GCACCACTGATGTGATGATGAAATGAAATATCTCCAAATTCCTGTGGATAGGATGCAC     | 3027 |
| QY | 1021 | LysGlyValAlaTrpValLysArgLysLleTrpGluPheIleGlnGlnSerPheIleArg   | 1040 |
| Db | 3028 | AAAGAGTAGCTTGTGTGAAAGAAAGAAATATATGATTTATTCACAGCTTCATTATGG      | 3087 |
| QY | 1041 | LysGlnLysLleLeuAspGluIleLysProLeuAspAspLeuAsnLysLysAspSer      | 1060 |
| Db | 3088 | AAACAAAGATTTAGTATGAAATTTAAACCACTTGAGATCTTAACACAGAAACACAGT      | 3147 |
| QY | 1061 | CysMetSerAsnHisTrp***GluIleGlyLysAspLeuAspTrpLeuLysAspValAsn   | 1080 |
| Db | 3148 | TGTATGTCCATCATACARAGAAATTTGGGAAAGATCTTGACTATCTTTAAAGATGTAAAT   | 3207 |
| QY | 1081 | GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTrpIleIleAspLysSer   | 1100 |
| Db | 3208 | GGAACTACAAAGTGGTATAGAACTGGCAGACAGTGTGAAGAAATACATTATGTGTAAGT    | 3267 |
| QY | 1101 | AspTrpMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly   | 1120 |
| Db | 3268 | GATTACATGTTCATTCATTAACCAACCCCACTTACTGTGCTACGTACCAATGTGCTGTA    | 3327 |
| QY | 1121 | GluSerAspPheGlnAsnLeuAsnThrGluAspPheSerSerGlnSerAspLeuGlnGlu   | 1140 |
| Db | 3328 | GAACTGTACCTTGAATTTTAAACACGGGAAGACTTTAGTAGTGAATCCGATCTGGAAACA   | 3387 |
| QY | 1141 | SerLysGlnLysLeuAsnGlnSerSerSerSerGlnGlySerThrValAspIleGly      | 1160 |
| Db | 3388 | AGCAAAAGAAACGAAATGAACCAACAGTACTCATCGAAGGTAGACATGTGGACATCGGC    | 3447 |
| QY | 1161 | AlaProValGlnGlnGlnProValValGluProGluGlnThrLeuGlnProGluAlaCys   | 1180 |
| Db | 3448 | GCACCTGTAAAGAACGCCCGCTAGTGGAACTGGAAGAACTTTGAACACGAAGCTTGT      | 3507 |
| QY | 1181 | PheThrGlnGlyCysValGlnAargPheLysCysCysGlnIleAsnValGlnGlnLysArg  | 1200 |
| Db | 3508 | TTCTCTGAAGCGCTGTGTACAAAGATTCAAGTGTGTTCATCAATCAATGTGGAAAGACGCA  | 3567 |
| QY | 1201 | GlyLysGlnTrpTrpAsnLeuAargArgTrpCysPheArgIleValGlnHisAsnTrpPhe  | 1220 |
| Db | 3568 | GGAAACAAATGTGTGAACCTGAGAAAGAGAGTGTTCGCCAATATGTTGAACATAACTGGTTT | 3627 |



|||||  
Db 5668 GTCCTACAGCAATCACTACTTAAAAAGAAAGAGAACTATCTGCTGC 5727  
OY 1921 llellelnarAlaTyrArgHisLeuLeuLysArgThrValLysGlnAAserPhe 1940  
Db 5728 ATTATTCAGCGCTTACAGAGCCCTTTTAAAGCAAGTAAAGAACTCTCTT 5787  
OY 1941 ThrTyrAsnLysAsnLysLleLysGlyLysLysLeuLeuLleLysGlnAspMetIle 1960  
Db 5788 AGTACAAATTAACAAATCAAGGTGGGCTATCTTATTAAGAAAGACATGATA 5847  
OY 1961 lleasparGileasnGlnAsnSerIleThrGluLys 1972  
Db 5848 ATTGACAGATTAATGAAACCTTATTACAGAAAA 5883

## RESULT 8

US-09-930-871-5  
; Sequence 5, Application US/09930871  
; Patent No. US20020076780A1  
; GENERAL INFORMATION:  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Mathur, Daniel  
; APPLICANT: Mathur, Brian  
; TITLE OF INVENTION: No. US20020076780A1 Human Ion Channel Proteins and Polynucleot  
; TITLE OF INVENTION: Same  
; FILE REFERENCE: LEX-0216-USA  
; CURRENT APPLICATION NUMBER: US/09/930,871  
; PRIOR FILING DATE: 2001-08-14  
; PRIOR APPLICATION NUMBER: US 60/225,989  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 4329  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-09-930-871-5

## Alignment Scores:

Pred. No.: 0 Length: 4329  
Score: 763.00 Matches: 1429  
Percent Similarity: 98.82% Conservative: 0  
Best Local Similarity: 98.82% Mismatches: 17  
Query Match: 37.98% Indels: 17  
DB: Gaps: 0

US-09-930-871-12 (1-2009) x US-09-930-871-5 (1-4329)

OY 1 MetGlnGlnThrValLeuValProProGlyProAspSerPheAsnPhetheThrArgGlu 20  
Db 1 ATGAGCAAGAGCTGCTGTACACAGAGCTGACAGCTTCACTTCTTCCAGAGAA 60  
OY 21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40  
Db 61 TCTCTGGGGCTATTGAAAGAGCAATTCAGAAAGAAAGCAAAATCCCAACCAAGAC 120  
OY 41 LysLysAspAspAspGlnAsnGlyProLysProAsnSerAspLeuGlnAlaGlyLysAsn 60  
Db 121 AAAAAAGATGACAGCAAAATGCCCCAAGCCAAATAGTACTTGAGAGCTGGAAAGAAC 180  
OY 61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGlnAspLeu 80  
Db 181 CTTCATTTATTTATGAGACATCTCCAGAGATGGTGTAGAGCCCTGGAGAGCTG 240  
OY 81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100  
Db 241 GACCCCTACTATATCAAAAGAAACTTTTATAGTATGAATTAAGGAGAGCCATCTTC 300  
OY 101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuAlaGlyIle 120  
Db 301 CGGTTCATGCGCACTCTGCGCTGTACATTTTAACTCCCTTCAATCCCTTAAGGAAATA 360  
OY 121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140

|||||  
Db 361 GCATTTAGACTTTTGGTACTTCACTTATTTACAGATGCTAATATATGCACTATTGACA 420  
OY 141 AsnCysValPheMetThrMetSerAsnProProAspTyrThrLysAsnValGluTyrThr 160  
Db 421 AACTGTGTGTATGACAAATGAGTAACCCCGATGATGAGCAAGAAATGAGATGACATACACC 480  
OY 161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180  
Db 481 TTCACAGGATATATCTTTGATCACTTATTAATAATATTCACAGGGGATCTGTGTA 540  
OY 181 GluAspPheThrPheLeuArgAspProTyrAsnThrLeuAspPheThrValIleThrPhe 200  
Db 541 GAAGATTTTACTTCTCTGGGATCCATGAGACCTGGCTGATTCACGTCACTTACATTT 600  
OY 201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220  
Db 601 GGTACGTACAGAGTTTGTGACCTGGGCAATGTCTCGGCATTTGAGAAACATTCAGAGTT 660  
OY 221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240  
Db 661 CTCGAGCAATGAAAGCAATTCAGATTCAGATTCAGGCTGAAAACCATGTGGAGAGCCCTG 720  
OY 241 lleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260  
Db 721 ATCCAGTCTGTGAGAGAGCTCTCAGATGTATATATCTGCTGTCTGTACAGCGTA 780  
OY 261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280  
Db 781 TTTGCTCTAATTTGGCTGACAGTGTTCATGCGGCACTGAGCAATTAATGATACAAATG 840  
OY 281 ProProThrAsnAlaSerLeuGlnGluHisSerIleGluLysAsnIleThrValAsnTyr 300  
Db 841 CCTCCCAACCAATGCTCTCTGGAGCAATATGATGAAGAAATATTACTGTGAATTAAT 900  
OY 301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTyrLysSerTyrIleGlnAsp 320  
Db 901 AATGTACACTTATTAATTAATGAACCTGCTTGTGACTTGTGACGACATATATTCAGAT 960  
OY 321 SerArgTyrHisTyrPheLeuGlnGlyPheLeuAspAlaLeuLeuGlyLysSerSer 340  
Db 961 TCAAGATATCATATTTCTCTGGAGGGTTTATAGATGCACTACTATGTGAAATACCTCT 1020  
OY 341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360  
Db 1021 GATGACAGGCCAATGTCACAGGATATATGTGTGAAAAGCTGTGGAATCCCAATTAAT 1080  
OY 361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380  
Db 1081 GGTACACACAGCTTGTATACCTTCACTTGTGGCTTTTGTGTCTGTGCTGCAATATGACT 1140  
OY 381 GlnAspPheTrpGlnAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400  
Db 1141 CAGGACTCTGGGAAATCTTTATCAACATGACATTAACGTGCTGGGAAACGTACAG 1200  
OY 401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420  
Db 1201 AATATTTTGTGTGTCTTTTCTTGTGGCTCATTTCTTACATATTAATTTGATCCCGGCT 1260  
OY 421 ValValAlaMetAlaTyrGlnGlnGlnAsnGlnAlaThrLeuGlnGlnLysGlnLys 440  
Db 1261 GTGGTGGCCATGGCTACAGAGACAGAAATCAGGCCACTTGGAAAGACACAGACAGAA 1320  
OY 441 GluAlaGluPheGlnGlnMetIleGlnGlnLeuLysGlnGlnGlnLysAlaGlnGln 460  
Db 1321 GAGGCCGAATTTACACAGATGATTAACAGCTTAATAAACAACAGAGAGCAGCTGACAG 1380  
OY 461 AlaAlaThrAlaThrAlaSerGlnHisSerArgGluProSerAlaAlaGlyArgLeuSer 480  
Db 1381 GCAGCAAGGCAAGTGCCTCAGACATTCACAGAGCCCAAGTGCAGCAGGAGGCTCTCA 1440  
OY 481 AspSerSerSerGluAlaSerLysLeuSerLysSerLysSerAlaLysGluArgArgAsnArg 500



Db 961 TCACATATCATTTATTTCTCGAGGGCTTTTATAGATGCACACTACTATGTGAAATAGCTCT 1020  
 QY 341 AspalaglyInCysProgluIyTyMetCysValIyAlaGlyArgAsnProAsnTyR 360  
 Db 1021 GATGACGGCCAAATGTCAGAGGGAATATATGTGTGAAAGCTGTGAGAAATCCCAATAT 1080  
 QY 361 GlyTyThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380  
 Db 1081 GGCTACACAGCTTGATACCTTCACCTGAGCTTTTCTTTCTGTTGACCTAATGACT 1140  
 QY 381 GluAspPheTrpGluAsnLeuTyRGlueuThrLeuArgAlaAlaGlyTyRThrTyMet 400  
 Db 1141 CAGGACTTCTGGGAAATCTTATACACTGACATTAAGTGTGCGGGGAAACGTACAG 1200  
 QY 401 IlePhePheValLeuValIlePheLeuGlySerPheTyRLeuIleAsnLeuIleLeuAla 420  
 Db 1201 ATATTTTGTGTGTGTATTTTCTTGGCTCATTTCTACCTAATATAATTGATCTGGCT 1260  
 QY 421 ValValAlaMetAlaTyRGlueuGluGlnAsnGlnAlaThrLeuGluGluAlaGluGln 440  
 Db 1261 GTGGTGGCCATGCGCTACAGAGAACAGATACGGCCACTTGGAAAGACAGACAGAA 1320  
 QY 441 GluAlaGluPheGluGlnMetIleGluGlnLeuTyRGlueuGluGluAlaAlaGluGln 460  
 Db 1321 GAGGCCGAATTCACAGATGATGACAGCTTAAAGAACACAGAGAGGACAGCTCAGCAG 1380  
 QY 461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480  
 Db 1381 GCAGACAGGCACTGCTCAGAACATTCACAGAGCCAGAGCCAGGCGAGCTGTCTCA 1440  
 QY 481 AspSerSerSerGluAlaSerLysLeuSerLysSerLysSerAlaLysGluArgArgAsnArg 500  
 Db 1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAGAGCGCTAAGAAAGAAAGAAATCGG 1500  
 QY 501 ArgIyLysArgGlyGluGlnGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520  
 Db 1501 AGCAAGAAACAAACAAACAAAGACAGCTGCTGGGGAAGAAAGAAAGATGAGATGAATTC 1560  
 QY 521 GlnLysSerGluSerGluAspSerIleArgArgGlyGlyPheArgPheSerIleGluGly 540  
 Db 1561 CAAAATCTGAATCTGAGAGACAGCATCAGAGAGAAAGTTTGGCTTCTCCATTTCAAGGG 1620  
 QY 541 AsnArgLeuThrTyRGlueuArgTyRSerSerProHisGlnSerLeuLeuSerIleArg 560  
 Db 1621 AACCGATTGACATATGAAAGAGTACTCTCCACACACAGACTTTTGTGAGCATCCGT 1680  
 QY 561 GlySerLeuPheSerProArgArgAsnSerArgTyRThrSerLeuPheSerPheArgGlyArg 580  
 Db 1681 GGTCTCCCTATTTTCAACCAAGCGAATAGCAGAACACAGCTTTTCAAGCTTATAGAGGGCA 1740  
 QY 581 AlaLysAspValIySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600  
 Db 1741 GCAAAAGATGTGGATCTGAGAACACACTTCGACATGTGACACAGACACCTTTTCAGAT 1800  
 QY 601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620  
 Db 1801 AACAGAGCCCTAGAGATCTCTTGTGTGTGCTGCCCGACACACAGAGAGACAGCACAGCC 1860  
 QY 621 AsnLeuSerGluThrSerArgSerSerArgMetLeuAlaValPheProAlaAsnGlyLys 640  
 Db 1861 AACCTGAGTCAGACACAGTAGTCAATCCCGATGCTGCGCAGTGTTCACGCAATGGGAG 1920  
 QY 641 MethHisSerThrValAspCysAsnGlyValAlaSerLeuValIyGlyProSerValPro 660  
 Db 1921 ATGTGACAGCAGCTGTGATGCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1980  
 QY 661 ThrSerProValIyGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680  
 Db 1981 ACATCGCTGTGTG--G--A--C--A--G--C--T--T--C--T--G--C--C--A--G-- 2008  
 QY 681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerPheHisValSer 700

Db 2009 AG-GGAACACACCTGAAATGAAATGAGAAAGAGAGTCAATGCTTCCAGCTTCC 2067  
 QY 701 MetAspPheLeuGluAspProSerGlnArgGlnAlaGluMetSerIleAlaSerIleLeu 720  
 Db 2068 ATGACTTTCTAGAGATCTCTTCCAAAGGCAACGACAGCATGATATACACAGCATTTCA 2127  
 QY 721 ThrAsnThrValIyGluGluGluGluSerArgGlnLysCysProProCysTrpTyR 740  
 Db 2128 ACATATACAGTGAAGAACTTGAAAGATTCAGAGCAAGAAATGCCACCTGTGTGTATA 2187  
 QY 741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyRTrpLeuLysValIyHisVal 760  
 Db 2188 TTTTCCAAATATCTTATATCTGAGACGTGTCTCATATATGTTTAAATGAAACATGTT 2247  
 QY 761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780  
 Db 2248 GTCAACCGGTGTGATGACCATATTTGTGACCTGGCCATCATCATCTGTATGCTTA 2307  
 QY 781 AsnThrLeuPheMetAlaMetGluHisTyRProMetThrAspHisPheAsnAsnValLeu 800  
 Db 2308 AATACTTCTTTCAGGCGCATGAGCATATCCAAATGAGGACCATTTCAATATGTGCTT 2367  
 QY 801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820  
 Db 2368 ACAGTAGGAACCTTGCTTTCACCTGGATCTTTACAGCAGAAATGTTCTGAAATATAT 2427  
 QY 821 AlaMetAspProTyRTrpTyRThrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840  
 Db 2428 GCCATGATCTCTTACTATATTTTCCAAAGGCTGGAATATCTTGACGGTTTATTTG 2487  
 QY 841 ThrLeuSerLeuValGluGluGlyLeuAlaAsnValIyGlyLeuSerValLeuArgSer 860  
 Db 2488 ACGCTTACCTCTGAGTACACTTGACCTGCCAATGTGGAAGGTTATCTGTCTCCGTTA 2547  
 QY 861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880  
 Db 2548 TTTTCGATTGTGCGAGTTTTCAGGTGCAAAATCTTGCCCAACTTAAATATGCTAATA 2607  
 QY 881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900  
 Db 2608 AAGATCATCGGCATATCCGTGGGGCTCTGGAAATTTAAACCTCTGTGGCCATATC 2667  
 QY 901 ValPheIlePheAlaValAlaIyMetGlnLeuPheGlyLysSerTyRAspCysVal 920  
 Db 2668 GTCTTCATTTTTCGCGGTGCTGCGCATGCACTTTGTGTAAGGTACAAATATGTGTC 2727  
 QY 921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPheHisSer 940  
 Db 2728 TGCAAGATCGCCAGATGTGCACTCCACGCTGCCACATGATGACTTCTCCACTCC 2787  
 QY 941 PheLeuIleValPheArgValLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 960  
 Db 2788 TTTCTGATGTGTGCTCCGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2847  
 QY 961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValIleGlyLysn 980  
 Db 2848 GAGGTGCTGCTCAACCATATGCTTACTCTTCAAGATGATGATGATGATGATGATGATG 2907  
 QY 981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu\*\*SerSerPheSerAlaAspAsnLeu 1000  
 Db 2908 CTACTGTGCTGATATCTTCTTCTGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2967  
 QY 1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020  
 Db 2968 GCAGCCACCTGATGTGATATGAAATGATATATCTCCAAATGCTGTGGAGATGATGATG 3027  
 QY 1021 LysGlyValAlaTyRValLysArgLysIleTyRGlueuPheIleGlnSerPheIleArg 1040  
 Db 3028 AAAGGATGACTTATGTGAAAGAAATATATATATATATATATATATATATATATATAT 3087  
 QY 1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysAspSer 1060  
 Db 3088 AAACAAAGATTTTATGATGAAATTAACCACTTATGATGATGATGATGATGATGATGAT 3147

QY 1221 GluThrPheIleValPheMetIleLeuIleuSerSerGlyAlaLeuAlaPheGluAspIle 1240  
 DB 3628 GAAACCTTCATGTTTTCATGATTCCTCTAGTAGTGGTGTCTGGCATTTGAAGATATA 3687  
 QY 1241 TyrIleAspGlnArgIleYsrIleYsrThrMetLeuGluYrAlaAspIleValPheThr 1260  
 DB 3688 TATATGATCATGCGAAGAGATTAAGCATGTGGAAATAGCTGACAAAGTTTCCACT 3747  
 QY 1261 TyrIlePheIleLeuGluMetIleuLeuIleYsrValAlaYrGlyYrGlnThrThrPhe 1280  
 DB 3748 TACATTTTCATTCGTGAAAGCTTCTAAAGGGGTGGCAATAGGCTATCAACATATTTTC 3807  
 QY 1281 ThrAsnAlaIlePyrCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300  
 DB 3808 ACCAATGCCGTGGTGTGGTGGCTCTTATATTTGATGTGTTGATGGTTAAACA 3867  
 QY 1301 AlaAsnAlaLeuGluYrYsrSerGluLeuGlyAlaIleYsrSerLeuArgThrLeuArgAla 1320  
 DB 3868 GCAAAATGCCCTGGGTACTCAGAACTTGAGCCATCAATCTCTCAGGACACTAAGACT 3927  
 QY 1321 LeuArgProLeuArgAlaLeuSerArgPheGluGluMetArgValAlaValAsnAlaLeu 1340  
 DB 3928 CTAGAGACCTCTAAGAGCTTATCTGCAATTTGAAAGGATGAGGGGTGGTGAATGCCCTT 3987  
 QY 1341 LeuGlyAlaIleProSerIleMetAsnValIleuLeuValCysLeuIlePheThrIleuIle 1360  
 DB 3988 TTAGGACCATTTCCATCCATCATGAAATGTCTTGTGGTTGTCTTAATTTCTGGCTTAAT 4047  
 QY 1361 PheSerIleMetGlyValAsnLeuPheAlaGlyYsrPheYrHisCysIleAsnThrThr 1380  
 DB 4048 TTCAGCATCATGGGCGGCAATTTGTGTGGCAATTTCAACCATGATTAACACACACA 4107  
 QY 1381 ThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuYsrLeuIle 1400  
 DB 4108 ACTGGTGACGGTTTGGACATCGAAGAGGTGAATATCATCTGATTCCTGCTAACTATA 4167  
 QY 1401 GluArgAsnGluThrAlaArgTrpIleAsnValIleValAsnPheAspAsnValGlyPhe 1420  
 DB 4168 GAAAGAAATACAGACTGCTCATGGAATAATGTGAAAGTAACTTTGATATGTAGGATTT 4227  
 QY 1421 GlyTyrLeuSerLeuLeuGluValAlaThrPheYsrGlyYrMetAspIleMetYrAla 1440  
 DB 4228 GGGTATCTCTCTTGGCTCAAGTGCACATTCAAAGATGATGATATATGATGACA 4287  
 QY 1441 AlaValAspSerArgAsn 1446  
 DB 4288 CAGATTGATTCAGAAAT 4305

## RESULT 9

US-09-930-871-7

Sequence 7, Application US/09930871

Patent No. US20020076780A1

GENERAL INFORMATION:

APPLICANT: Turner, C. Alexander Jr.

APPLICANT: Mathur, Daniel

APPLICANT: Mathur, Brian

TITLE OF INVENTION: No. US20020076780A1 Human Ion Channel Proteins and Polynucleoti

FILE REFERENCE: LEX-0216-USA

CURRENT APPLICATION NUMBER: US/09/930/871

PRIOR APPLICATION NUMBER: US 60/225,989

PRIOR FILING DATE: 2000-08-16

NUMBER OF SEQ ID NOS: 20

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 7

LENGTH: 4146

TYPE: DNA

ORGANISM: homo sapiens

US-09-930-871-7

Alignment Scores:

Pred. No.: 0

Length:

4146

Score: 701.00 Matches: 1367  
 Percent Similarity: 98.77% Conservative: 0  
 Best Local Similarity: 98.77% Mismatches: 17  
 Query Match: 34.89% Indels: 17  
 DB: 10 Gaps: 0

US-09-930-871-12 (1-2009) x US-09-930-871-7 (1-4146)

QY 1 MetGluGlnThrValIleuValIleProGluYrProAspSerPheAsnPheThrArgGlu 20  
 DB 1 ATGAGAGCAAAAGCTGCTTGTACCAACAGACCTGACACCTTCAACTTTCACACAGAA 60  
 QY 21 SerIleuAlaIleGluArgArgIleAlaGluGluYsrAlaYsrProAspProAsp 40  
 DB 61 TCTCTTGGCTTATTTGAAAGAGCAATGTCAGAGAAAGGCAAGAAATCCCAACCAAGAC 120  
 QY 41 LysIleAspAspAspGluAsnGlyProIleProAsnSerAspLeuGluAlaGlyAsn 60  
 DB 121 AAAAAGATGACGAGCAAAATGGCCAAAGCCAAATAGTACTTGGAAAGCTGGAAGAAC 180  
 QY 61 LeuProPheIleYrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80  
 DB 181 CTTCATTTATTTATGAGACATTCCTCCAGACATGTGTCCAGAGCCCTGAGGACCTG 240  
 QY 81 AspProYrYrIleAsnYsrThrPheIleValIleuAsnYsrGlyYsrAlaIlePhe 100  
 DB 241 GACCCCTACTATATCAATAAAGAAACTTTATATATGAAATGAAGGAGGACCATCTTC 300  
 QY 101 ArgPheSerAlaThrSerAlaLeuYrIleuThrProPheAsnProLeuArgLysIle 120  
 DB 301 CGGTGATGTCACCTGCTGCCCTGATTAATCTCCCTTCAATCTCTTATGAAATA 360  
 QY 121 AlaIleYsrIleuValHisSerIlePheSerMetLeuIleMetCysThrIleuThr 140  
 DB 361 GCTATTAAGATTTTGTATCATTTATTCAGATGCTAATATATGACATATTTTGACA 420  
 QY 141 AsnGlyValPheMetThrMetSerAspProProAspTrpThrIleAsnValGluYrThr 160  
 DB 421 AACTGTGTGTTAGACAATGATGATACCTCTCTATTTGGACAAAGAAATGATGAATACCC 480  
 QY 161 PheThrGlyIleYrThrPheGluSerLeuIleYsrIleIleAlaArgGlyPheCysLeu 180  
 DB 481 TTCACAGAAATATATCTTTGATCACTATTAATAATATATGACAGGATTTCTGTTA 540  
 QY 181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200  
 DB 541 GAGATTTTACTTCTCTCGGATCCATGGAACCTGCTCATTTCACTGATTAACATTT 600  
 QY 201 AlaTrpValThrGluPheValAspLeuGlyAsnValSerIleAlaArgTrpPheArgVal 220  
 DB 601 GCGTAGCTCACAGAGTTGTGGACCTGGCAATGCTCGCATTTGAGAACTTCAGAGTT 660  
 QY 221 LeuArgAlaLeuYsrThrIleSerValIleProGlyLeuYsrThrIleValGlyAlaLeu 240  
 DB 661 CTCGAGCATGGAAGAGATTTGATGATCCAGGCTGAAAACATTTGGGGGCCCTG 720  
 QY 241 IleGlnSerValYsrYsrLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260  
 DB 721 ATCCAGCTCTGTGAAGAGCTCTCAGATGATATGATCTGACTGTCTGTGAGCGTA 780  
 QY 261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnYsrIleGlnTrp 280  
 DB 781 TTGCTTAAATTTGGCTGACGCTGTATGATGGCACTGAGGAAATATGATATCAATGG 840  
 QY 281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluYsrAsnIleThrValAspYr 300  
 DB 841 CCTGCCACCAATGCTCTCTGGAGAACATATGATATGATATTAATCTGTAATAT 900  
 QY 301 AsnGlyThrIleuIleAsnGluThrValPheGluPheAspTrpYsrYrIleGlnAsp 320  
 DB 901 AATGTACACTTATTAATGAAGAACTGCTTACATTTGACATGAGATCATATATCAAGAT 960  
 QY 321 SerArgTrpHisYrPheLeuGluGlyPheLeuAspAlaLeuLeuYsrGlyAsnSerSer 340

QY 221 LeuArgAlaLeuYThrIleSerValIleProGlyLeuYThrIleValAlaLeu 240  
 |||||  
 Db 661 CTCGGAGCAATGAGACGATTCAGTCATCCAGCCCTGAACCATGTCGGAGCCCTG 720  
 QY 241 IleGlnSerValIlySylsLeuSerAspValMetIleIleuThrValPheCysLeuSerVal 260  
 |||||  
 Db 721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTATATGATCCTGACGTGTCTCTGAGAGCTA 780  
 QY 261 PheAlaLeuIleGlyLeuGlnIleuPheMetGlyAsnLeuArgAsnYsCysIleGlnTrp 280  
 |||||  
 Db 781 TTTGCTCTAATGGCTGAGCTGTTCATGGCAACCTGAGGAATAAATATTAACAATGG 840  
 QY 281 ProProThrAsnAlaSerLeuGlnIleuHisSerIleGlyAsnIleThrValAsnTrp 300  
 |||||  
 Db 841 CCTCCACCAATGCTCTTCCTGGAGGAACATATATAGAAAAGATATATACCTGCAATTA 900  
 QY 301 AsnGlyThrLeuIleAsnGlnTrpValPheGluPheAspTrpIlySerTrpIleGlnAsp 320  
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 Db 901 AATGGTACACTATTAATGAAGAACTGCTTGAATTCAGTGAAGATATATATCAAGAT 960  
 QY 321 SerArgTrpHisTrpPheLeuGlnIlyPheLeuAspAlaLeuLeuYsGlyAsnSerSer 340  
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 Db 961 TCAAGATATATATATCTCTGAGGGGTTTTTGTATGACACTATATGTGGAATATAGCTCT 1020  
 QY 341 AspAlaGlyValIleCysProGlnIlyTrpMetCysValIlySylsAlaGlyArgAsnProAsnTrp 360  
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 Db 1021 GATGCGAGCCCAATGTCACAGAGCATATATGTGTGAAACCTGTGTGAATATCCCAATTA 1080  
 QY 361 GlyTrpTrpSerPheAspTrpPheSerTrpAlaPheLeuSerLeuPheArgLeuMetTrp 380  
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 Db 1081 GGCTACACAAGCTTGTATACCTTCAGTGTGGCTTTTGTCTGTTGTCACATTAAGACT 1140  
 QY 381 GlnAspPheTrpGlnAsnLeuTrpGlnIleuThrLeuArgAlaAlaGlySylsTrpTrpMet 400  
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 Db 1141 CAGGACTTCTGGAAATCTTTATCAACATGACATTCAGTCTCTGGGAAACAGTCAATG 1200  
 QY 401 IlePhePheValIleuValIlePheLeuGlySerPheTrpIleuIleAsnLeuIleAla 420  
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 Db 1201 AATATTTTGTGTGTCTATTTCTTCTGGGCTCTTCTACTAATTAATTTGATCCGTGCT 1260  
 QY 421 ValValAlaMetAlaTrpGlnIleuGlnAsnGlnAlaThrLeuGlnIleuAlaGlnIlySyls 440  
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 Db 1261 GTGGTGCCCATGGCTTCAGAGCAAGAAATCAAGCCACCTTGGAGAGCAAGCAAGAAA 1320  
 QY 441 GlnAlaGlnPheGlnIleuMetIleGlnIleuIlySylsGlnIleuAlaAlaGlnIleu 460  
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 Db 1321 GAGGCCGAATTTTCAGAGATGATTTGAACAGCTTAAAGCAACAGGAGGCTCAGCAG 1380  
 QY 461 AlaAlaThrAlaThraIaSerGlnHisSerArgGluProSerAlaAlaGlyArgLeuSer 480  
 |||||  
 Db 1381 GCAGCAAGCGCAACTGCTCAGAACATTCAGAGAGCCCAAGTCCAGCAGGAGGCTCTCA 1440  
 QY 481 AspSerSerSerGlnAlaSerIlySylsLeuSerSerIlySylsAlaGlyArgArgAsnArg 500  
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 Db 1501 AGGAAGAAAAGAAAAGAAAAGAGCTGTGTGGGGAAGAAAAGATGGATGGATTAATTC 1560  
 QY 521 GlnIlySerGlnSerGlnAspSerIleArgArgIlySylsPheArgPheSerIleGlnIly 540  
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 Db 1561 CAAAATCTGATCTGAGAGACAGCATCAGAGAGAAAGTTTTCGCTTCCATTTGAAGG 1620  
 QY 541 AsnArgLeuThrTrpGlnIlySylsArgTrpSerSerProHisGlnSerLeuSerIleArg 560  
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 Db 1621 AACCCATTGACATGATGAAAAGAGGTACTCTCCACACACAGCTTTGTTGACATCCGT 1680  
 QY 561 GlySerLeuPheSerProArgArgAsnSerArgTrpSerLeuPheSerPheArgGlyArg 580  
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 Db 1681 GGCTCCCTATTTTTCACCAAGGGGAAATAGCAGAAACAGCTTTTACGCTTTAGAGGGGCA 1740  
 QY 581 AlaIlyAspValAlaGlySerGlnAsnAspPheAlaAspAspGlnHisSerThrPheGlnAsp 600

Db 1741 GCAAGAGATCTGGATGTGAAACGACTTGCAGATGATAGACACACCTTTGAGAT 1800  
 QY 601 AsnGlnSerArgArgAspSerLeuPheValProArgArgIlySylsIleuArgArgAsnSer 620  
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 Db 1801 AACGAGAGCCGTAGAGATCTCTGTTGTGCCCCGAGACAGAGAGAGAACCAACAGC 1860  
 QY 621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaAlaPheProAlaAsnGlyIlySyls 640  
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 Db 1861 AACCTGAGTCAGACCACTAGATCCGATCCGATGCTGGCACTGTTCCAGGAATGGAG 1920  
 QY 641 MetHisSerThrValAspCysAsnGlyValAlaSerLeuValGlyIlyProSerValPro 660  
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 Db 1921 ATGCACAGCAGCTGATTCATATGCTGTGCTTCTCTGTTGTGGACCTTCAGTTCCT 1980  
 QY 661 ThrSerProValGlyIleuLeuProGlnValIleIleAspIlyProAlaTrpAspAsp 680  
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 Db 1981 ACATCGCCCTTGG--G--A--C--A--G--C--T--C--T--G--C--C--A--G-- 2008  
 QY 681 AsnGlyThrThrTrpGlnIleuThrGlnMetArgIlyArgArgSerSerPheHisValSer 700  
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 Db 2009 AG--GGAACAACCACTGAACCTGAATGAGAAAGAGAGGCAAGTCTTCCACGTTTCC 2067  
 QY 701 MetAspPheLeuGlnAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720  
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 Db 2068 ATGACCTTTCTAAGACATCTTCCCAAGGCAAGGCAAGCAATGAGATAGCCAGATTTCA 2127  
 QY 721 ThrAsnThrValGlnIleuGlnIleuSerArgGlnIlySylsCysProCysTrpIlySyls 740  
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 Db 2128 ACAATATACACTAGACAGAACTTGAAGATCCAGGACAGAAAGCCACCTTGTGTATTA 2187  
 QY 741 PheSerAsnIlePheLeuIleTrpAspCysSerProTrpTrpLeuIlySylsValIlyHisVal 760  
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 Db 2188 TTTTCCAACTATCTTAACTATCTGGACTGTTCCTCAATATGGTAAAGGAAACAATGTT 2247  
 QY 761 ValAsnLeuValAlaMetAspProPheValAspLeuAlaIleThrIleCysIleValIleu 780  
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 Db 2248 GTCAACTGCTGTGTGATGACCACTTGTGTGACCTGCCATCCATCTTATATGCTTA 2307  
 QY 781 AsnThrLeuPheMetAlaMetGlnHisTrpProMetThrAspHisPheAsnValIleu 800  
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 Db 2308 AATACCTTTTCACTGAGCAGAGCACTATCCAAATGACGAGACCATTTCAATATATGCTT 2367  
 QY 801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGlnMetPheLeuIlyIle 820  
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 Db 2368 ACAGTGGAAACATGTTGTTCACTGGAGATCTTACAGCAGAAATGTTTCAAAATTAAT 2427  
 QY 821 AlaMetAspProTrpTrpTrpPheGlnIleuGlyTrpAsnIlePheAspGlyPheIleVal 840  
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 Db 2428 GCCATGATCTTACTATTAATTTTCCAAAGAGCTGCAATATCTTGAACGTTTATATG 2487  
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 Db 2488 ACCTTAGGCTGTGTAGAACTTGAGCTGCCAATGTGAAGATTAATCTGTTCCTGCTCA 2547  
 QY 861 PheArgLeuLeuArgValPheIlySylsAlaIlySerTrpProThrLeuAsnMetLeuIle 880  
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 Db 2548 TTTGATGTGCTGGAGATTTTCAAGTTGGCAAAATCTTGGCAACGTTAAATATGCTTAATA 2607  
 QY 881 IlyIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValIleuAlaIleIle 900  
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 Db 2608 AAGATATGCGCATTCCTCGGGGGCTGTGGGAATTAATTAACCTGCTTGGCCATCAATC 2667  
 QY 901 ValPheIlePheAlaValAlaGlyMetGlnIleuPheGlyIlySerTrpIlySylsCysVal 920  
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 Db 2668 GTCTTCAATTTTGGCCGTGGTCGAGCAGCTCTTGTGTAAGAGTAAAGATGATGTGTC 2727  
 QY 921 CysIlyIleAlaSerAspCysGlnIleuProArgTrpHisMetAsnAspPhePheHisSer 940  
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 Db 2728 TGCAGATGCCAGATGATGTCAATCCACAGCTGGCAATGAATATCACTTCCACTCC 2787  
 QY 941 PheLeuIleValPheArgValLeuCysGlyIleuTrpIleGlnThrMetTrpAspCysMet 960

QY 1061 CyswSerSerAsnHisThr\*\*\*\*GluIleGlyLysAspLeuAspTyrIleuLysAspValAsp 1080  
 DB 3148 TGAATGTCATCATACACAGAAATGGGAAAGATCTTGACTATCTTAAGAGATGAAT 3207  
 QY 1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100  
 DB 3208 GGAACATCAAGTGTATAGAGACAGCGAGCTGTGAAAATATCATTTATGATGAAGCT 3267  
 QY 1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120  
 DB 3268 GAATACATGTCATCAATCAAAACACCCAGCTTACTGTACTGACCAATGCTGTAGGA 3327  
 QY 1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerGluSerGluAspLeuGlu 1140  
 DB 3328 GAATGTCATCTGAAAATTTAAACACGAAAGACTTATGATGTAAGATGATGGAAGAA 3387  
 QY 1141 SerLysGluLysLeuAsnGluSerSerSerSerGluGlySerThrValAspIleGly 1160  
 DB 3388 AGCAAGAGAAACGATGATGAAGAGAGCTCATCAGACAGATGACATGCGCATCGGC 3447  
 QY 1161 AlaProValGluGluGluProValValGluProGluGluThrLeuGluProGluAlaCys 1180  
 DB 3448 GCACTCTAGACAGAACGCCCGTAGCTGAACTGAAACAACTCTTGAACAGAGCTTGT 3507  
 QY 1181 PheThrGluGlyCysValGluArgPheLysCysGluIleAsnValGluGluLysArg 1200  
 DB 3508 TTACTCTGAAGGCTGTGTACAAAGTTCAAGTGTGTCAAAATCATGTGGAAGAGGAGA 3567  
 QY 1201 GlyLysGluThrPyrAsnLeuArgThrCysPheArgIleValGluHisAsnTyrPhe 1220  
 DB 3568 GGAACAAATGCGTGAACCTGAGAGAGAGCTGTTCCGAATGATGAACTAATCTGTTT 3627  
 QY 1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240  
 DB 3628 GAGACCTCTCTGTTTCAAGATCTCTCTAGAGTGTCTCTGCGATTTGGAAGATATA 3687  
 QY 1241 TyrIleAspGluThrLysThrIleLysThrMetLeuGluThrAlaAspLysValPheThr 1260  
 DB 3688 TAAATTCATCAGCGAAAGAGATTAAGACATGTTGGAATATCTGACAGAGTTTCTACT 3747  
 QY 1261 TyrIlePheIleLeuGluMetLeuLeuLysTyrValAlaTyrGlyThrThrTyrPhe 1280  
 DB 3748 TACATTTTCACTCTGGAATGCTTCTTAATGGGTGGCATATGCGATCAACATATTC 3807  
 QY 1281 ThrAsnAlaTyrPyrAsnLeuAspPheIleValAlaAspValSerLeuValSerLeuThr 1300  
 DB 3808 ACCAATGCTGTGTGGTGGCTGACTCTTAATGTTGATGTTTCAATGTCAGTTTAAACA 3867  
 QY 1301 AlaAsnAlaLeuGlyLysThrGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320  
 DB 3868 GCAAAATGCTGTGGTACTCAGAACCTTGAGCCATCAATCTCTCAGAGACATGAAGCT 3927  
 QY 1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValAlaAsnAlaLeu 1340  
 DB 3928 CTCAGAGCTCTTAGAGCTTATCTCGATTTGAAGGATGAGGTGGTGGATGTCCTT 3987  
 QY 1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheThrPheIle 1360  
 DB 3988 TTAGAGCAATTCATCATTCAATCAAGATGCTCTGCTGTGTATATCTGCGTAATTT 4047  
 QY 1361 PheSerIleMetGlyAlaAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThr 1380  
 DB 4048 TTCAGCATCATGGCGCTAAATTTGTTGCTGGCAATTTCAACACTGTATTAACACACACA 4107  
 QY 1381 ThrGlyAspArg 1384  
 DB 4108 ACTGCTGACAGG 4119

RESULT 10  
 US-09-930-871-9  
 ; Sequence 9, Application US/09930871  
 ; Patent No. US20020076780A1

; GENERAL INFORMATION:  
 ; APPLICANT: Turner, C. Alexander Jr.  
 ; APPLICANT: Mathur, Daniel  
 ; APPLICANT: Mathur, Brian  
 ; TITLE OF INVENTION: No. US20020076780A1el Human Ion Channel Proteins and Polynuci  
 ; FILE REFERENCE: Same  
 ; CURRENT APPLICATION NUMBER: US/09/930,871  
 ; PRIOR FILING DATE: 2001-08-14  
 ; PRIOR APPLICATION NUMBER: US 60/225,989  
 ; NUMBER OF SEQ ID NOS: 20  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 9  
 ; LENGTH: 4164  
 ; TYPE: DNA  
 ; ORGANISM: homo sapiens  
 ; US-09-930-871-9  
 Alignment Scores:  
 Pred. No.: 0 Length: 4164  
 Score: 670.00 Matches: 1317  
 Percent Similarity: 98.73% Conservative: 0  
 Best Local Similarity: 98.73% Mismatches: 17  
 Query Match: 33.35% Indels: 17  
 DB: 10 Gaps: 0  
 US-09-930-871-12 (1-2009) x US-09-930-871-9 (1-4164)  
 QY 1 MetGluGluThrValLeuValProProGlyProAspSerPheAsnPheThrArgGlu 20  
 DB 1 ATGAGCAAAACAGTCTCTTGACCAACAGAGCTGACAGCTTCACTTCTTACCAGAGAA 60  
 QY 21 SerLeuAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40  
 DB 61 TCTCTGGCGCTATGAAAGACGATTCGAGAGAAAGCAAGAGATCCCAACAGAC 120  
 QY 41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60  
 DB 121 AAAAAAGATGACAGCAAAATGGCCCAAGCCAAATAGTACTTGGAAGCTGGAAGAAC 180  
 QY 61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80  
 DB 181 CTTCATTTATTTATGAGAGCATCTCTCCAGAGATGTGTGACAGCCCTGGAGGACTG 240  
 QY 81 AspProTyrTyrIleAsnLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100  
 DB 241 GACCCCTACTATATCAATGAAGAACTTTATAGTATGATGAATGAAGGAGGCACTTC 300  
 QY 101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120  
 DB 301 CGGTTAGTGCACCTGTGCTGCAATTTTAATCCCTCAATCTCTTAGGAAATA 360  
 QY 121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140  
 DB 361 GCATTTAAGATTTTGGTATCATTCATTTATTCAGCATCTAATTAATGCGCACTATTGGACA 420  
 QY 141 AsnCysValPheMetThrMetSerAsnProProAspTyrThrLysAsnValGluTyrThr 160  
 DB 421 AACTGTGTATATGACATGATGATACCTCCGATTTGACAAAGAAATGAGAAATACACC 480  
 QY 161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180  
 DB 481 TTACAGCAATATATATCTTTGATCATCTATTAATAAATTAATGCAAGGGAATCTGTTTA 540  
 QY 181 GluAspPheThrPheLeuArgAspProTyrAsnTyrLeuAspPheThrValIleThrPhe 200  
 DB 541 GAAAGATTTACTTCTCTGGATTCATGCACTGCACTGCTGATTTCTGCTCATATATTT 600  
 QY 201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220  
 DB 601 GGTACGTACAGAGATTTGTGAGACCTGGCAATGTCTCGGCAATTTGAGAACATTCAGAGTT 660









Db 435 AGAGGTGACCGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGTTCTAGGA 376

PRIOR APPLICATION NUMBER: 2001-01-01

ORGANISM: Rattus norvegicus  
FEATURE:  
OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM\_013119  
US-09-917-800A-1604

## Alignment Scores:

|                        |          |               |      |
|------------------------|----------|---------------|------|
| Pred. No.:             | 1.55e-90 | Length:       | 6822 |
| Score:                 | 99.00    | Matches:      | 99   |
| Percent Similarity:    | 100.00%  | Conservative: | 0    |
| Best Local Similarity: | 100.00%  | Mismatches:   | 0    |
| Query Match:           | 4.938    | Indels:       | 0    |
| DB:                    | 10       | Gaps:         | 0    |

US-09-930-871-12 (1-2009) x US-09-917-800A-1604 (1-6822)

OY 1598 TyrTyrPheThrIleGlyTyrPheAsnIlePheAspPheValValIleIleuSerIleVal 1617  
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DB 5013 TACTACTTCACGATAGGGGAGAACATCTTGACTTGTGTGTGATCTCTCGATTGTA 5072  
OY 1618 GlyMetPheLeuAlaGluLeuIleGluLysTyrPheValSerProThrIleuPheArgVal 1637  
|||||  
DB 5073 GGAATGTTTCGCGAGACTGATAGAGATTTGTTGTTCCCTACCTGTTCCGAGTC 5132  
OY 1638 IleArgLeuAlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArg 1657  
|||||  
DB 5133 ATCCGCTGGCCAGATGGAGCATCTACGCCCTGATCAAGGCCCAAGGGGATCCGC 5192  
OY 1658 ThrIleuPheAlaLeuMetMetSerLeuProAlaLeuPheAsnIleGlyLeuLeu 1677  
|||||  
DB 5193 ACTCGCTCTTGGCTTGTATGATGTCCTTCCTGCGCTGTTCAACATCGGCTCCTGCTT 5252  
OY 1678 PheLeuValMetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLys 1696  
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DB 5253 TTCCGGTCATGTCATCTACGCCATCTTTGGGATGTCACACTTGGCTAAGTTAA 5309

Search completed: April 23, 2003, 10:35:09  
Job time : 713 secs

GenCore version 5.1.4-p5\_4578  
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## OM nucleic - nucleic search, using sw model

Run on: April 22, 2003, 06:22:18 ; Search time 10003 Seconds

(Without alignments)  
17543.729 Million cell updates/sec

Title: US-09-930-871-11

Perfect score: 6030

Sequence: 1 atggagcaacaagctgtgtf.....aaaagcaagaaggaataa 6030

Scoring table:

IDENTITY\_NNC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:\*

- 1: gb\_da:\*
- 2: gb\_hcg:\*
- 3: gb\_in:\*
- 4: gb\_ov:\*
- 5: gb\_ov:\*
- 6: gb\_pat:\*
- 7: gb\_ph:\*
- 8: gb\_pl:\*
- 9: gb\_pr:\*
- 10: gb\_ro:\*
- 11: gb\_sts:\*
- 12: gb\_sy:\*
- 13: gb\_un:\*
- 14: gb\_vl:\*
- 15: em\_ba:\*
- 16: em\_fun:\*
- 17: em\_hum:\*
- 18: em\_in:\*
- 19: em\_mu:\*
- 20: em\_om:\*
- 21: em\_or:\*
- 22: em\_ov:\*
- 23: em\_pat:\*
- 24: em\_ph:\*
- 25: em\_pl:\*
- 26: em\_ro:\*
- 27: em\_sts:\*
- 28: em\_un:\*
- 29: em\_vl:\*
- 30: em\_hcg\_hum:\*
- 31: em\_hcg\_inv:\*
- 32: em\_hcg\_other:\*
- 33: em\_hcg\_mus:\*
- 34: em\_hcg\_pin:\*
- 35: em\_hcg\_rtd:\*
- 36: em\_hcg\_mam:\*
- 37: em\_hcg\_vrt:\*
- 38: em\_sy:\*
- 39: em\_hggo\_hum:\*
- 40: em\_hggo\_mus:\*
- 41: em\_hggo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score  | Query Match | Length | DB ID       | Description        |
|------------|--------|-------------|--------|-------------|--------------------|
| 1          | 6028.8 | 100.0       | 6030   | 6 AX391140  | AX391140 Sequence  |
| 2          | 6015.2 | 99.8        | 8378   | 6 AX164171  | AX164171 Sequence  |
| 3          | 5963.2 | 98.9        | 8378   | 6 AX164172  | AX164172 Sequence  |
| 4          | 5952.8 | 98.7        | 5997   | 6 AX391130  | AX391130 Sequence  |
| 5          | 5941.2 | 98.5        | 6046   | 6 AY043484  | AY043484 Homo sapi |
| 6          | 5917.4 | 98.1        | 8131   | 9 AF225985  | AF225985 Homo sapi |
| 7          | 5915.8 | 98.1        | 5932   | 6 AX391142  | AX391142 Sequence  |
| 8          | 5839.8 | 96.8        | 5889   | 6 AX391132  | AX391132 Sequence  |
| 9          | 5062.4 | 84.0        | 8398   | 10 RATNCP1R | X03638 Rat brain m |
| 10         | 5062.4 | 84.0        | 8399   | 10 RATNCP1R | M22253 Rat brain m |
| 11         | 4336.8 | 71.9        | 4362   | 6 AX391144  | AX391144 Sequence  |
| 12         | 4260.8 | 70.7        | 4339   | 6 AX391134  | AX391134 Sequence  |
| 13         | 4219   | 70.0        | 8349   | 6 AX164203  | AX164203 Sequence  |
| 14         | 4219   | 70.0        | 8349   | 6 AX164204  | AX164204 Sequence  |
| 15         | 4217.4 | 69.9        | 6328   | 9 HUMHBA1X  | M94055 Human volta |
| 16         | 4150.8 | 68.8        | 4179   | 6 AX391146  | AX391146 Sequence  |
| 17         | 4074.8 | 67.6        | 4146   | 6 AX391136  | AX391136 Sequence  |
| 18         | 4057.8 | 67.3        | 4197   | 6 AX391148  | AX391148 Sequence  |
| 19         | 4045   | 67.1        | 9123   | 9 AF225987  | AF225987 Homo sapi |
| 20         | 3981.8 | 66.0        | 4164   | 6 AX391138  | AX391138 Sequence  |
| 21         | 3959.8 | 65.7        | 8552   | 10 RATNCP1R | X03639 Rat brain m |
| 22         | 3949.4 | 65.5        | 8976   | 9 AF225986  | M22254 Rat brain m |
| 23         | 3787.8 | 62.8        | 8976   | 9 AF225986  | AF225986 Homo sapi |
| 24         | 3785.4 | 62.8        | 9112   | 6 AX164235  | AX164235 Sequence  |
| 25         | 3771.8 | 62.6        | 6599   | 9 HSA251507 | AJ251507 Homo sapi |
| 26         | 3758.2 | 62.3        | 9112   | 6 AX164236  | AX164236 Sequence  |
| 27         | 3563.8 | 59.1        | 6822   | 6 AX401928  | AX401928 Sequence  |
| 28         | 3563.8 | 59.1        | 6822   | 10 RNSC1R1  | Y00766 Rat mRNA fo |
| 29         | 3544.8 | 58.8        | 6404   | 6 AR107906  | AR107906 Sequence  |
| 30         | 3543   | 58.8        | 8378   | 5 AF123593  | AF123593 Cyrops py |
| 31         | 3477.2 | 57.7        | 5955   | 4 OC035238  | U35238 Oryctolagus |
| 32         | 3476.8 | 57.7        | 6371   | 6 AR107905  | AR107905 Sequence  |
| 33         | 3476.8 | 57.7        | 6371   | 9 HSVASCSAS | X82835 H.sapiens m |
| 34         | 3412   | 56.6        | 9316   | 10 AF000368 | AF000368 Rattus no |
| 35         | 3410.4 | 56.6        | 5952   | 10 RMT79568 | U79568 Rattus norv |
| 36         | 3410.4 | 56.6        | 6452   | 6 AR107904  | AR107904 Sequence  |
| 37         | 2821.2 | 46.8        | 7008   | 9 AB027567  | AB027567 Homo sapi |
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## ALIGNMENTS

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DEFINITION Sequence 11 from Patent WO0214498.  
ACCESSION AX391140  
VERSION AX391140.1 GI:19584237  
KEYWORDS  
SOURCE  
ORGANISM human.  
Human sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE  
1 Turner, C.A., Mathur, B. and Mathur, D.  
Novel human ion channel proteins and polynucleotides encoding the  
same

PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
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APPLICANT: Mendrick, Donna  
APPLICANT: Porter, Mark  
APPLICANT: Johnson, Kory  
APPLICANT: Castle, Arthur  
APPLICANT: Elashoff, Michael  
TITLE OF INVENTION: Molecular Toxicology Modeling  
FILE REFERENCE: 44921-5038-US  
CURRENT APPLICATION NUMBER: US/09/917,800A  
CURRENT FILING DATE: 2001-07-31  
PRIOR APPLICATION NUMBER: US 60/222,040  
PRIOR FILING DATE: 2000-07-31  
PRIOR APPLICATION NUMBER: US 60/222,880  
PRIOR FILING DATE: 2000-11-02  
PRIOR APPLICATION NUMBER: US 60/290,029  
PRIOR FILING DATE: 2001-05-11  
PRIOR APPLICATION NUMBER: US 60/290,645  
PRIOR FILING DATE: 2001-05-15  
PRIOR APPLICATION NUMBER: US 60/292,336  
PRIOR FILING DATE: 2001-05-22  
PRIOR APPLICATION NUMBER: US 60/295,798  
PRIOR FILING DATE: 2001-06-06  
PRIOR APPLICATION NUMBER: US 60/297,457  
PRIOR FILING DATE: 2001-06-13  
PRIOR APPLICATION NUMBER: US 60/298,884  
PRIOR FILING DATE: 2001-06-19  
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PRIOR FILING DATE: 2001-07-09  
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SOFTWARE: PatentIn Ver. 2.1  
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LENGTH: 6822  
TYPE: DNA

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Query Match 100.0%; Score 6028.8; DB 6; Length 6030;  
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 DB 6001 GGCAGAGATGAAAAAGCCAAAGGAAATTA 6030

RESULT 2  
 AX164171  
 LOCUS 8378 bp DNA linear PAT 22-JUN-2001  
 DEPOSITION Sequence 1 from Patent WO0138564.  
 ACCESSION AX164171  
 VERSION AX164171.1 GI:14545110  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1 (bases 1 to 8378)  
 AUTHORS Rouleau, G.A., Lafreniere, R.G., Rochefort, D., Cossette, P. and  
 Ragsdale, D.  
 TITLE Loci for idiopathic generalized epilepsy, mutations thereof and  
 method using same to assess, diagnose, prognosis or treat epilepsy  
 JOURNAL Patent: WO 0138564-A 1 31-May-2001;  
 McGill University (CA)  
 FEATURES  
 Location/Qualifiers  
 source 1..8378

/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
BASE COUNT 2496 a 1575 c 1782 g 2525 t  
ORIGIN

Query Match 99.8%; Score 6015.2; DB 6; Length 8378;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 6025; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 1 ATGAGCAAAAGCTCTGTACACAGAGACCTGACAGCTTCACTTCCACAGAGAA 60  
DB ATGAGCAAAAGCTCTGTACACAGAGACCTGACAGCTTCACTTCCACAGAGAA 325  
QY 61 TCTCTGGGGGCTATGAAAGCGCATGTGAGAAAGAAAGGCAAAATCCCAACAGAC 120  
DB TCTCTGGGGGCTATGAAAGCGCATGTGAGAAAGAAAGGCAAAATCCCAACAGAC 385  
QY 121 AAAAAAGATGAGAGCAAGAAATGGCCCAAGCCAAATAGTGAAGCTGGAAGAAC 180  
DB AAAAAAGATGAGAGCAAGAAATGGCCCAAGCCAAATAGTGAAGCTGGAAGAAC 445  
QY 181 CTTCATTATTTATGAGACATTCCTCCAGAGATGTGTGAGAGCCCTGGAGACCTG 240  
DB CTTCATTATTTATGAGACATTCCTCCAGAGATGTGTGAGAGCCCTGGAGACCTG 505  
QY 241 GACCCCTACTATATCAATTAAGAAACCTTTATAGTATGAATTAAGGAGGACCTTTC 300  
DB GACCCCTACTATATCAATTAAGAAACCTTTATAGTATGAATTAAGGAGGACCTTTC 565  
QY 301 CGGTTCAAGTGCACCTCGCCCTGTACATTTTAACCTCCCAATCCTTGAAGAAATA 360  
DB CGGTTCAAGTGCACCTCGCCCTGTACATTTTAACCTCCCAATCCTTGAAGAAATA 625  
QY 361 GCTTTTAAGATTTTGTGATCATTCAATTAATGACATGTAATATGTGACATTTTGACA 420  
DB GCTTTTAAGATTTTGTGATCATTCAATTAATGACATGTAATATGTGACATTTTGACA 685  
QY 421 AACGTGCTTTATGACAAATAGTAAGCCTCTGTATGAGAAAGATGAATACACC 480  
DB AACGTGCTTTATGACAAATAGTAAGCCTCTGTATGAGAAAGATGAATACACC 745  
QY 481 TTCACAGAAATATATCTTTTGAATCACTTAATTAATTAATTAATTAATTAATTAAT 540  
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QY 541 GAAATTTTACTTCTCTGGGATTCATGAACTGCTGATTCATCTGATTAATCAATTT 600  
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QY 601 GCGTACGTCACAGAGTTGTGACCTGGGCAATGTCTGGGATGAGAAACATTCAGAGTT 660  
DB GCGTACGTCACAGAGTTGTGACCTGGGCAATGTCTGGGATGAGAAACATTCAGAGTT 925  
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QY 781 TTTCTCTAATTTGGGCGACACTGTTCATGGGCAACCTGAGAGAAATATATCAATGG 840  
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QY 901 AATGTACACTTAAATGAAGAACTGTCTTGAAGTTTGAAGTCAATATATCAAGAT 960  
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QY 961 TCAAGATATCATATTTCTCTGAGGGTTTTTATAGATCCATCAATATGTGAATAAGCTCT 1020  
DB TCAAGATATCATATTTCTCTGAGGGTTTTTATAGATCCATCAATATGTGAATAAGCTCT 1285  
QY 1021 GATGAGGCCAATGTCCAGAGAGGATATATGTGTGAAGCTGTGTGAATATCCCAATTA 1080  
DB GATGAGGCCAATGTCCAGAGAGGATATATGTGTGAAGCTGTGTGAATATCCCAATTA 1345  
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DB GGCATACAAAGCTTGTATACCTTCAGTTGGGCTTTTGTCTTGTCTGTAATGACT 1405  
QY 1141 CAGAGACTCTGGGAAATCTTTATACACTGACATTAAGTGTCTGTGGAAACGTATATG 1200  
DB CAGAGACTCTGGGAAATCTTTATACACTGACATTAAGTGTCTGTGGAAACGTATATG 1465  
QY 1201 ATATTTTGTGTGTATTTCTTGGGCTATCTACCTTAATTAATTTGATCCGCT 1260  
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QY 1261 GTGTGGCCATGGCTTACAGAGAACAGATACAGCCACCTTGAAGAAAGCAGAACAGAA 1320  
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DB GCAGCAAGGCAATGCTCTGAAACATTCAGAGAGCCAGTGGACAGGAGGCTCTCA 1705  
QY 1441 GACAGCTCATGTGAAGCCTTAAGTTGATTCAGAGTGTCTAAGAAAGAAAGAAATGCG 1500  
DB GACAGCTCATGTGAAGCCTTAAGTTGATTCAGAGTGTCTAAGAAAGAAAGAAATGCG 1765  
QY 1501 AGAAGAAAGAAAGAAAGAAAGAGAGCTGTGGGGAAGAAAGATGAGATGAATTC 1560  
DB AGAAGAAAGAAAGAAAGAAAGAGAGCTGTGGGGAAGAAAGATGAGATGAATTC 1825  
QY 1561 CAAAATCTGATCTGAGAGACATTCAGAGAGAAAGGTTTTGCTCTCCATGAAGG 1620  
DB CAAAATCTGATCTGAGAGACATTCAGAGAGAAAGGTTTTGCTCTCCATGAAGG 1885  
QY 1621 AACGATGACATATGAAGAAAGAGTACTCTCCCAACACAGCTTTTGTGACATCCGT 1680  
DB AACGATGACATATGAAGAAAGAGTACTCTCCCAACACAGCTTTTGTGACATCCGT 1945  
QY 1681 GGCCTCCATTTTCAACCAAGGCGAAATAGCAAGAACCTTTTACGTTTGAAGGCGA 1740  
DB GGCCTCCATTTTCAACCAAGGCGAAATAGCAAGAACCTTTTACGTTTGAAGGCGA 2005  
QY 1741 GCAAGAGATGTGGGATCTGAGAACACTTGCAGATGATGAGCAACAGACCTTGAGAT 1800  
DB GCAAGAGATGTGGGATCTGAGAACACTTGCAGATGATGAGCAACAGACCTTGAGAT 2065  
QY 1801 AACGAGAGCCGTAGAGATTCCTTGTGTGCCCCGACAGCAAGAGAGAGAGCAAGC 1860  
DB AACGAGAGCCGTAGAGATTCCTTGTGTGCCCCGACAGCAAGAGAGAGAGCAAGC 2125  
QY 1861 AACCTGAGTCAAGACAGTATGCTATCCCGGATGCTGGCAGTGTTCACAGCAATGGGAG 1920  
DB AACCTGAGTCAAGACAGTATGCTATCCCGGATGCTGGCAGTGTTCACAGCAATGGGAG 2185  
QY 1921 ATGCAAGCACTGTGTGATGCAATGAGTGTGCTTCTGCTGTGGAGCTTCAGTCCCT 1980  
DB ATGCAAGCACTGTGTGATGCAATGAGTGTGCTTCTGCTGTGGAGCTTCAGTCCCT 2245  
QY 1981 ACATGCGCTGTGGACAGCTTCTGCAAGAGTGTATATAGATTAAGCCAGCTACTGATAC 2040  
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QY 2041 AATGGAACCAACCACTGAACCTGAATAGAAAGAAAGGTCAGCTTCTTCCAGCTTCC 2100

|   |      |   |      |
|---|------|---|------|
| D | 2306 | AAATGGAACAAACCACTGAAATCTGAATATAGAAAGGAAGGTCMAAGTCTTTCCACGTTTCC  | 2365 |
| Q | 2101 | ATGGACTTTCTAGAGATCTTCCCAAGCCAAAGCAGCAATGAGTATAGCCACATTTCTA      | 2160 |
| D | 2366 | ATGAGACTTTCTAAGATATCTTCCCAAGGCCAAAGCAATAGATATAGCAGCATTTCTA      | 2425 |
| Q | 2161 | ACAAATACAGTATAGAAAGCTGGAAGAAATCCAGGACAGAAAGCCACCCCTGTGGTATATAA  | 2220 |
| D | 2426 | ACAAATACAGTATAGAAAGCTGGAAGAAATCCAGGACAGAAAGCCACCCCTGTGGTATATAA  | 2485 |
| Q | 2221 | TTTTCCAAACATATTTCTTAATCTGGGACTGTCTCCATATTTGGTTAAAAAGTAAACATGTT  | 2280 |
| D | 2486 | TTTTCCAAACATATTTCTTAATCTGGGACTGTCTCCATATTTGGTTAAAAAGTAAACATGTT  | 2545 |
| Q | 2281 | GTCACCTGGTGTGATGAGACCATTTGTTGACTGGCCATCACATCTGATTTGCTTTA        | 2340 |
| D | 2546 | GTCACCTGGTGTGATGAGACCATTTGTTGACTGGCCATCACATCTGATTTGCTTTA        | 2605 |
| Q | 2341 | AATACTTTTTTCATGCGCATGAGACACTATACATAGCAGACCAATTCATTAATATGCTCT    | 2400 |
| D | 2606 | AATACTTTTTTCATGCGCATGAGACACTATACATAGCAGACCAATTCATTAATATGCTCT    | 2665 |
| Q | 2401 | ACAGTAGGAAACTTGGTTTTCACATGGGATCTTTACAGACAGAAATGTTTCTGAAAATTTAT  | 2460 |
| D | 2666 | ACAGTAGGAAACTTGGTTTTCACATGGGATCTTTACAGACAGAAATGTTTCTGAAAATTTAT  | 2725 |
| Q | 2461 | GCCATGAGATCCTACTATATATTTTCCAAAGAGCGTGGAATATCTTGACGGTTTTATTTGTG  | 2520 |
| D | 2726 | GCCATGAGATCCTACTATATATTTTCCAAAGAGCGTGGAATATCTTGACGGTTTTATTTGTG  | 2785 |
| Q | 2521 | ACGCTTAGCCTGGTAGAACTTGGACTCGCCAAATGTGAGAGATTAATCTGTTCOCGTTCA    | 2580 |
| D | 2786 | ACGCTTAGCCTGGTAGAACTTGGACTCGCCAAATGTGAGAGATTAATCTGTTCOCGTTCA    | 2845 |
| Q | 2581 | TTTTGATCTCTGGGAACTTTTCCAAAGTGGGCAAAATCTTGGCCAAAGTTAATATGCTATA   | 2640 |
| D | 2846 | TTTTGATCTCTGGGAACTTTTCCAAAGTGGGCAAAATCTTGGCCAAAGTTAATATGCTATA   | 2905 |
| Q | 2641 | AAGATCATGGGCAATTCOCGTGGGGGCTCTGGGAAATTTAACCTCGTGGGCATCATC       | 2700 |
| D | 2906 | AAGATCATGGGCAATTCOCGTGGGGGCTCTGGGAAATTTAACCTCGTGGGCATCATC       | 2965 |
| Q | 2701 | GTCCTATTTTTGCCGTGGTCCGGCATGCACTCTTTTGGTAAAGCTACAAAGATTTGTGTC    | 2760 |
| D | 2966 | GTCCTATTTTTGCCGTGGTCCGGCATGCACTCTTTTGGTAAAGCTACAAAGATTTGTGTC    | 3025 |
| Q | 2761 | TGCACATGCGCCAGTATTTGTCAACTCCCAAGCTGGGACATGTAATGACTCTTCCACTCC    | 2820 |
| D | 3026 | TGCACATGCGCCAGTATTTGTCAACTCCCAAGCTGGGACATGTAATGACTCTTCCACTCC    | 3085 |
| Q | 2821 | TTTCCGATTTGTGTTCCCGCTGCTGTGTGGGAGTGAATAGAACCATGTTGGACTGTATG     | 2880 |
| D | 3086 | TTTCCGATTTGTGTTCCCGCTGCTGTGTGGGAGTGAATAGAACCATGTTGGACTGTATG     | 3145 |
| Q | 2881 | GAGGTGCTGGTCAACCAATGTCCTTACTGCTTCAATATAGTCAATGGTCAATGGATTTGGAAC | 2940 |
| D | 3146 | GAGGTGCTGGTCAACCAATGTCCTTACTGCTTCAATATAGTCAATGGTCAATGGATTTGGAAC | 3205 |
| Q | 2941 | CTAGTGTCTGTAATCTTTCTGTGGCCTTGCTMTGAGCTCATTTAGTGCAGCAACCTT       | 3000 |
| D | 3206 | CTAGTGTCTGTAATCTTTCTGTGGCCTTGCTMTGAGCTCATTTAGTGCAGCAACCTT       | 3265 |
| Q | 3001 | GGAGCCATGATGATGATATGAAATGAATATCTCCAAATTTGCTGTGGATAGAGTGCAC      | 3060 |
| D | 3266 | GGAGCCATGATGATGATATGAAATGAATATCTCCAAATTTGCTGTGGATAGAGTGCAC      | 3325 |
| Q | 3061 | AAAGAGTAGTATATGTGAAGAAATATATGAATTTATTCACAGTCCCTCATTAGG          | 3120 |
| D | 3326 | AAAGAGTAGTATATGTGAAGAAATATATGAATTTATTCACAGTCCCTCATTAGG          | 3385 |
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Query Match 98.9%; Score 5963.2; DB 6; Length 8378;  
 Best Local Similarity 99.5%; Pred. No. 0;  
 Matches 5999; Conservative 3; Mismatches 26; Indels 2; Gaps 2;

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QY 61 TCTCTTGGGCTATTGAAAGACGATTGCAAGAAAGCAAGAAATCCCAACAGAC 120  
 DB 326 TCTCTTGGGCTATTGAAAGACGATTGCAAGAAAGCAAGAAATCCCAACAGAC 385

QY 121 AAAAAAGATGACGCAAGAAATGGCCCAAGCAAAATAGTACTTGGAGTGGAAAGAAC 180  
 DB 386 AAAAAAGATGACGCAAGAAATGGCCCAAGCAAAATAGTACTTGGAGTGGAAAGAAC 445

QY 181 CTTCATTTATTTATGAGACATTTCTCCAGAGATGCTGACAGCCCTGAGAGACTG 240  
 DB 446 CTTCATTTATTTATGAGACATTTCTCCAGAGATGCTGACAGCCCTGAGAGACTG 505

QY 241 GACCCCTACATATATCAATAGAAACCTTTATATGATATGAATTAAGGGAAGCCATCTTC 300  
 DB 506 GACCCCTACATATATCAATAGAAACCTTTATATGATATGAATTAAGGGAAGCCATCTTC 565

QY 301 CGGTTGAGTCCACCTGCTGCTGATCAATTTAACTCCCTCAATCCTCTTAGAAATA 360  
 DB 566 CGGTTGAGTCCACCTGCTGCTGATCAATTTAACTCCCTCAATCCTCTTAGAAATA 625

QY 361 GCTATTAAGATTTTGTGATCATTTATTTACAGCATGCTAATTAATGACACTATTTTGACA 420  
 DB 626 GCTATTAAGATTTTGTGATCATTTATTTACAGCATGCTAATTAATGACACTATTTTGACA 685

QY 421 AACTGTGTTTTTATGCAATAGATTAACCCCTGATTTGCAAGAAATGTAATACACC 480  
 DB 686 AACTGTGTTTTTATGCAATAGATTAACCCCTGATTTGCAAGAAATGTAATACACC 745

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 DB 746 TTTCACAGAAATATATCTTTTGAATCACTTATAAAATTAATTCAGAGGGATCTGTTTA 805

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 DB 806 GAAGATTTTACTTCTCTGCGGATCCATGGAACCTGCTGATTTCACTGTCATTACATTT 865

QY 601 GGTGAGTCAAGAGATTTTGTGAGACCTGCGCAATGCTCGGCAATTGGAACATTACAGATT 660  
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QY 661 CTCGAGCAATTTGAAGAGATTTTCACTGATTTCCAGGCTGAAAACCAATTTGGAGCCCTG 720  
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QY 781 TTGTGCTTAATTTGGGCTGAGCTGTTTCATGAGGCAACCTAGGAATAATGATATACAAATG 840  
 DB 1046 TTGTGCTTAATTTGGGCTGAGCTGTTTCATGAGGCAACCTAGGAATAATGATATACAAATG 1105

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 DB 1106 CCTCCACCAATGCTTCTTTGAGAGCAATAGATATGAAAGAAATTAATCTGTAATAT 1165

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QY 1081 GGTGACCAAGCTTTGATATCTTCACTTGTGAGCTTTTGTGCTTTGCTTTGCTGACTATGACT 1140  
 DB 1346 GGTGACCAAGCTTTGATATCTTCACTTGTGAGCTTTTGTGCTTTGCTTTGCTGACTATGACT 1405

QY 1141 CAGGACTTCTGGGAAATCTTTATCACTGACATTAAGTACGCTGCTGGGAAAGCTATAGT 1200  
 DB 1406 CAGGACTTCTGGGAAATCTTTATCACTGACATTAAGTACGCTGCTGGGAAAGCTATAGT 1465

QY 1201 ATATTTTGTGTGTGATATTTCTTGGGCTCAATTTCACTTAATTAATTTGATCTGCT 1260  
 DB 1466 ATATTTTGTGTGTGATATTTCTTGGGCTCAATTTCACTTAATTAATTTGATCTGCT 1525

QY 1261 GTGTGCTCATGAGCTTACGAGAAACAGAAATCAGGCTTGTGAAGAGCAAGACAGAA 1320  
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QY 1321 GAGGCGAATTTACGAGATGATTAACACGCTTAAAAAGCAAGAGGACGCTCAGCAG 1380  
 DB 1586 GAGGCGAATTTACGAGATGATTAACACGCTTAAAAAGCAAGAGGACGCTCAGCAG 1645

QY 1381 GCAGCAAGGCACTGCTCAGAAATTTCCAGAGAGCCGCTGACAGAGGCTCTCA 1440  
 DB 1646 GCAGCAAGGCACTGCTCAGAAATTTCCAGAGAGCCGCTGACAGAGGCTCTCA 1705

QY 1441 GACAGCTCATCTGAGAGCTTAAAGTTGATTTCCAAAGAGTCTTAAGAAAGAAATACGG 1500  
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QY 1501 AGGAAAGAAAGAAACAGAAAGAGAGCTGTGTGGGAGAGAAAGATGAGATGAATTC 1560  
 DB 1766 AGGAAAGAAAGAAACAGAAAGAGAGCTGTGTGGGAGAGAAAGATGAGATGAATTC 1825

QY 1561 CAAAAATCTGAATCTGAGGACAGATCAGGAGAAAGCTTGTGCTTCATTTGAAGGG 1620  
 DB 1826 CAAAAATCTGAATCTGAGGACAGATCAGGAGAAAGCTTGTGCTTCATTTGAAGGG 1885

QY 1621 AACCGATGACATATGAAAGAGAGTACTCTCCCAACACAGCTTTGTTGAGCATCCGT 1680  
 DB 1886 AACCGATGACATATGAAAGAGAGTACTCTCCCAACACAGCTTTGTTGAGCATCCGT 1945

QY 1681 GGTCTCCATTTTCCACCAAGGCGAAATAGCAGAACAAAGCTTTTACGCTTTAGAGGCGA 1740  
 DB 1946 GGTCTCCATTTTCCACCAAGGCGAAATAGCAGAACAAAGCTTTTACGCTTTAGAGGCGA 2005

QY 1741 GCAAAAGATGTGGGATCTGGAAGCACTTGGAGATGATGAGACAGCACTTTGAGGAT 1800  
 DB 2006 GCAAAAGATGTGGGATCTGGAAGCACTTGGAGATGATGAGACAGCACTTTGAGGAT 2064

QY 1801 AACGAGAGCGTAGAGATTTCTTTGTTGCTCCCGAGACACACGAGAGAGACCAACAGC 1860  
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QY 1861 AACCTGAGTCAACACAGTATGATCTCCGAGATCTGCGAGCTTTTCCAGGAATGGAGAG 1920  
 DB 2125 AACCTGAGTCAACACAGTATGATCTCCGAGATCTGCGAGCTTTTCCAGGAATGGAGAG 2184

QY 1921 ATGCACAGACATGTGATGATGCAATGCTGTGTTCTCTGTTGGTGGAGACCTTACGTTCT 1980  
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QY 1981 ACATGCTGTGTGGAGAGCTTCTGCAAGGTGATATATGATTAAGACAGTACTGATGAC 2040  
 DB 2245 ACATGCTGTGTGGAGAGCTTCTGCAAGGTGATATATGATTAAGACAGTACTGATGAC 2304

QY 2041 AATGGAACACACATGAAATGAAATGAGAAAGAGGTCAGATTCTTTCCAGCTTTCC 2100  
 DB 2305 AATGGAACACACATGAAATGAAATGAGAAAGAGGTCAGATTCTTTCCAGCTTTCC 2364

QY 2101 ATGAGCTTCTTGAAGATCTTCCCAAGGCAAGCAAGATGATATGACAGCATTTCA 2160



Db 2365 ATGACCTTCAGAGATCCTCCCAAGGAGAGAGATATGCCAGCTTCTA 2424  
Qy 2161 ACAAAATACAGTAGAAGAACTTGAGAAATCCAGGCGAGAAATGCCACCTGTTGTATAAA 2220  
Db 2425 ACAAAATACAGTAGAAGAACTTGAGAAATCCAGGCGAGAAATGCCACCTGTTGTATAAA 2484  
Qy 2221 TTTTCCAAATATCTTATATGCGGAGCTGTTCTCCATATATGTTTAAAGTAAACATGTT 2280  
Db 2485 TTTTCCAAATATCTTATATGCGGAGCTGTTCTCCATATATGTTTAAAGTAAACATGTT 2544  
Qy 2281 GTCAACCTGCTGTGATGAGACCATTTGTTGACCTGACCATCACCATCTGATTTGCTTA 2340  
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Qy 2341 AATATCTTTTCATGAGCCATGAGACATATCCATATGACGACCATTTCAATATATGCTT 2400  
Db 2605 AATATCTTTTCATGAGCCATGAGACATATCCATATGACGACCATTTCAATATATGCTT 2664  
Qy 2401 ACAGTAGAGAACTTGGTTTCCAGTGGAGCTTTACAGAGAAATGTTCTGAAATATAT 2460  
Db 2665 ACAGTAGAGAACTTGGTTTCCAGTGGAGCTTTACAGAGAAATGTTCTGAAATATAT 2724  
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Qy 3541 TTCACTGAGGCTGTGTACAAAGATTTCAAGTGTGTCAATCAATGTGAGAAAGGACAG 3600  
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Qy 3601 GGAAGAACTGTGGAACCTGAGAGAGAGCTGTTCCGAAATAGTTGAACATATCTGTTT 3660  
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Qy 3661 GAGACCTCATTTGTTTATGATCTCTCTTACTGATGCTGCTGGCATTTAAATATAT 3720  
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Qy 3781 TACATTTTCATTTGGAATGCTTCTTAAATGCTGGCATATGCTATCAAAATATTC 3840  
Db 4045 TACATTTTCATTTGGAATGCTTCTTAAATGCTGGCATATGCTATCAAAATATTC 4103  
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 Homo sapiens  
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 Turner, C.A., Mathur, B. and Mathur, D.  
 Novel human ion channel proteins and polynucleotides encoding the  
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 JOURNAL Lexicon Genetics Incorporated (US)  
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Query Match 98.7%; Score 5952.8; DB 6; Length 5997;  
 Best Local Similarity 99.5%; Pred. No. 0;  
 Matches 5997; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

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| QY | 1    | ATGGAGCAAAACAGTGGCTGTGTACACACAGACCTTACAGCTTCAACTTCTTACACAGAA  | 60   |
| Db | 1    | ATGGAGCAAAACAGTGGCTGTGTACACACAGACCTTACAGCTTCAACTTCTTACACAGAA  | 60   |
| QY | 61   | TCCTCTGGCGCCATATGGAAGAAGCATTTGACAGAAAGAAAGGCAAGAAATCCAAACAGAC | 120  |
| Db | 61   | TCCTCTGGCGCCATATGGAAGAAGCATTTGACAGAAAGAAAGGCAAGAAATCCAAACAGAC | 120  |
| QY | 121  | AAAAAAGATGACAGCAAAAAAGGCCAAAGCAAAATAGTACTTGGAACTGGAAAGAC      | 180  |
| Db | 121  | AAAAAAGATGACAGCAAAAAAGGCCAAAGCAAAATAGTACTTGGAACTGGAAAGAC      | 180  |
| QY | 181  | CTTCCATTTATTTATGAGACATTTCTCCAGAGATGCTGTACAGGCCCTGGAGACCTG     | 240  |
| Db | 181  | CTTCCATTTATTTATGAGACATTTCTCCAGAGATGCTGTACAGGCCCTGGAGACCTG     | 240  |
| QY | 241  | GACCCCTACTATATCAATAAAGAAACCTTATATGTATGATTAAGGAAAGGCCATCTTC    | 300  |
| Db | 241  | GACCCCTACTATATCAATAAAGAAACCTTATATGTATGATTAAGGAAAGGCCATCTTC    | 300  |
| QY | 301  | CGGTTACAGTGCACACTCGCCCTGTACATTTTAACTCCCTCAATCCTCTTAGAAGAAATA  | 360  |
| Db | 301  | CGGTTACAGTGCACACTCGCCCTGTACATTTTAACTCCCTCAATCCTCTTAGAAGAAATA  | 360  |
| QY | 361  | GCTATTAAGATTTTGTGACATTCATTAATACAGATGCTAATTAATGTGACATATTTTGACA | 420  |
| Db | 361  | GCTATTAAGATTTTGTGACATTCATTAATACAGATGCTAATTAATGTGACATATTTTGACA | 420  |
| QY | 421  | AACSTGTGTTTATGACAAATGAAATACCCTCGATTTGGACAAAGAAATGAAATACAC     | 480  |
| Db | 421  | AACSTGTGTTTATGACAAATGAAATACCCTCGATTTGGACAAAGAAATGAAATACAC     | 480  |
| QY | 481  | TTACAGAGAAATATATACTTTTGAATCACTATATAAAATTTTTCAGAGGATTCGTTTA    | 540  |
| Db | 481  | TTACAGAGAAATATATACTTTTGAATCACTATATAAAATTTTTCAGAGGATTCGTTTA    | 540  |
| QY | 541  | GAAATTTTACTTTCCTCGGGATTCACATGACATCGCTCGATTTCACTGTCAATTAATTT   | 600  |
| Db | 541  | GAAATTTTACTTTCCTCGGGATTCACATGACATCGCTCGATTTCACTGTCAATTAATTT   | 600  |
| QY | 601  | GCGTACGTACAGAGTTGTGAGACCTGAGCAATGTCTCGGCANTTGGAAATTCAGAGTT    | 660  |
| Db | 601  | GCGTACGTACAGAGTTGTGAGACCTGAGCAATGTCTCGGCANTTGGAAATTCAGAGTT    | 660  |
| QY | 661  | CTCCAGCATTTGAAGACGATTTCACTGATTTCCAGGCTGAAACCAATTTGGAGACCCG    | 720  |
| Db | 661  | CTCCAGCATTTGAAGACGATTTCACTGATTTCCAGGCTGAAACCAATTTGGAGACCCG    | 720  |
| QY | 721  | ATCCAGTGTGTGAAGAAAGCTCTCAGATGTATGATATCCATGCTGTCTGTGTGACGTA    | 780  |
| Db | 721  | ATCCAGTGTGTGAAGAAAGCTCTCAGATGTATGATATCCATGCTGTCTGTGTGACGTA    | 780  |
| QY | 781  | TTTGCTCTAATTTGGGCGAGCTGTTCATGAGGCAACCTGAGAAATTAAGTATACAATGG   | 840  |
| Db | 781  | TTTGCTCTAATTTGGGCGAGCTGTTCATGAGGCAACCTGAGAAATTAAGTATACAATGG   | 840  |
| QY | 841  | CTCTCCACCAATGCTTCCCTTGGAGAGAACATAGTATAGAAAAGAAATTAACCTGGAATAT | 900  |
| Db | 841  | CTCTCCACCAATGCTTCCCTTGGAGAGAACATAGTATAGAAAAGAAATTAACCTGGAATAT | 900  |
| QY | 901  | AATGGTACCTTATTAATAATGAACCTGTCTTGAATTTGACTGGAAGTCAATATATTCAGAT | 960  |
| Db | 901  | AATGGTACCTTATTAATAATGAACCTGTCTTGAATTTGACTGGAAGTCAATATATTCAGAT | 960  |
| QY | 961  | TCAAGATATCATTTTTCCTGGAGAGGTTTTTATGATGCACTACTATGTGGAATATGCTCT  | 1020 |
| Db | 961  | TCAAGATATCATTTTTCCTGGAGAGGTTTTTATGATGCACTACTATGTGGAATATGCTCT  | 1020 |
| QY | 1021 | GATGAGGCCAATATCCAGAGAGGATATATGTGTGTAAGTCTGTGTGAAATATCCCAATAT  | 1080 |
| Db | 1021 | GATGAGGCCAATATCCAGAGAGGATATATGTGTGTAAGTCTGTGTGAAATATCCCAATAT  | 1080 |
| QY | 1081 | GCGTACACAGCCTTTGATACCTTCAGTTGGGCTTTTGTGCTGTGTTGCACTAATAGCT    | 1140 |

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| Db | 1081 | GCCTCACAAAGCTTTCAGATCCCTTCAGTTGGGCTTTTTCCTTTGTCCTTTGTCATTAAGACT | 11440 |
| Oy | 1141 | CAGGACCTTGGGAAAAAATCTTATCACTCAATACATTAACGTCGTCGGGAAAAACGTACAG   | 12007 |
| Db | 1141 | CAGGACCTTGGGAAAAAATCTTATCACTCAATTAAGTCGTCGGGAAAAACGTACAG        | 12007 |
| Oy | 1201 | ATATTTTGTGTGTGTCATTTTCTTGGGGCTCATTCACCTAATAATTAATTGATCCGAGCT    | 1266  |
| Db | 1201 | ATATTTTGTGTGTGTCATTTTCTTGGGGCTCATTCACCTAATAATTAATTGATTCGAGCT    | 1266  |
| Oy | 1261 | GTGTGGCCATGGCTTACGAGGAACAGAATCAGGCCACCTTGGAAAGAACAGACAGAAA      | 1320  |
| Db | 1261 | GTGTGGCCATGGCTTACGAGGAACAGAATCAGGCCACCTTGGAAAGAACAGACAGAAA      | 1320  |
| Oy | 1321 | CAGGCCAAATTTTCAGCAGATGATTAAGAACACTTAAAAAGCACAGAGGCACTCAGCAG     | 1380  |
| Db | 1321 | CAGGCCAAATTTTCAGCAGATGATTAAGAACACTTAAAAAGCACAGAGGCACTCAGCAG     | 1380  |
| Oy | 1381 | GCAGCAAGGCAATCGCTCAGAACATTCAGAGAGCCCAAGTCAGCAGGCAAGGCTCTCA      | 1440  |
| Db | 1381 | GCAGCAAGGCAATCGCTCAGAACATTCAGAGAGCCCAAGTCAGCAGGCAAGGCTCTCA      | 1440  |
| Oy | 1441 | GACAGCTCATCTGAGAGCCCTTAAGTGAATTCAGAAAGTCTTAAGAAAGAAAGAAATCGG    | 1500  |
| Db | 1441 | GACAGCTCATCTGAGAGCCCTTAAGTGAATTCAGAAAGTCTTAAGAAAGAAAGAAATCGG    | 1500  |
| Oy | 1501 | AGGAAGAAAAAACAAGAAAGAGCACTCTGTGTGGGAAAGAAAGATGAGATCAATTC        | 1560  |
| Db | 1501 | AGGAAGAAAAAACAAGAAAGAGCACTCTGTGTGGGAAAGAAAGATGAGATCAATTC        | 1560  |
| Oy | 1561 | CAAAAATCTGAATCTGAGAGCAGCATCAGAGGAAGAAAGTTTTCGCTCCATTAAGG        | 1620  |
| Db | 1561 | CAAAAATCTGAATCTGAGAGCAGCATCAGAGGAAGAAAGTTTTCGCTCCATTAAGG        | 1620  |
| Oy | 1621 | AAACGATTCAGATATGAAAAGAGTACCTCCACACACAGTCTTTGTTGAGCATCCGT        | 1680  |
| Db | 1621 | AAACGATTCAGATATGAAAAGAGTACCTCCACACACAGTCTTTGTTGAGCATCCGT        | 1680  |
| Oy | 1681 | GGCTCCCTATTTTACCAAGGCGCAATAGCAAAACGCTTTTCACTTTAGAGGCGCA         | 1740  |
| Db | 1681 | GGCTCCCTATTTTACCAAGGCGCAATAGCAAAACGCTTTTCACTTTAGAGGCGCA         | 1740  |
| Oy | 1741 | GCAAAAGATGTGGGATCTGAGAAAGCACTTCCAGATGATGACACAGACCTTTAGGAT       | 1800  |
| Db | 1741 | GCAAAAGATGTGGGATCTGAGAAAGCACTTCCAGATGATGACACAGACCTTTAGGAT       | 1800  |
| Oy | 1801 | AACGAGACCCGTAGAGATCCTTGTGTGTGCCCCCGACGACAGGAGAGAGCAACAGC        | 1860  |
| Db | 1801 | AACGAGACCCGTAGAGATCCTTGTGTGTGCCCCCGACGACAGGAGAGAGCAACAGC        | 1860  |
| Oy | 1861 | AACTGAGTCAGACCATAGTATCTCCGGATGCTGGAGTCTTTCACCGAATGGAG           | 1920  |
| Db | 1861 | AACTGAGTCAGACCATAGTATCTCCGGATGCTGGAGTCTTTCACCGAATGGAG           | 1920  |
| Oy | 1921 | ATGCACAGCACTGTGGAATTCATATGGTGTGTCTTCTTGTTGGTGAGCACTTCAGTTC      | 1980  |
| Db | 1921 | ATGCACAGCACTGTGGAATTCATATGGTGTGTCTTCTTGTTGGTGAGCACTTCAGTTC      | 1980  |
| Oy | 1981 | ACATCGCTGTGGACAGCTTCTGCGCAGAGGTGATTAATGATTAACCCAGCTACTGATGAC    | 2040  |
| Db | 1981 | ACATCGCTGTGGACAGCTTCTGCGCAGAGGTGATTAATGATTAACCCAGCTACTGATGAC    | 2040  |
| Oy | 2041 | AATGGAAACACACTGAAATCTGAATAGAGAAAGAGAGTCAAGTTCTTCCAGCTTCC        | 2100  |
| Db | 2041 | AATGGAAACACACTGAAATCTGAATAGAGAAAGAGAGTCAAGTTCTTCCAGCTTCC        | 2100  |
| Oy | 2101 | ATGGAATCTTCTAGAAAGATCTTCCCAAGGCAACGAGCAATGATGATGCAAGATTCCTA     | 2160  |
| Db | 2101 | ATGGAATCTTCTAGAAAGATCTTCCCAAGGCAACGAGCAATGATGATGCAAGATTCCTA     | 2160  |
| Oy | 2161 | ACAAATACAGTGAAGAACTTGAAGATCCAGGACAGAAATGCCACCTGTTGGTATAAA       | 2220  |
| Db | 2161 | ACAAATACAGTGAAGAACTTGAAGATCCAGGACAGAAATGCCACCTGTTGGTATAAA       | 2220  |

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| D | b | 2128 | ACAAATACAGTAAAGAAAGACTGGAAGATTCAGAGCAAGGAAAGGCCACCCTGTTGGTTAA  | 218 |
| O | y | 2221 | TTTTCCAAACAATATCTTAATCTGGAGACTGTTCACATATTTGGTTAAAGTAACATGTT    | 228 |
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| O | y | 2401 | ACAGTAGGAACAATGGTTTTCACTGGAGTCTTTACAGCAGAAATGTTCTGAAATTAAT     | 246 |
| D | b | 2368 | ACAGTAGGAACAATGGTTTTCACTGGAGTCTTTACAGCAGAAATGTTCTGAAATTAAT     | 242 |
| O | y | 2461 | GCATATGGATCCTTACATATATTTTCCAAAGAGCTGGAAATCTTTACGCTTTATGTGTG    | 252 |
| D | b | 2428 | GCCAATGATCCTTACATATATTTTCCAAAGAGCTGGAAATCTTTACGCTTTATGTGTG     | 248 |
| O | y | 2521 | ACGCTTACCTGGTAGAAGCTTGACCTGGCAATGTGGAAAGGATTAATCTGTCCGTTCA     | 258 |
| D | b | 2488 | ACGCTTACCTGGTAGAAGCTTGACCTGGCAATGTGGAAAGGATTAATCTGTCCGTTCA     | 254 |
| O | y | 2581 | TTTTGATTTGCTGCGAGTTTTCACATTTGGCAAAATCTTGGCCAACTTAAATATGTCAATA  | 264 |
| D | b | 2548 | TTTTGATTTGCTGCGAGTTTTCACATTTGGCAAAATCTTGGCCAACTTAAATATGTCAATA  | 260 |
| O | y | 2641 | AAGATCATCGGCATTTCCGTGGGGGCTCTGGAAATTTAACTCGTCTTGGCCATCATC      | 270 |
| D | b | 2608 | AAGATCATCGGCATTTCCGTGGGGGCTCTGGAAATTTAACTCGTCTTGGCCATCATC      | 266 |
| O | y | 2701 | GCTTCATTTTGGCCGTGGTGGCATGCACCTCTTTGGTAAAGACCAAAATATGTGTC       | 276 |
| D | b | 2668 | GCTTCATTTTGGCCGTGGTGGCATGCACCTCTTTGGTAAAGACCAAAATATGTGTC       | 272 |
| O | y | 2761 | TGCAAGATCGCAGTGTATGTCAACTCCACGCTGGCACATGATGACTTCTTCCACTCC      | 282 |
| D | b | 2728 | TGCAAGATCGCAGTGTATGTCAACTCCACGCTGGCACATGATGACTTCTTCCACTCC      | 278 |
| O | y | 2821 | TTTCTGATTTGTTCCTCCGCTGTGTGTGGGGAATGATATAGACCATGTGGGACTGTATG    | 288 |
| D | b | 2788 | TTTCTGATTTGTTCCTCCGCTGTGTGTGGGGAATGATATAGACCATGTGGGACTGTATG    | 284 |
| O | y | 2881 | GAGGTGCTGGTCAAGCATGTGCTTACTGTCTTATATAGTGTCAATGGTATTTGGAAAC     | 294 |
| D | b | 2848 | GAGGTGCTGGTCAAGCATGTGCTTACTGTCTTATATAGTGTCAATGGTATTTGGAAAC     | 290 |
| O | y | 2941 | CTAGTGTCTGCAATCTCTTCTTGAGCTTCTTMTAGCTCAATTTAGTGTCAACAACCTT     | 300 |
| D | b | 2908 | CTAGTGTCTGCAATCTCTTCTTGAGCTTCTTMTAGCTCAATTTAGTGTCAACAACCTT     | 296 |
| O | y | 3001 | GCAGCACTGATGTGATGATTAATGAAATGAAATATCTCCAAATTTGCTGTGGATAGATGCAC | 306 |
| D | b | 2968 | GCAGCACTGATGTGATGATTAATGAAATGAAATATCTCCAAATTTGCTGTGGATAGATGCAC | 302 |
| O | y | 3061 | AAAGAGTAGCTTATGTGAAAGAAAGAAATATATGATTTATTCACACAGCTCTTCAATAGG   | 312 |
| D | b | 3028 | AAAGAGTAGCTTATGTGAAAGAAAGAAATATATGATTTATTCACACAGCTCTTCAATAGG   | 308 |
| O | y | 3121 | AAACAAAGATTTTATGATGAAATTTAAACCACTTGATGATCTTAAACAACAAGAAACAGT   | 318 |
| D | b | 3088 | AAACAAAGATTTTATGATGAAATTTAAACCACTTGATGATCTTAAACAACAAGAAACAGT   | 314 |
| O | y | 3181 | TGTATGTCCATCATATACACAGAAATTTGGAAAGATCTTGACTATCTTAAAGATGTAAT    | 324 |
| D | b | 3148 | TGTATGTCCATCATATACACAGAAATTTGGAAAGATCTTGACTATCTTAAAGATGTAAT    | 320 |
| O | y | 3241 | GGAACTTCAAAAGTGTATAGGAACCTGGCACAGCTTGAAAAATTAATATTTATGTAGAAAGT | 330 |
| D | b | 3208 | GGAACTTCAAAAGTGTATAGGAACCTGGCACAGCTTGAAAAATTAATATTTATGTAGAAAGT | 326 |

|    |      |   |      |
|----|------|---|------|
| QY | 3301 | GATPACATGTCATTCATTAACAACCCCAAGCTTACTGTGACGTGTACCAATTCGTGTGAGA | 3360 |
| Db | 3268 | GATTTCATGTCATTCATTAACAACCCCAAGCTTACTGTGACGTGTACCAATTCGTGTGAGA | 3327 |
| QY | 3361 | GAATCTGACTTGTGAAATTTTAAACAGGAAAGACTTGTAGTAGGATCGGATCTGGAGA    | 3420 |
| Db | 3328 | GAATCTGACTTGTGAAATTTTAAACAGGAAAGACTTGTAGTAGGATCGGATCTGGAGA    | 3387 |
| QY | 3421 | AGCAAGAGAACTGGAATGAAGCACTAGCTCATCAGAAGGTAGCATTGTGACATCGGC     | 3480 |
| Db | 3388 | AGCAAGAGAACTGGAATGAAGCACTAGCTCATCAGAAGGTAGCATTGTGACATCGGC     | 3447 |
| QY | 3481 | GCACCTGTAGAAAGACGCCCGTAGTGGAAAGCTGAAAGAACTCTTGAACCGAAGCTGT    | 3540 |
| Db | 3448 | GCACCTGTAGAAAGACGCCCGTAGTGGAAAGCTGAAAGAACTCTTGAACCGAAGCTGT    | 3507 |
| QY | 3541 | TTCACTGAAGGCTGTGTACCAAGATTCGAATGTGTCAATCAATGTGGAAAGGCGAGA     | 3600 |
| Db | 3508 | TTCACTGAAGGCTGTGTACCAAGATTCGAATGTGTCAATCAATGTGGAAAGGCGAGA     | 3567 |
| QY | 3601 | GAAAAACAATGTGTGAACCTGTGAAGGAGCTGTTCGCCAATGTGTAACAATPACTGTTT   | 3660 |
| Db | 3568 | GAAAAACAATGTGTGAACCTGTGAAGGAGCTGTTCGCCAATGTGTAACAATPACTGTTT   | 3627 |
| QY | 3661 | GAGACTTCATGTGTTTCATGATTCCTTAGTAGGAGGCTGTGGATTTGGAAGATTA       | 3720 |
| Db | 3628 | GAGACTTCATGTGTTTCATGATTCCTTAGTAGGAGGCTGTGGATTTGGAAGATTA       | 3687 |
| QY | 3721 | TATATTGATACGGAAAGACGATTAAAGACGATTGGAAATGCTGACAAAGTTTCACT      | 3780 |
| Db | 3688 | TATATTGATACGGAAAGACGATTAAAGACGATTGGAAATGCTGACAAAGTTTCACT      | 3747 |
| QY | 3781 | TACATTTTCATCTCGGAAAGCTCTTCAAATGGGGGCATATGCTATCAACAATATTC      | 3840 |
| Db | 3748 | TACATTTTCATCTCGGAAAGCTCTTCAAATGGGGGCATATGCTATCAACAATATTC      | 3807 |
| QY | 3841 | ACCAATGCTGTGTGTGGCTGACCTCTTAATGTGTGATGTTTCATTGGTCAGTTTACA     | 3900 |
| Db | 3808 | ACCAATGCTGTGTGTGGCTGACCTCTTAATGTGTGATGTTTCATTGGTCAGTTTACA     | 3867 |
| QY | 3901 | GCAATGCTGTGGGTATCTACAAACCTTGGAGGCATCAAACTCTCAGACACTAAGACT     | 3960 |
| Db | 3868 | GCAATGCTGTGGGTATCTACAAACCTTGGAGGCATCAAACTCTCAGACACTAAGACT     | 3927 |
| QY | 3961 | CTGAGACCTCTTAAGACCTTATCTCGAATTGAAGGATGAGGAGGTGTGAATGCCCT      | 4020 |
| Db | 3928 | CTGAGACCTCTTAAGACCTTATCTCGAATTGAAGGATGAGGAGGTGTGTGAATGCCCT    | 3987 |
| QY | 4021 | TTAGAGCAATTCATCATCATGAAATGTCTTCTGTGTTGTCTAATATTCGTGCTAAT      | 4080 |
| Db | 3988 | TTAGAGCAATTCATCATCATGAAATGTCTTCTGTGTTGTCTAATATTCGTGCTAAT      | 4047 |
| QY | 4081 | TTGACATCATGAGGCGCTAAATTTGTTGCTGGCAATCTCCACCTGATTAACACACA      | 4140 |
| Db | 4048 | TTGACATCATGAGGCGCTAAATTTGTTGCTGGCAATCTCCACCTGATTAACACACA      | 4107 |
| QY | 4141 | ACTGTGTACAGGTTTGACATTCGAACGCTGAATATTCATCTGATGGCTTAAACTATA     | 4200 |
| Db | 4108 | ACTGTGTACAGGTTTGACATTCGAACGCTGAATATTCATCTGATGGCTTAAACTATA     | 4167 |
| QY | 4201 | GAAGAAGATGAGCTCTCGATGTGAAAAATGTGAAAGTAACTTTGATATGTGCAATTT     | 4260 |
| Db | 4168 | GAAGAAGATGAGCTCTCGATGTGAAAAATGTGAAAGTAACTTTGATATGTGCAATTT     | 4227 |
| QY | 4261 | GGGTATCTCTTTGCTTCAATTCGCCACATTCAAAGATGATGATTAATATGTATGCA      | 4320 |
| Db | 4228 | GGGTATCTCTTTGCTTCAATTCGCCACATTCAAAGATGATGATTAATATGTATGCA      | 4287 |
| QY | 4321 | GCAGTTGATTCAGAAATGTGAACTCAGCCCTAAGTATGAAGAAAGTCTGTACATGTAT    | 4380 |
| Db | 4288 | GCAGTTGATTCAGAAATGTGAACTCAGCCCTAAGTATGAAGAAAGTCTGTACATGTAT    | 4347 |

|    |      |  |        |
|----|------|--|--------|
| OY | 4381 | CTTTCACCTTTGGATTATTTTCAACATCCTTTGGGCTCCTTCCACCTGAAACCTGTTATTTGGT | 4440.0 |
| Db | 4348 | CTTTACCTTTGGATTATTTTCAACATCCTTTGGGCTCCTTCCACCTGAAACCTGTTATTTGGT  | 4407.0 |
| OY | 4441 | GTCAATCAGATGATATTTTCAACACGACGAAAAAAGACTTTGGAGGTCAAGACATCTTATG    | 4500.0 |
| Db | 4408 | GTCAATCAGATGATATTTTCAACACGACGAAAAAAGACTTTGGAGGTCAAGACATCTTATG    | 4467.0 |
| OY | 4501 | ACGAGAAACAGAAAGAAATCTATATATGCAATGAAAAAATTTAGATCGAAAAACCGCA       | 4560.0 |
| Db | 4468 | ACAGAAAGAAACAGAAAGAAATCTATATATGCAATGAAAAAATTTAGATCGAAAAACCGCA    | 4527.0 |
| OY | 4561 | AAGCCTATACCTGCACACGAGAAACAAATTTCAAGSAAAGCTGTTTGACTGTCTGTACACGA   | 4620.0 |
| Db | 4528 | AAGCCTATACCTGCACACGAGAAACAAATTTCAAGSAAAGCTGTTTGACTGTCTGTACACGA   | 4587.0 |
| OY | 4621 | CAAGTTTGTGACATTAACATCATCATGATTCATCTGCTTAACATGATGGTCAATGATGGTG    | 4680.0 |
| Db | 4588 | CAAGTTTGTGACATTAACATCATCATGATTCATCTGCTTAACATGATGGTCAATGATGGTG    | 4647.0 |
| OY | 4681 | GAACACAGTACACGAGTGAATATGTGACTACCAATTTGTCAAGCAATCTGGTGTTC         | 4740.0 |
| Db | 4648 | GAACACAGTACACGAGTGAATATGTGACTACCAATTTGTCAAGCAATCTGGTGTTC         | 4707.0 |
| OY | 4741 | ATTGCGCATTTACTGAGAGGTGTGTACTGAAACATCATCTCTCTACGCCATTTATTTT       | 4800.0 |
| Db | 4708 | ATTGCGCATTTACTGAGAGGTGTGTACTGAAACATCATCTCTCTACGCCATTTATTTT       | 4767.0 |
| OY | 4801 | ACCATTGGATGGAATATTTTGGATTTTGGTGTGTCATCTCTCCATTGTGTGATGTTT        | 4860.0 |
| Db | 4768 | ACCATTGGATGGAATATTTTGGATTTTGGTGTGTCATCTCTCCATTGTGTGATGTTT        | 4827.0 |
| OY | 4861 | CTTGCCGAGCTGATAGAAAAGTATTTCTGTCTCCCTACCCCTGTTCCGAGTATCCGTTT      | 4920.0 |
| Db | 4828 | CTTGCCGAGCTGATAGAAAAGTATTTCTGTCTCCCTACCCCTGTTCCGAGTATCCGTTT      | 4887.0 |
| OY | 4921 | GCTAGGATTTGGCCGAATCTCTACGTCTGTGATCAAAAGAGCAAGGGATCTCCACGCTGCTC   | 4980.0 |
| Db | 4888 | GCTAGGATTTGGCCGAATCTCTACGTCTGTGATCAAAAGAGCAAGGGATCTCCACGCTGCTC   | 4947.0 |
| OY | 4981 | TTTCTCTTGAAGATGTCCTCTCCCTGCTGTTTAAACATCGGCTCTCTACTTCTCTAGTC      | 5040.0 |
| Db | 4948 | TTTCTCTTGAAGATGTCCTCTCCCTGCTGTTTAAACATCGGCTCTCTACTTCTCTAGTC      | 5007.0 |
| OY | 5041 | ATGTTCATCTACGCGCATCTTTGGATGTCCAACTTGGCTATGTTAAGAGGGAAGTTGGG      | 5100.0 |
| Db | 5008 | ATGTTCATCTACGCGCATCTTTGGATGTCCAACTTGGCTATGTTAAGAGGGAAGTTGGG      | 5067.0 |
| OY | 5101 | ATTCATGACATGTTCAACTTTAGACCTTTGGCAACAGACATGATCTGCTATTTCCAAAT      | 5160.0 |
| Db | 5068 | ATTCATGACATGTTCAACTTTAGACCTTTGGCAACAGACATGATCTGCTATTTCCAAAT      | 5127.0 |
| OY | 5161 | ACAACCTCTGCTGGCTGGGATGGATGTCTAAGAACCCATTCTCAACAGTAACGACCCGAC     | 5220.0 |
| Db | 5128 | ACAACCTCTGCTGGCTGGGATGGATGTCTAAGAACCCATTCTCAACAGTAACGACCCGAC     | 5187.0 |
| OY | 5221 | TGTGACCCTATAAAGTTAAACCTGTGAAGCTCAGTTAAGAGAGATGTGGGAACCCATCT      | 5280.0 |
| Db | 5188 | TGTGACCCTATAAAGTTAAACCTGTGAAGCTCAGTTAAGAGAGATGTGGGAACCCATCT      | 5247.0 |
| OY | 5281 | GTTTGGATTTTCTTTTGTGACGATTACATCATCATATCTCTCTGTGTGTGTGTAACATG      | 5340.0 |
| Db | 5248 | GTTTGGATTTTCTTTTGTGACGATTACATCATCATCATATCTCTCTGTGTGTGTGTAACATG   | 5307.0 |
| OY | 5341 | TACATCGCGGTACCTCGGAGAACTTCACTGTTGCTACTGAAAGAAAGTGCAGAACCTCTG     | 5400.0 |
| Db | 5308 | TACATCGCGGTACCTCGGAGAACTTCACTGTTGCTACTGAAAGAAAGTGCAGAACCTCTG     | 5367.0 |
| OY | 5401 | AGTAGAGATGACTTTGAGATGTTTCTATAGAGTTTGGAGAAAGTTTGATCCCGATGCAACT    | 5460.0 |
| Db | 5368 | AGTAGAGATGACTTTGAGATGTTTCTATAGAGTTTGGAGAAAGTTTGATCCCGATGCAACT    | 5427.0 |
| OY | 5461 | CAGTTACAGAAATTTGAAAAATTAATCTCAGTTTGACAGCTGCGCTTGAACCGCTCTCAAT    | 5520.0 |

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Db 5488 CTGGCCACAACCAAAACAACATCCAGCTCAATGGCATGGATTTGGCCATGGATGGTGCAC 5547  
Oy 5581 CGGATCCCATCTGCTTATATATCTTATTTGCTTTTACAAAGCGGCTCTAGACAGACTGA 5640  
Db 5548 CGGATCCCATCTGCTTATATCTTATTTGCTTTTACAAACGGGCTCTAGAGAGACTGA 5607  
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|            |   |
|------------|---|
| RESULT     | 5   |
| A0043484   |   |
| LOCUS      |   |
| DEFINITION | 6046 bp mRNA linear PRI 24-APR-2002<br>Homo sapiens voltage-gated sodium channel type I mRNA, complete cds.   |
| ACCESSION  | AY043484  |
| VERSION    | AY043484  |
| KEYWORDS   | GI:15421161   |
| SOURCE     |   |
| ORGANISM   | Homo sapiens.<br>Homo sapiens.<br>Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;<br>Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.<br>1 (bases 1 to 6046)<br>Sugawara,T., Mazaki-Miyazaki,E., Fukushima,K., Shimonura,J.,<br>Fujiwara,T., Hamano,S., Inoue,Y. and Yamakawa.K.<br>Frequent mutations of SCN1A in severe myoclonic epilepsy in infancy<br>Neurology 58 (7), 1122-1124 (2002) |
| TITLE      |   |
| JOURNAL    |   |
| MEDLINE    | 21938587  |
| PUBMED     | 11940708  |
| REFERENCE  | 2 (bases 1 to 6046)<br>Sugawara,T., Mazaki,E.M. and Yamakawa,K.<br>Homo sapiens neuronal voltage-gated sodium channel type I (Nav1.1) mRNA  |
| AUTHORS    | Unpublished<br>3 (bases 1 to 6046)<br>Sugawara,T., Mazaki,E.M. and Yamakawa,K.<br>Direct Submission<br>Submitted (03-JUL-2001) Neurogenetics, BSI, RIKEN, 2-1 Hirosawa,<br>Wako, Saitama 351-0198, Japan  |
| JOURNAL    |   |
| FEATURES   | Location/Qualifiers<br>1..6046  |
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 FMGIYFESLKIILANGFCEDEPTELRODMNMLDVFITPAVTEVDIGSALATP  
 RYLRALKTSVIGKILYAGLISYKISDMILVPLSLPALIGLIPGONLANK  
 CLOMPPTNALSLEHSIEKNTYNTNIGTLINETVEEDMSTYIDSHYHLEFSDAL  
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BASE COUNT 1808 a 1188 c 1345 g 1704 t 1 others

Query Match 98.5%; Score 5941.2; DB 9; Length 6046;  
 Best Local Similarity 99.3%; Pred. No. 0;  
 Matches 5986; Conservative 4; Mismatches 7; Indels 33; Gaps 1;

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 1201 ATATTTTGTGTGATCATTTCTTGGGCTCAATTCATTAATTAATTTGATCGGGCT 1260  
 1261 GTGTGTGCTATGCTTACAGAGAGCAAGAAATCAGGCACTTGGAAAGAGCAAGAA 1320  
 1261 GTGTGTGCTATGCTTACAGAGAGCAAGAAATCAGGCACTTGGAAAGAGCAAGAA 1320  
 1321 GAGGCGGAATTTGAGAGAGATGATGAGCACTTAAAGAAAGAGAGAGAGAGAGAG 1380  
 1321 GAGGCGGAATTTGAGAGAGATGATGAGCACTTAAAGAAAGAGAGAGAGAGAGAG 1380  
 1381 GAGGCGGAATTTGAGAGAGATGATGAGCACTTAAAGAAAGAGAGAGAGAGAGAG 1440  
 1381 GAGGCGGAATTTGAGAGAGATGATGAGCACTTAAAGAAAGAGAGAGAGAGAGAG 1440



|    |      |   |      |
|----|------|---|------|
| OY | 1441 | GACAGCTCATCGAAGCCCTAGTGGATGCTCCAGAAGTCGAAGAAAGCAAAATCGG       | 1500 |
| Db | 1441 |   |      |
| OY | 1441 | GACAGCTCATCGAAGCCCTAGTGGATGCTCCAGAAGTCGAAGAAAGCAAAATCGG       | 1500 |
| Db | 1441 |   |      |
| OY | 1501 | AGGAAGAAAAGAAACAGAAAGAGCAGTGTGTGGGAGAGAAAGATGAGATGCAATTC      | 1560 |
| Db | 1501 |   |      |
| OY | 1561 | CAAAAATCTGAATCTGAGAGACAGCATCAGAGAGAAAGTTTGCTTCATTGGAAGGG      | 1620 |
| Db | 1561 |   |      |
| OY | 1621 | AACCGATTACATPATAAGAAAGGTACTCTGCCACACAGCTTTGTTGAGCATCCGT       | 1680 |
| Db | 1621 |   |      |
| OY | 1681 | GCGTCCCTATTTTTCACCAGGCGGAATATAGACAACAAGCCTTTTACAGTTTAGAGGCGA  | 1740 |
| Db | 1681 |   |      |
| OY | 1741 | GCAAAGGATGTGGATCTGAGAACGACTTTCGAGATGATGACACAGCACCTTTAGAGAT    | 1800 |
| Db | 1741 |   |      |
| OY | 1801 | AACGAGAGCCGTAGAGATTCCTTTGTTGGCCCCGAGCAGCAGGAGAGAGAGCAACAGC    | 1860 |
| Db | 1801 |   |      |
| OY | 1861 | AACCTGAGTCAGACACAGTATGATCCCGAATGCTGGCAGTGTTCACAGGAATGGGAAG    | 1920 |
| Db | 1861 |   |      |
| OY | 1921 | ATGCACAGACTGTGGATTTGCAATGGTGTGTTTCTGTGGTTGGTGGACTTATGTTCT     | 1980 |
| Db | 1921 |   |      |
| OY | 1981 | ACATGGCCTGTGGACAGCTTCTGCAGAGGTGATTAATAGATTAAGCAGCACTACTGATGAC | 2040 |
| Db | 1981 |   |      |
| OY | 2041 | AATGGAACAACCATGAAATCTGAATGAGAAAGAGAGSTCAAGTTCTTCCAGCTTTCC     | 2100 |
| Db | 2041 |   |      |
| OY | 2101 | ATGSACTTCTGAGAGATCCTCCCAAGGCAAGCAGCAATAGTATAGCCAGCATTCRA      | 2160 |
| Db | 2101 |   |      |
| OY | 2161 | ACAATATACAGTGAAGAACTTGAAGATCCAGGACAGAAATGCCACCTGTGGTATTA      | 2220 |
| Db | 2161 |   |      |
| OY | 2221 | TTTTCCAACATATCTTAATCTGGGACGTGTCTCATATTTGGTTAAAGTGAACATGTT     | 2280 |
| Db | 2221 |   |      |
| OY | 2281 | GTCACCTGTGTATGAGAACCATTTGTGACCTGGCCATCACCATCTGATGCTTA         | 2340 |
| Db | 2281 |   |      |
| OY | 2341 | AATATCTTTTCATGGCCATGAGACATATCCAAATGACGACCATTTCAATATGTCCT      | 2400 |
| Db | 2341 |   |      |
| OY | 2401 | ACAGATGAGAAATGTGGTTTTCATGCGGATCTTTACAGCAGAAATGTTTCTGAATATAT   | 2460 |
| Db | 2401 |   |      |
| OY | 2461 | GCCATGATTCCTTACTATATATTTCCAGAAGGCTGGAATATCTTTGACGTTTATGTTG    | 2520 |
| Db | 2461 |   |      |
| OY | 2521 | GGCAATGATTCCTTACTATATATTTCCAGAAGGCTGGAATATCTTTGACGTTTATGTTG   | 2580 |
| Db | 2521 |   |      |



VLNLFLLALLSSFSADWLAATDDNENANNLOIADPRHAKGVAAYKRIYEIPEOIOSFR  
KOKLIDIEKPLDLDNKKDSOMSHTEIEKDKLDLDVNGTGTGGGDSVEKYLII  
ESDMSPFINNPSLTVYPIVAVGESDFDPEPSSDSSEKRIENESSSEST  
VGRHAPEROBPOYBERTEIIPACFTTCGVOFRCCOINVEBGRKWMNLRRCPI  
VENHMEPTIYPMALLSSGALAFEDTITDOKITIKTMELETAOKFTTITLEMLKAV  
AIGIOTIFINAMCMLDPLIVDSLVLSLNAHNGISELGAIKSLTLPYLRRLSRE  
EGKRWVNNALLGALPSLIMNVLVCLLEWLFISMGVNLFGFKETHCINTYVGRDFIE  
DVNNHDDCLKLEIERNETARKNRVNDVNGFGLSLNOVATKRGKGDOWIAYADNSO  
VELDOPKEESLIMYLIVFPIIFGSPFTLNLFGVILIDNNOOKRKGGOIPEWESQ  
KOSYNNARKKLGSRKPOKPIPRPGKPGMAGFEDTPOVPIISIMILLCLNMTYAVET  
DDSEVYTTLSIRINLIVEFPGTCECVLILNHYFTYGMNLEFVVVYLISVGEK  
LAELIEKYPFVSPLEFVIRIARIGIRILIRIKGAGGIMTLEALMSAPLENGILF  
LWELIYVIFGMSNFAVYKREMGIDNEFGSMGLCOITTSAGMDLAPILINS  
KSPDPCDNKRNPPSSVGGDCGNPSVGIJFEFVYYSILVANNVYATILENVSVAPE  
ESAPDLESDEPEMPEYMEREPDPAOGFEMFERLISORAALEPLINPOIRKQILIAM  
DLWVSGDRIRHICDLIDLEAFTRKVLGSGEGBDMLRIQREPRMANSBKSVOITPITTL  
KRODEEYSAVUIORATRNHLLKRVKAVSPFYNNKIRKGANLITIKEDMTIDIRINENS  
ITTEETDITJMSJTAACPSPIYDRVYKPIVYKHOEGBDEKAVAK\*

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|----|------|--|------|
| QY | 721  | ATCCAGTCTGTGAAGAGCTCTCAGATGTATATGATCTCTGACTGTCTTGTCTGAGGCTA    | 760  |
| Db | 739  | ATCCAGTCTGTGAAGAGCTCTCAGATGTATATGATCTCTGACTGTCTTGTCTGAGGCTA    | 798  |
| QY | 781  | TTTCTCTAATTTGGGGTGGAGCTGTTCATGGGGCAACCTGAGAAATTAATGTATCAATGG   | 840  |
| Db | 799  | TTTCTCTAATTTGGGGTGGAGCTGTTCATGGGGCAACCTGAGAAATTAATGTATCAATGG   | 858  |
| QY | 841  | CTTCCCAACAATGGTCTCTTGGAGGACATAGTATAGAAAAGAAATTAATCTGTAATTTAT   | 900  |
| Db | 859  | CTTCCCAACAATGGTCTCTTGGAGGACATAGTATAGAAAAGAAATTAATCTGTAATTTAT   | 918  |
| QY | 901  | AATGGTACACTTATTAATTAATGAAACTGTCTTGTGATTTGATCGAATCTATATATTCAGAT | 960  |
| Db | 919  | AATGGTACACTTATTAATTAATGAAACTGTCTTGTGATTTGATCGAATCTATATATTCAGAT | 978  |
| QY | 961  | TCAGATATCATTTATTTTCCGAGAGGGTTTTTATGATGACTACTATGTGAAATAGCTCT    | 1020 |
| Db | 979  | TCAGATATCATTTATTTTCCGAGAGGGTTTTTATGATGACTACTATGTGAAATAGCTCT    | 1038 |
| QY | 1021 | GATGAGGCCAATGTCCAGAGGGATATATGTGTGTAAAGCTGTGTAGAAATCCCAATTAAT   | 1080 |
| Db | 1039 | GATGAGGCCAATGTCCAGAGGGATATATGTGTGTAAAGCTGTGTAGAAATCCCAATTAAT   | 1098 |
| QY | 1081 | GGCTACACAACTTTGATTTACTCTCAGTGGGGCTTTTTTGTCTCTGTTTCGACTAATGACT  | 1140 |
| Db | 1099 | GGCTACACAACTTTGATTTACTCTCAGTGGGGCTTTTTTGTCTCTGTTTCGACTAATGACT  | 1158 |
| QY | 1141 | CAGGACTTTGGGAAAATCTTTATCAACATGACATTAACGTCTGTGGGAAAACGTACATG    | 1200 |
| Db | 1159 | CAGGACTTTGGGAAAATCTTTATCAACATGACATTAACGTCTGTGGGAAAACGTACATG    | 1218 |
| QY | 1201 | ATATTTTGTGTGTGTCTATTTTCTTGGGCTACTTCTACTTAATTAATTTGATCTGTGCT    | 1260 |
| Db | 1219 | ATATTTTGTGTGTGTCTATTTTCTTGGGCTACTTCTACTTAATTAATTTGATCTGTGCT    | 1278 |
| QY | 1261 | GTGTGGCCATGSCCTACGAGGAAACAGATCAGGCCACTTGGAGAAAGCAACACAA        | 1320 |
| Db | 1279 | GTGTGGCCATGSCCTACGAGGAAACAGATCAGGCCACTTGGAGAAAGCAACACAA        | 1338 |
| QY | 1321 | GAGGCCAAATTTCAAGAGATGATTTGAACACTTAAATAACAACAGAGGACAGCTCAGAG    | 1380 |
| Db | 1339 | GAGGCCAAATTTCAAGAGATGATTTGAACACTTAAATAACAACAGAGGACAGCTCAGAG    | 1398 |
| QY | 1381 | GCAGCAACGGCACTGCTCAGAACATTCAGAGAGCCCAAGTGCACAGCAGGCTCTCA       | 1440 |
| Db | 1399 | GCAGCAACGGCACTGCTCAGAACATTCAGAGAGCCCAAGTGCACAGCAGGCTCTCA       | 1458 |
| QY | 1441 | GACAGCTCATGTGAAGCTCTAAGTTGAGTCCAAAGAGGTCTAAGGAAAGAAATAGG       | 1500 |
| Db | 1459 | GACAGCTCATGTGAAGCTCTAAGTTGAGTCCAAAGAGGTCTAAGGAAAGAAATAGG       | 1518 |
| QY | 1501 | AGGAAGAAAAGAAAACAGAAAGAGCACTCTGTGTGGGGAAGAGAAAGATAGAGTAATTC    | 1560 |
| Db | 1519 | AGGAAGAAAAGAAAACAGAAAGAGCACTGTGTGTGGGGAAGAGAAAGATAGAGTAATTC    | 1578 |
| QY | 1561 | CAAAAATCTGAATCTGAGAGCAGATATAGAGGAAAGTTTTGCTCTCCATTTAAAGG       | 1620 |
| Db | 1579 | CAAAAATCTGAATCTGAGAGCAGATATAGAGGAAAGTTTTGCTCTCCATTTAAAGG       | 1638 |
| QY | 1621 | AACCGATTGACATTTGAAAAGAGGTACTCTCTCCCAACACAGTCTTTGTTGAGCAATCCGT  | 1680 |
| Db | 1639 | AACCGATTGACATTTGAAAAGAGGTACTCTCTCCCAACACAGTCTTTGTTGAGCAATCCGT  | 1698 |
| QY | 1681 | GGCTCCCTAATTTTCAACAGGCGCAAAATAGCAAAACAAGCCTTTTACGCTTTAGAGGCGA  | 1740 |
| Db | 1699 | GGCTCCCTAATTTTCAACAGGCGCAAAATAGCAAAACAAGCCTTTTACGCTTTAGAGGCGT  | 1758 |
| QY | 1741 | GCAAAAGATTTGGGCTGTGAAAGCAATTCGCAAGATGATGAGAGACAGCACTTTAGAGAT   | 1800 |
| Db | 1759 | GCAAAAGATTTGGGCTGTGAAAGCAATTCGCAAGATGATGAGAGACAGCACTTTAGAGAT   | 1818 |
| QY | 1801 | AACGAGACCGTAGATTTCCGTTTGTGCCCCGACGACAGGACAGACGCAACAGC          | 1860 |

|    |      |   |      |
|----|------|---|------|
| Db | 1819 | AACGAGACCGCTGAGATTCTTTGTGTGCCCCGACACACACGAGAGACGACAC          | 1878 |
| Qy | 1861 | AACCTGATCAGACACAGTAGTCATCCGGATGCTGGCAGTGTTCACAGCAATGGGAG      | 1920 |
| Db | 1879 | AACCTGATCAGACACAGTAGTCATCCGGATGCTGGCAGTGTTCACAGCAATGGGAG      | 1938 |
| Qy | 1921 | ATGACACGACCTGTGTGATTCGCAATGCTGTGCTTCCTTGTTGGGACCTTCAGTTC      | 1980 |
| Db | 1939 | ATGACACGACCTGTGTGATTCGCAATGCTGTGCTTCCTTGTTGGGACCTTCAGTTC      | 1998 |
| Qy | 1981 | ACATCGCCTTGTGACAGCTTCGCGACAGAGTGATTAAGATTAAGCCAGCTACGATGAC    | 2040 |
| Db | 1999 | ACATCGCCTTGTGACAGCTTCGCGAGG-----                              | 2028 |
| Qy | 2041 | AATGGACAACACCTGAAACTGAATGAGAAAGAGAGTCAGTTCCTTCACAGTTCC        | 2100 |
| Db | 2029 | ---GGAAACAACCACTGAACTGAAAGAAAGAAAGAAAGTCAAGTCTTCACAGTTCC      | 2085 |
| Qy | 2101 | ATGACATTTTACAGATGCTCTCCCAAAGCAACGACAATGATATGACAGATTCCTA       | 2160 |
| Db | 2086 | ATGACATTTTACAGATGCTCTCCCAAAGCAACGACAATGATATGACAGATTCCTA       | 2145 |
| Qy | 2161 | ACAATATCAGTAGAGACTTGAAGATTCAGGACGAGAAATGCCACCTGTGTGATAAA      | 2220 |
| Db | 2146 | ACAATATCAGTAGAGAACTTGAAGATTCAGGACGAGAAATGCCACCTGTGTGATAAA     | 2205 |
| Qy | 2221 | TTTTCCAAACATTTCTTAATCTGGGACTGTCCATATATGTGTTAAAGTGAACATGT      | 2280 |
| Db | 2206 | TTTTCCAAACATTTCTCAATCTGGGACTGTTCCTCCATATGTGTTAAAGTGAACATGT    | 2265 |
| Qy | 2281 | GTCAACCTGCTGTGTATGAGACCCATTTGTGACCTGGCCATCACCATCTGTATGTCTTA   | 2340 |
| Db | 2266 | GTCAACCTGCTGTGTATGAGACCCATTTGTGACCTGGCCATCACCATCTGTATGTCTTA   | 2325 |
| Qy | 2341 | AATCTCTTTTCAATGCGCATGAGGACACTATCCAAATGACGACATTCCTAAATATGTCTT  | 2400 |
| Db | 2326 | AATCTCTTTTCAATGCGCATGAGGACACTATCCAAATGACGACATTCCTAAATATGTCTT  | 2385 |
| Qy | 2401 | ACAATGAGAAACTGTGTTTTCACTGGGATCTTTACAGCAGAAATGTTCTCGAAATATTT   | 2460 |
| Db | 2386 | ACAATGAGAAACTGTGTTTTCACTGGGATCTTTACAGCAGAAATGTTCTCGAAATATTT   | 2445 |
| Qy | 2461 | GCCATGATCCTTACTATATATTTTCCAAAGAGCTGGAATATCTTTGACGGTTATATGTCG  | 2520 |
| Db | 2446 | GCCATGATCCTTACTATATATTTTCCAAAGAGCTGGAATATCTTTGACGGTTATATGTCG  | 2505 |
| Qy | 2521 | ACGCTTACCGTGTGAGAACTTGGACTGCGCAATGTGGAAGATTAATCTGTCTCCGTCA    | 2580 |
| Db | 2506 | ACGCTTACCGTGTGAGAACTTGGACTGCGCAATGTGGAAGATTAATCTGTCTCCGTCA    | 2565 |
| Qy | 2581 | TTTGCATTTGCTGCGAGTTTCCAAAGTTGGCAAAATCTTGCGCAACGTTAAATATGCTATA | 2640 |
| Db | 2566 | TTTGCATTTGCTGCGAGTTTCCAAAGTTGGCAAAATCTTGCGCAACGTTAAATATGCTATA | 2625 |
| Qy | 2641 | AAGATCATCGGCATTTCCGTGGGGGCTGTGGAAATTTAAACCTGCTGTGGCAATCATC    | 2700 |
| Db | 2626 | AAGATCATCGGCATTTCCGTGGGGGCTGTGGAAATTTAAACCTGCTGTGGCAATCATC    | 2685 |
| Qy | 2701 | GTTCTCATTTTTGCGCGTGTGCGGACTGACAGCTCTTTGTAAAAAGCTACAAAGATGTGTC | 2760 |
| Db | 2686 | GTTCTCATTTTTGCGCGTGTGCGGACTGACAGCTCTTTGTAAAAAGCTACAAAGATGTGTC | 2745 |
| Qy | 2761 | TGCAAGATCGCAGATGATTCGAAACATGCC---ACGTGGCAATGAAGATCTCTTCAC     | 2817 |
| Db | 2746 | TGCAAGATCGCAGATGATTCGAAACATGCCAGCGTGGCAATGAAGATCTCTTCAC       | 2805 |
| Qy | 2818 | TCTTCTCCTGATTGTGTCCTCGCTGCTGTGTGTGGGAGTGAATGAGACCATGTGGGACTGT | 2877 |
| Db | 2806 | TCTTCTCCTGATTGTGTCCTCGGCTGTGTGTGGGAGTGAATGAGACCATGTGGGACTGT   | 2865 |
| Qy | 2878 | ATGAGAGTGTGTGATCAAGCATGTGCTTACTGTCTTATATATGTCATGTGATTTGGA     | 2937 |

Db 2866 ATGGAGGTCGTGCTCAAGCCATGTCCTTACTGCTTCATGATGTCATGCTGATTTGGA 2925  
 Oy 2938 AACCTAGGTGCTGTAATCTCTTCTGACCTCTCTTGTAGCTCATTTAGTCAGACAAC 2997  
 Db 2926 AACCTAGGTGCTGTAATCTCTTCTGACCTCTCTTGTAGCTCATTTAGTCAGACAAC 2985  
 Oy 2998 CTTGACGCACTGATGATGATTAATGAATGATTAATCTCCAAATTCCTGATAGGATG 3057  
 Db 2986 CTTGACGCACTGATGATGATTAATGAATGATTAATCTCCAAATTCCTGATAGGATG 3045  
 Oy 3058 CACAAAGAGTACTATGTAAGAAAATTAATGATTTATGTAACAGCTTCAT 3117  
 Db 3046 CACAAAGAGTACTATGTAAGAAAATTAATGATTTATGTAACAGCTTCAT 3105  
 Oy 3118 AGAAACAAAGATTTTATGATGTAATTAACCACTGATGATCTTAACACAGAAAGAC 3177  
 Db 3106 AGAAACAAAGATTTTATGATGTAATTAACCACTGATGATCTTAACACAGAAAGAC 3165  
 Oy 3178 ACTGTATGTCATCATACACAGAAATGGGAAAGATCTTACTATCTTAAAGATGA 3237  
 Db 3166 ACTGTATGTCATCATACACAGAAATGGGAAAGATCTTACTATCTTAAAGATGA 3225  
 Oy 3238 AATGAACTACAAAGTGTATAGAACTGGCAGACAGTGTGAAGAAATACATTTATGATGA 3297  
 Db 3226 AATGAACTACAAAGTGTATAGAACTGGCAGACAGTGTGAAGAAATACATTTATGATGA 3285  
 Oy 3298 ACTGATTTACATGCTATTAACCAACCCAGCTCTTACTGATGATCTTAACCAATGCTGA 3357  
 Db 3286 ACTGATTTACATGCTATTAACCAACCCAGCTCTTACTGATGATCTTAACCAATGCTGA 3345  
 Oy 3358 GGAGAACTGACTTTGAAAAATTTAAACAGGAAAGACTTATGATGAAATCGATCTGAA 3417  
 Db 3346 GGAGAACTGACTTTGAAAAATTTAAACAGGAAAGACTTATGATGAAATCGATCTGAA 3405  
 Oy 3418 GAAAGAAAGAAATGATGATGAAAGCACTACTGATGAAAGTACAGCTGTGACATC 3477  
 Db 3406 GAAAGAAAGAAATGATGATGAAAGCACTACTGATGAAAGTACAGCTGTGACATC 3465  
 Oy 3478 GCGCAGACCTGTAGAAAGACCCGCTGATGAAAGCTGAAAGAACTTTGAAACAGAGCT 3537  
 Db 3466 GCGCAGACCTGTAGAAAGACCCGCTGATGAAAGCTGAAAGAACTTTGAAACAGAGCT 3525  
 Oy 3538 TGTTCACCTGAAAGCTGTGTACAAAGATTCAAAGTGTGTCAATCAATGTGAAAGAGC 3597  
 Db 3526 TGTTCACCTGAAAGCTGTGTACAAAGATTCAAAGTGTGTCAATCAATGTGAAAGAGC 3585  
 Oy 3598 AGAGGAAACAAATGGTGAAGCTGAAAGAGAGCTTTCCGAAATGTTGAATAATACCTG 3657  
 Db 3586 AGAGGAAACAAATGGTGAAGCTGAAAGAGAGCTTTCCGAAATGTTGAATAATACCTG 3645  
 Oy 3658 TTTGAGACCTTATGTTTTCATGATTCCTTATGATGAGTGTCTGTGCACTTTGAAGAT 3717  
 Db 3646 TTTGAGACCTTATGTTTTCATGATTCCTTATGATGAGTGTGTCTGTGCACTTTGAAGAT 3705  
 Oy 3718 ATATATATGATCAGGAAAGACATTAAGACATGTGGAATATGCTGACAAAGTTTTTC 3777  
 Db 3706 ATATATATGATCAGGAAAGACATTAAGACATGTGGAATATGCTGACAAAGTTTTTC 3765  
 Oy 3778 ACTTACATTTTCAATCTGGAATGCTTCAAAATGGTGGCATATGAGCATATCAACATAT 3837  
 Db 3766 ACTTACATTTTCAATCTGGAATGCTTCAAAATGGTGGCATATGAGCATATCAACATAT 3825  
 Oy 3838 TTTACCAATGCTGTGTGTGTGCTGACTTCTTAATTTGTTGATGTTTCAATTTGCTAGTTTA 3897  
 Db 3826 TTTACCAATGCTGTGTGTGTGCTGACTTCTTAATTTGTTGATGTTTCAATTTGCTAGTTTA 3885  
 Oy 3898 ACAGCAATGCTGT 3957  
 Db 3886 ACAGCAATGCTGT 3945  
 Oy 3958 GCTGTGAGACCTTAAGAGACCTTATCTGATTTGAAGGATGAGGTTGTGTGTGTGTGTGTGT 4017  
 Db 3946 GCTGTGAGACCTTAAGAGACCTTATCTGATTTGAAGGATGAGGTTGTGTGTGTGTGTGTGT 4005

Oy 4018 CTTTATGAGCAATTTCCATCATCATGAATGTGCTTCTGTGTTGTCTTATATTTGTGGCTA 4077  
 Db 4006 CTTTATGAGCAATTTCCATCATCATGAATGTGCTTCTGTGTTGTCTTATATTTGTGGCTA 4065  
 Oy 4078 ATTTTCAGCATATGAGGCTAAATTTTGTGTGCTGGCAAAATTTCCACATGCTATTAACACC 4137  
 Db 4066 ATTTTCAGCATATGAGGCTAAATTTTGTGTGCTGGCAAAATTTCCACATGCTATTAACACC 4125  
 Oy 4138 ACAACTGTGACAGTTTGATCATCGAAGCTGATTAATCATCTGATTTGCTTAAACTA 4197  
 Db 4126 ACAACTGTGACAGTTTGATCATCGAAGCTGATTAATCATCTGATTTGCTTAAACTA 4185  
 Oy 4198 ATAGAAAGAAATGAGACTCTGATGAAATATGTAAGTAACTTTGATTAATGAGGA 4257  
 Db 4186 ATAGAAAGAAATGAGACTCTGATGAAATATGTAAGTAACTTTGATTAATGAGGA 4245  
 Oy 4258 TTTGGTATCTCTCTTCTGCTCAAGTTGCCACATTCOAAGATGATGATATTAATGAT 4317  
 Db 4246 TTTGGTATCTCTCTTCTGCTCAAGTTGCCACATTCOAAGATGATGATATTAATGAT 4305  
 Oy 4318 GCAGCAGTTGATTCAGAAATGTGGAATCTCCAGCTTAATGATGAAAGTCTGATCATG 4377  
 Db 4306 GCAGCAGTTGATTCAGAAATGTGGAATCTCCAGCTTAATGATGAAAGTCTGATCATG 4365  
 Oy 4378 TATCTTACTTTGTTATTTTCAATCATCTTGGGCTCTCTCACTTGAACCTGTTAT 4437  
 Db 4366 TATCTTACTTTGTTATTTTCAATCATCTTGGGCTCTCTCACTTGAACCTGTTAT 4425  
 Oy 4438 GGTGCATCATGATTAATTTCAACAGCAGAAAGAAAGATTTGAGCTCAAGCATCTT 4497  
 Db 4426 GGTGCATCATGATTAATTTCAACAGCAGAAAGAAAGATTTGAGCTCAAGCATCTT 4485  
 Oy 4498 ATGACAGAAAGACAGAAATATCTTAATGCAATGAAAAATTTAGATCGAAAAACCG 4557  
 Db 4486 ATGACAGAAAGACAGAAATATCTTAATGCAATGAAAAATTTAGATCGAAAAACCG 4545  
 Oy 4558 CAAAAGCTATCTCTGACAGAAACAAATTTCAAGGAATGGTCTTGAATCTGTAAC 4617  
 Db 4546 CAAAAGCTATCTCTGACAGAAACAAATTTCAAGGAATGGTCTTGAATCTGTAAC 4605  
 Oy 4618 AGACAAGTTTTCATTAACATCATGATTCATCTGCTTAACATGCTCAATGATG 4677  
 Db 4606 AGACAAGTTTTCATTAACATCATGATTCATCTGCTTAACATGCTCAATGATG 4665  
 Oy 4678 GTGGAACAGATGACCAAGTGAATGTGATGATCTATTTGTACGATCAATCTGTG 4737  
 Db 4666 GTGGAACAGATGACCAAGTGAATGTGATGATCTATTTGTACGATCAATCTGTG 4725  
 Oy 4738 TTTCAATTTGCTTATTTACTGGAAGTGTGATGAAACCTCATCTGTACGCCATTTAT 4797  
 Db 4726 TTTCAATTTGCTTATTTACTGGAAGTGTGATGAAACCTCATCTGTGTAGCCATTTAT 4785  
 Oy 4798 TTTACCATTTGATGGAATATTTTGAATTTGTGTGTGCTTCAATCTGTGTAGTATG 4857  
 Db 4786 TTTACCATTTGATGGAATATTTTGAATTTGTGTGTGCTTCAATCTGTGTAGTATG 4845  
 Oy 4858 TTTCTGCGAGCTGATGAAAGATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4917  
 Db 4846 TTTCTGCGAGCTGATGAAAGATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4905  
 Oy 4918 CTTGCTAGATTTGGCCGAATCTTACGTGATCAAGGAAAGGAAAGGATTCGCAAGCTG 4977  
 Db 4906 CTTGCTAGATTTGGCCGAATCTTACGTGATCAAGGAAAGGAAAGGATTCGCAAGCTG 4965  
 Oy 4978 CTTCTTCTTGTGATGATGCTCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5037  
 Db 4966 CTTCTTCTTGTGATGATGCTCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5025  
 Oy 5038 GTCATGTTCACTACGCCATCTTTGGGATGTCCAACTTGTCTATGTTAAAGGGAAGTT 5097  
 Db 5026 GTCATGTTCACTACGCCATCTTTGGGATGTCCAACTTGTCTATGTTAAAGGGAAGTT 5085



|    |      |   |      |
|----|------|---|------|
| OY | 5038 | GGGATCGATGACATGTTCAACTTGGACCTTTGGCAACAGATGATGCCATATCCAA       | 5157 |
| Db | 5086 | GGGATCGATGACATGTTCAACTTGGACCTTTGGCAACAGATGATGCCATATCCAA       | 5145 |
| OY | 5158 | ATTACAACTCTGCTGGCGGGATGGATTGCTAGACACCCATTTCTCAACAGTAAGCCACCC  | 5217 |
| Db | 5146 | ATTACAACTCTGCTGGCGGGATGGATTGCTAGACACCCATTTCTCAACAGTAAGCCACCC  | 5205 |
| OY | 5218 | GACTGTGACCCCTAATTAAGTTAACTTGAAGCTCAGTTAAAGGAGACGTGGGAACCA     | 5277 |
| Db | 5206 | GACTGTGACCCCTAATTAAGTTAACTTGAAGCTCAGTTAAAGGAGACGTGGGAACCA     | 5265 |
| OY | 5278 | TCTGTGGAAATTTCTTTTGTGTCAGTTTCATCATCATATATCCCTCCGTGGTGGGTGAAC  | 5337 |
| Db | 5266 | TCTGTGGAAATTTCTTTTGTGTCAGTTTCATCATCATATATCCCTCCGTGGTGGGTGAAC  | 5325 |
| OY | 5338 | ATGTACATTCGGGTCATCCCTGGAGAATCTCAGTGTGCTACTGAAAGAAAGTCAGAGCCT  | 5397 |
| Db | 5326 | ATGTACATTCGGGTCATCCCTGGAGAATCTCAGTGTGCTACTGAAAGAAAGTCAGAGCCT  | 5385 |
| OY | 5398 | CTGAGTGAAGATGACTTGTAGATGTTCTATGAGGTTTGGGAGAAGTTGATCCCATGCA    | 5457 |
| Db | 5386 | CTGAGTGAAGATGACTTGTAGATGTTCTATGAGGTTTGGGAGAAGTTGATCCCATGCA    | 5445 |
| OY | 5458 | ACTGATTCATGGAAATTTGAAAATTAATCTAGTTTGCAGCGCGCTTGAACCGGCTCTGC   | 5517 |
| Db | 5446 | ACTGATTCATGGAAATTTGAAAATTAATCTAGTTTGCAGCGCGCTTGAACCGGCTCTGC   | 5505 |
| OY | 5518 | AATCTGCCACAACCAACCAACTCCAGCTCATGTGCATAGATTTGGCCATGGTGAAGTGT   | 5577 |
| Db | 5506 | AATCTGCCACAACCAACCAACTCCAGCTCATGTGCATAGATTTGGCCATGGTGAAGTGT   | 5565 |
| OY | 5578 | GACCGGATCCACTGTCCTTGATATCTTATTTGCTTTTACAAAGCGGGTCTAGAGAGAGT   | 5637 |
| Db | 5566 | GACCGGATCCACTGTCCTTGATATCTTATTTGCTTTTACAAAGCGGGTCTAGAGAGAGT   | 5625 |
| OY | 5638 | GGAGAGATGGATGCTCTTCGGAATPACAGATGGAAGAGCGATTATGGCTTCCAACTCTTC  | 5697 |
| Db | 5626 | GGAGAGATGGATGCTCTTCGGAATPACAGATGGAAGAGCGATTATGGCTTCCAACTCTTC  | 5685 |
| OY | 5698 | AAGGTCCTCTTACAGCCATCACTACTACTTAAACGAAAACAAGAGAGAAATATCTGCT    | 5757 |
| Db | 5686 | AAGGTCCTCTTACAGCCATCACTACTACTTAAACGAAAACAAGAGAGAAATATCTGCT    | 5745 |
| OY | 5758 | GTCATTATTCAGCGTGTTCACAGACGCCACTTTTAAAGCGAATGTAAACCAAGCTTCC    | 5817 |
| Db | 5746 | GTCATTATTCAGCGTGTTCACAGACGCCACTTTTAAAGCGAATGTAAACCAAGCTTCC    | 5805 |
| OY | 5818 | TTTACGTCATTAATAAAACAAAATCAAAGGTGGGGCTATCTCTTATATAAAGAACATG    | 5877 |
| Db | 5806 | TTTACGTCATTAATAAAACAAAATCAAAGGTGGGGCTATCTCTTATATAAAGAACATG    | 5865 |
| OY | 5878 | ATAATGTACAGAAATTAATGAAGAACTCTATTAAGAAAAAAACGTATCGACCTGTCCACT  | 5937 |
| Db | 5866 | ATAATGTACAGAAATTAATGAAGAACTCTATTAAGAAAAAAACGTATCGACCTGTCCACT  | 5925 |
| OY | 5938 | GCAGCTGTCCACCTTCTCTATGACCGGGGTGAACCAAGCCAAATTTGGAAAAACATGAGCA | 5997 |
| Db | 5926 | GCAGCTGTCCACCTTCTCTATGACCGGGGTGAACCAAGCCAAATTTGGAAAAACATGAGCA | 5985 |
| OY | 5998 | GAAAGCAAAAGATGAAAAAGCCAAAGGGAAAAATA 6030                      |      |
| Db | 5986 | GAAAGCAAAAGATGAAAAAGCCAAAGGGAAAAATA 6018                      |      |

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| RESULT     | 7                                  |
| AX391142   |                                    |
| LOCUS      | AX391142                           |
| DEFINITION | Sequence 13 from Patent WO0214498. |
| ACCESSION  | AX391142                           |
| VERSION    | AX391142.1                         |
| KEYWORDS   | GI:19584238                        |
| SOURCE     | human.                             |
| DNA        | 5922 bp                            |
| linear     | PAT 19-MAR-2002                    |

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| ORGANISM                   | Homo sapiens  |
| REFERENCE                  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;   |
| AUTHORS                    | Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.   |
| TITLE                      | 1<br>Turner,C.A., Mathur,B. and Mathur,D.<br>Novel human ion channel proteins and polynucleotides encoding the same |
| JOURNAL                    | Patent: WO 0214498-A 13 21-FEB-2002;<br>Lexicon Genetics Incorporated (US)  |
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| Oy                         | 181 CTTCATTTATTTATGAGAGACATTCCTCCAGAGATGTGTCTAGAGCCCTCGAGAGACCTG 240  |
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| Oy                         | 301 CGGTTCAGTAGGCCACMCCTGGCCCTGTACAATTTAACTCCCTCAATCCCTTGAAGAAATA 360   |
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| Oy                         | 781 TTTCGCTTAATTTGGGCTGACCTGTTCAATGGGCAACCTGAGGAATTAATGATTAACAATGG 840  |







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RESULT 8
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LOCUS AX391132
DEFINITION Sequence 3 from Patent W00214498.
ACCESSION AX391132
VERSION AX391132.1 GI:19584233
KEYWORDS
ORGANISM human.
SOURCE Homo sapiens
human.
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Turner,C.A., Mathur,B. and Mathur,D.
TITLE Novel human ion channel proteins and polynucleotides encoding the
same
JOURNAL Patent: WO 0214498-A 3 21-FEB-2002;
FEATURES
SOURCE Location/Dualifiers
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Best Local Similarity 99.4%; Pred. No. 0;
Matches 5884; Conservative 0; Mismatches 0; Indels 33; Gaps 1;
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 ACCESSION X03638  
 VERSION X03638.1 GI:57216  
 KEYWORDS glycoprotein; sodium channel.  
 SOURCE Rattus norvegicus.  
 ORGANISM Rattus norvegicus.  
 Eukaryota; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 8398)  
 AUTHORS Node, M., Ikeda, T., Kayano, T., Suzuki, H., Takeshima, H., Kurasaki, M., Takahashi, H. and Numu, S.

TITLE Existence of distinct sodium channel messenger RNAs in rat brain  
 JOURNAL Nature 320 (6058), 188-192 (1996)  
 MEDLINE 86146901  
 PUBMED 3754035

## FEATURES

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Query Match 84.0%: Score 5062.4; DB 10; Length 8399;  
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 Db 4032 TACATTTTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4091  
 Oy 3841 ACCAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3900  
 Db 4092 ACCAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4151  
 Oy 3901 GCAATGCTTGGGTTTACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3960  
 Db 4152 GCAATGCTTGGGTTTACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 4211







VERSION AX91144.1 GI:19584239  
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 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE  
 1 Turner,C.A., Mathur,B. and Mathur,D.  
 TITLE Novel human ion channel proteins and polynucleotides encoding the  
 JOURNAL same  
 PATENT: WO 0214498-A 15 21-FEB-2002;  
 FEATURES Lexicon Genetics Incorporated (US)  
 source location/Qualifiers  
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 Matches 4338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 61 TCTCTTCGGCGTATGAAAGCGATTCGAGAGAAAAGCGAAAGATCCCAACAGAC 120  
 QY 121 AAAAAAGATGACGACGAAAAATGGCCCAAGCAATAGTGACTGGAAGCTGGAAGAAC 180  
 Db 121 AAAAAAGATGACGACGAAAAATGGCCCAAGCAATAGTGACTGGAAGCTGGAAGAAC 180  
 QY 181 CTTCCATTTATTAATGAGACATTCCTCCAGAGATGGTGTGACAGCCCTGAGAGACTG 240  
 Db 181 CTTCCATTTATTAATGAGACATTCCTCCAGAGATGGTGTGACAGCCCTGAGAGACTG 240  
 QY 241 GACCCCTACATATGAAAGAAAGAACTTTATATGATTAAGAAAGGAGGCAATCTTC 300  
 Db 241 GACCCCTACATATGAAAGAAAGAACTTTATATGATTAAGAAAGGAGGCAATCTTC 300  
 QY 301 CGGTTGAGTGCACCTGCGCTGTACATTTAACTCCCTTCATTCCTTAGGAAATA 360  
 Db 301 CGGTTGAGTGCACCTGCGCTGTACATTTAACTCCCTTCATTCCTTAGGAAATA 360  
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 Db 361 GCTATTAAGATTTGGTACATTCATTAATGACATGCTAATTAATGTCACATTTTGA 420  
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 QY 961 TCAATATATATATTTCTGAGAGGTTTATAGATGCACTATGTCGAAATAGCTCT 1020  
 Db 961 TCAATATATATATTTCTGAGAGGTTTATAGATGCACTATGTCGAAATAGCTCT 1020  
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 Db 1021 GATGAGGCAATGTCAGAGGATATATGTCGAAAGCTGTAAGAAATCCCAATAT 1080  
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 Db 1081 GCGTACAGAGCTTGTATACCTTCAGTTGGGCTTTTGTCTGTTTCAGTAATGACT 1140  
 QY 1141 CAGGACTTCTGGGAAATCTTTATACATGACATTAAGTCTGTCGGGAAACGTACATG 1200  
 Db 1141 CAGGACTTCTGGGAAATCTTTATACATGACATTAAGTCTGTCGGGAAACGTACATG 1200  
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 QY 1321 GAGGCGCAATTTGACAGATGATTTGAACAGCTTAAAGAAAGCAACAGAGGCACTGACG 1380  
 Db 1321 GAGGCGCAATTTGACAGATGATTTGAACAGCTTAAAGAAAGCAACAGAGGCACTGACG 1380  
 QY 1381 GCAGCAAGGCAACTGCTCAGAACTTCAGAGAGCCAGGCGAGGAGGCTCTCA 1440  
 Db 1381 GCAGCAAGGCAACTGCTCAGAACTTCAGAGAGCCAGGCGAGGAGGCTCTCA 1440  
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 QY 1501 AGGAAGAAAGAAAGCAAGAGAGTCTGTGGGGAAGAAAGATGAGAGATATTC 1560  
 Db 1501 AGGAAGAAAGAAAGCAAGAGAGTCTGTGGGGAAGAAAGATGAGAGATATTC 1560  
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 QY 1621 AACCAGATGACATATGAAAGAGTACTCTCCCAACACAGTCTTGTGAGCATCCGT 1680  
 Db 1621 AACCAGATGACATATGAAAGAGTACTCTCCCAACACAGTCTTGTGAGCATCCGT 1680  
 QY 1681 GGGTCCCTATTTTACCAAGGCGAAATAGCAAGAACCTTTTACGTTTAGAGGGCGA 1740  
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 QY 1741 GCAAGAGATGAGGATCTGAAAGACATTCGAGATGATGAGCAGACCTTTGAGAGAT 1800  
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 QY 1801 AACGAGAGCCGTAGAGATTCCTTGTGTTGCTGCCGAGACACAGAGAGAGAGCAGCAGC 1860  
 Db 1801 AACGAGAGCCGTAGAGATTCCTTGTGTTGCTGCCGAGACACAGAGAGAGAGCAGCAGC 1860

|    |      |  |      |
|----|------|--|------|
| OY | 1861 | AACCTGAGTCAGACCACTAGCTACATCCCGGATGCTGGCACTGTTTCCAGCAATGGGAG    | 1920 |
| Db | 1861 | AACTGAGTCAGACCACTAGGTCATCCCGGATGCTGGCACTGTTTCCAGCAATGGGAG      | 1920 |
| OY | 1921 | ATGCACAGCACTGTGGATGTCAAAGGCTGTGTTTCCCTGGTGGTGCACTTCAGTTCCT     | 1980 |
| Db | 1921 | ATGCACAGCACTGTGGATGTCCAATGGCTGTGTTTCCCTGGTGGTGCACTTCAGTTCCT    | 1980 |
| OY | 1981 | ACATGCGCTGTGGACAGCTTTCGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC    | 2040 |
| Db | 1981 | ACATGCCCTGTGGACAGCTTTCGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC    | 2040 |
| OY | 2041 | AAAGSAAACAACCACTGAACTGAAATGAAAGAAAGAAAGGCAAGTTCCTTCCACGTTTCC   | 2100 |
| Db | 2041 | AAATGGAACAACAACCTGAAACTGAAATGAAAGAAAGGCAAGTTCCTTCCACGTTTCC     | 2100 |
| OY | 2101 | ATGAGCTTTCCTAGAGATCCCTTCCCAAAAGGCAACGAGCATTGAGTATAGCAGACATTCTA | 2160 |
| Db | 2101 | ATGAGCTTTCCTAGAGATCCCTTCCCAAAAGGCAACGAGCATTGAGTATAGCAGACATTCTA | 2160 |
| OY | 2161 | ACCAATACAGTACAGAGACTTGAAAGATCCAGCAGAGAAATGCCACCTGTGGTATAAA     | 2220 |
| Db | 2161 | ACAAATACAGTACAGAGAACTTGAAGATCCAGCAGAGAAATGCCACCTGTGGTATAAA     | 2220 |
| OY | 2221 | TTTTCCAACTATTCCTTAATCTGGGAGCTGTTCGCATATGGTGTAAAGGAAACAATGT     | 2280 |
| Db | 2221 | TTTTCCAACTATTCCTTAATCTGGGAGCTGTTCGCATATGGTGTAAAGGAAACAATGT     | 2280 |
| OY | 2281 | GTCACACCTGGTGTGATGAGCAACCATTTGTTGACCTGGCCATCCATCTGTATTGTCCTA   | 2340 |
| Db | 2281 | GTCACACCTGGTGTGATGAGCAACCATTTGTTGACCTGGCCATCCATCTGTATTGTCCTA   | 2340 |
| OY | 2341 | AAATACCTTTTCAATGGCCATGAGAGCACTATACAAATAGGCAACCATTTCAATATGTGCT  | 2400 |
| Db | 2341 | AAATACCTTTTCAATGGCCATGAGAGCACTATACAAATAGGCAACCATTTCAATATGTGCT  | 2400 |
| OY | 2401 | ACAGTAGGAAACTGTGTTTCACTGGGATCTTTCACAGCAAAATGTTTCAAAAATAT       | 2460 |
| Db | 2401 | ACAGTAGGAAACTGTGTTTCACTGGGATCTTTCACAGCAAAATGTTTCAAAAATAT       | 2460 |
| OY | 2461 | GCCATGAGATCCTTACTATATATTTCCAAAGAGGCTGCAATATCTTTGACGGTTTATGTG   | 2520 |
| Db | 2461 | GCCATGAGATCCTTACTATATATTTCCAAAGAGGCTGCAATATCTTTGACGGTTTATGTG   | 2520 |
| OY | 2521 | ACGCTTAGCCTGTGTAACCTTGGACTCGCCAATGTGGAAGATTAATCTGTTCCCGTCA     | 2580 |
| Db | 2521 | ACGCTTAGCCTGTGTAACCTTGGACTCGCCAATGTGGAAGATTAATCTGTTCCCGTCA     | 2580 |
| OY | 2581 | TTTTCGATTCCTGCGAGTTTCAAAGTTGGCAAAATCTTGGCCAACTGTAAATATGCTAATA  | 2640 |
| Db | 2581 | TTTTCGATTCCTGCGAGTTTCAAAGTTGGCAAAATCTTGGCCAACTGTAAATATGCTAATA  | 2640 |
| OY | 2641 | AAGATCATGGGCAATTCGCGGGGGGCTCGGGAAATTAACCTCGTCTGGGCATATC        | 2700 |
| Db | 2641 | AAGATCATGGGCAATTCGCGGGGGGCTCGGGAAATTAACCTCGTCTGGGCATATC        | 2700 |
| OY | 2701 | GTCCTCATTTTGGCCGTGTGCGGCATATGACAGCTTTTGATTAAGATACAAAGATTGTGTC  | 2760 |
| Db | 2701 | GTCCTCATTTTGGCCGTGTGCGGCATATGACAGCTTTTGATTAAGATACAAAGATTGTGTC  | 2760 |
| OY | 2761 | TGCAGATATGCCAGATATTTGTCAACTGCCACGCTGGCACATGATATCTTCCACTCC      | 2820 |
| Db | 2761 | TGCAGATATGCCAGATATTTGTCAACTGCCACGCTGGCACATGATATCTTCCACTCC      | 2820 |
| OY | 2821 | TTTCCGATTTGTGTCGCGGCTGTGGGGAGTGTGATAGAGACATGTGGGGACTATG        | 2880 |
| Db | 2821 | TTTCCGATTTGTGTCGCGGCTGTGTGGGGAGTGTGATAGAGACATGTGGGACTATG       | 2880 |
| OY | 2881 | GAGGTTGCTGTGACCAATGTGCTTACTGTCTTCAATGATGGTCAATGTGATGGAAAC      | 2940 |
| Db | 2881 | GAGGTTGCTGTGACCAATGTGCTTACTGTCTTCAATGATGGTCAATGTGATGGAAAC      | 2940 |

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|----|------|--|------|
| QY | 2941 | CTAGTGGTCCGGAATCTCTTCTCGGCTTGCTTGTAGCTCATTTAGTGCAGACAACCTT   | 3000 |
| Db | 2941 | CTAGTGGTCCGGAATCTCTTCTCGGCTTGCTTGTAGCTCATTTAGTGCAGACAACCTT   | 3000 |
| QY | 3001 | GCAGCCTGATGATGATTAATGAATGAATAACTCCAAATTCCTGTGATAGATGAC       | 3060 |
| Db | 3001 | GCAGCCTGATGATGATTAATGAATGAATAACTCCAAATTCCTGTGATAGATGAC       | 3060 |
| QY | 3061 | AAAGGATGCTTATGTGAAAAGAAAATATATGATTTATTCACAGCTCTTCATTAGG      | 3120 |
| Db | 3061 | AAAGGATGCTTATGTGAAAAGAAAATATATGATTTATTCACAGCTCTTCATTAGG      | 3120 |
| QY | 3121 | AAACAAAAGATTTTATGATGAAATTTAAACCACTGATGATCTAAACAAGAAACACGT    | 3180 |
| Db | 3121 | AAACAAAAGATTTTATGATGAAATTTAAACCACTGATGATCTAAACAAGAAACACGT    | 3180 |
| QY | 3181 | TGTATGTCCAAATCATACARCAAGAAATTTGGAAAGATCTTGACTATCTTAAAGATTAAT | 3240 |
| Db | 3181 | TGTATGTCCAAATCATACARCAAGAAATTTGGAAAGATCTTGACTATCTTAAAGATTAAT | 3240 |
| QY | 3241 | GGAATCTAATGGTATATRGAACTGGGACGACAGTGTGAAAATTTACTTATTTGATGAAGT | 3300 |
| Db | 3241 | GGAATCTAATGGTATATRGAACTGGGACGACAGTGTGAAAATTTACTTATTTGATGAAGT | 3300 |
| QY | 3301 | GATTACATGTCATTCATTAACCAACCCAGCTTACTGTGACGTACCAATTCGCTGTAGA   | 3360 |
| Db | 3301 | GATTACATGTCATTCATTAACCAACCCAGCTTACTGTGACGTACCAATTCGCTGTAGA   | 3360 |
| QY | 3361 | GAATCTGACTTTGAAAATTTAAACAGGGAAGACTTTAGTGAATCGGATCTGGAGAA     | 3420 |
| Db | 3361 | GAATCTGACTTTGAAAATTTAAACAGGGAAGACTTTAGTGAATCGGATCTGGAGAA     | 3420 |
| QY | 3421 | AGCAAGGAATCAAGATGGAAGAGAGTCAATCAGAGATGAGACATGTGACATCGGC      | 3480 |
| Db | 3421 | AGCAAGGAATCAAGATGGAAGAGAGTCAATCAGAGATGAGACATGTGACATCGGC      | 3480 |
| QY | 3481 | GCACCTGTAGGAAGACGCCGTATGTGGAACCTGAAGAAACTCTTGAACCAAGAACTTGT  | 3540 |
| Db | 3481 | GCACCTGTAGGAAGACGCCGTATGTGGAACCTGAAGAAACTCTTGAACCAAGAACTTGT  | 3540 |
| QY | 3541 | TTCACTGAAGCTGTGTACAAAGATTCAGTGTGTGCAAATCAATGTGGAAGAGCAGA     | 3600 |
| Db | 3541 | TTCACTGAAGCTGTGTACAAAGATTCAGTGTGTGTGCAAATCAATGTGGAAGAGCAGA   | 3600 |
| QY | 3601 | GGAAAACAATGTGTGAACCTGAGAGAGACGTGTTCCGAATAGTTGAACATTACTGCTT   | 3660 |
| Db | 3601 | GGAAAACAATGTGTGAACCTGAGAGAGACGTGTTCCGAATAGTTGAACATTACTGCTT   | 3660 |
| QY | 3661 | GAGACCTTCATTGTTTCATGATTTCTCTTATGATGTGTGCTCTGTGCAATTTGAAATATA | 3720 |
| Db | 3661 | GAGACCTTCATTGTTTCATGATTTCTCTTATGATGTGTGCTCTGTGCAATTTGAAATATA | 3720 |
| QY | 3721 | TATATGTATCGCAAGAGATTTAAGAGATTTGGAATATGTGCACAAGGTTTTCCT       | 3780 |
| Db | 3721 | TATATGTATCGCAAGAGATTTAAGAGATTTGGAATATGTGCACAAGGTTTTCCT       | 3780 |
| QY | 3781 | TACATTTTCATTGTGAATAGCTTCTAAAAATGGGTGGCATATGCTATCAACAATATTTTC | 3840 |
| Db | 3781 | TACATTTTCATTGTGAATAGCTTCTAAAAATGGGTGGCATATGCTATCAACAATATTTTC | 3840 |
| QY | 3841 | ACCAATGCTGGTGTGGCTGGACCTCTTAATTTGTGAATGTTTCAATGGTCAAGTTTACA  | 3900 |
| Db | 3841 | ACCAATGCTGGTGTGGCTGGACCTCTTAATTTGTGAATGTTTCAATGGTCAAGTTTACA  | 3900 |
| QY | 3901 | GCAATGCTTGGGTCTACTAGAACTTGGAGCATCAATCTCTAGACACTAAGAGCT       | 3960 |
| Db | 3901 | GCAATGCTTGGGTCTACTAGAACTTGGAGCATCAATCTCTAGACACTAAGAGCT       | 3960 |
| QY | 3961 | CTGAGACCTCAAGAGCCTTATCTGCATTTGAAGGATGAGGGTGGTGTGAAGGCCCTT    | 4020 |
| Db | 3961 | CTGAGACCTCAAGAGCCTTATCTGCATTTGAAGGATGAGGGTGGTGTGAAGGCCCTT    | 4020 |
| QY | 4021 | TTAGAGCAATTCATCATCATGATGATGTGCTTCTGTTTGTCTATATTTCTGCTAAT     | 4080 |

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Db 4021 TTAGAGCAATTCATCAATCATGAATGTGCTTCTGTTGTCTATATCTGGCTAAT 4080
OY 4081 TTACAGATATGCGGCTAAATTTGTTGCTGGCAAAATCTACACGCTATTAACACACA 4140
Db 4081 TTACAGATATGCGGCTAAATTTGTTGCTGGCAAAATCTACACGCTATTAACACACA 4140
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Db 4141 ACTGTCAGAGTTTACATCAGAGAGCTGAATATCATATCATATGCTTAAACTAATA 4200
OY 4201 GAAAGAAATGAGACTCTCGATGAGAAATGTGAAGTAACCTTGTATTAATGAGATT 4260
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OY 4261 GGGTATCTCTCTTCTGCTTCAAGTTCACACTTCAAAAGATGATGATATATGATGCA 4320
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LOCUS Sequence 5 from Patent WO0214498.
DEFINITION AX391134
ACCESSION AX391134
VERSION AX391134.1 GI:19584234
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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REFERENCE
1 Turner, C.A., Mathur, B. and Mathur, D.
AUTHORS Novel human ion channel proteins and polynucleotides encoding the
TITLE same
JOURNAL Patent: WO 0214498-A 5 21-FEB-2002;
FEATURES Lexicon Genetics Incorporated (US)
SOURCE 1. 4329
Location/Qualifiers

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BASE COUNT 1287 a 840 c 988 g 1211 t 3 others
ORIGIN

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Query Match 70.7%; Score 4260.8; DB 6; Length 4329;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 4305; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

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Db 61 TCTCTGCGGCTATTGAAGACGCTTGCAGAGAAAGGCAAAAGATCCCAACAGAC 120
OY 121 AAAAAAGATGACGAGCAAAATGGCCCAAGCCAAATAGTACTTGAAGCTGGAAGAAC 180
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OY 241 GAGCCCTACTATATCAATAGAAACTTTTATAGTATTAATTAAGGAGGCACTTTC 300
Db 241 GAGCCCTACTATATCAATAGAAACTTTTATAGTATTAATTAAGGAGGCACTTTC 300
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Db 361 GCTATTATAGATTTTGTGACTTTCATTTATGACAGTCTAATATATGTCACATTTTGAACA 420
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Db 421 AACTGTGTTTATGACATAGATTAACCCCTCGATGAGCAAAAGATATGATATACACC 480
OY 481 TTACAGAGATATATATCTTTTGAATCACTTATATAAATTTATGCAAGGGGATTCGTTTA 540
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OY 541 GAAGATTTTACTTCTCGGGATCCATGAGATGCTCGATTCATTCATTAATTT 600
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Db 721 ATTCAGTCTGTGAAGAACTCTCAGATGTATATGATATCTGATGCTGTGTCGAGCTTA 780
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Db 781 TTTGCTATATTTGGGCTGACGCTGTCATGAGGCACTGAGGAAATTAATATATACATGG 840
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Db 901 AATGTCACATTTATTAATGAAGTCTGTTGAGTTCAGTGAAGTATATTCAGAT 960
OY 961 TCAGATATCATATTTCTCGAGAGGTTTTTATGATGACCTATATGGAATATACCTCT 1020
Db 961 TCAGATATCATATTTCTCGAGAGGTTTTTATGATGACCTATATGGAATATACCTCT 1020
OY 1021 GATGAGGCAATGTCAGAGAGGATATATGTGTGAAGCTGTGAATCCCAATTA 1080
Db 1021 GATGAGGCAATGTCAGAGAGGATATATGTGTGAAGCTGTGAATCCCAATTA 1080
OY 1081 GGTATACAAAGCTTTATATCTTCACTGAGGCTTTTGTGCTGTTTTCAGTAAATGACT 1140
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OY 1321 GAGGCCAATTTACAGAGATGATGAAGCTTAATAAACAAGAGAGAGAGCTGAGAG 1380
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OY 1381 GCAGCAAGGCACTGCTCAGAACATTCAGAGAGCCAGTGCAGCAGGAGCTCTCA 1440

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|    |      |  |      |
|----|------|--|------|
| Db | 1381 | GAAGCAAGGGCAACTGCGCTCAGAAACANTCCAGAGAGGCCCAAGTGCAGCAGCGACTCTCA | 1440 |
| Qy | 1441 | GACAGCTCATCTGAAGCCTCTAAAGTTGATGTTCCAAAGAGTCTTAAGGAAGAAGAAATCGG | 1500 |
| Db | 1441 | GACAGCTCATCTGAAGCCTCTAAAGTTGATGTTCCAAAGAGTCTTAAGGAAGAAGAAATCGG | 1500 |
| Qy | 1501 | AGCAGAGAAAAGAAACAGAAAGAGCGAGTCTGGTGGGGAAAGAAAGATGTAGAGTAATTC   | 1560 |
| Db | 1501 | AGCAGAGAAAAGAAACAGAAAGAGCGAGTCTGGTGGGGAAAGAAAGATGTAGAGTAATTC   | 1560 |
| Qy | 1561 | CAAAAACTGAAATCTGAGGACAGCATCAGAGAGGAAAGGTTTGCTTCTCATTTGAAGGG    | 1620 |
| Db | 1561 | CAAAAACTGAAATCTGAGGACAGCATCAGAGAGGAAAGGTTTGCTTCTCATTTGAAGGG    | 1620 |
| Qy | 1621 | AACCGATTGACATATGAAAAAGAGTACTCTCCCAACACAGCTTTGTTGAGATCCGT       | 1680 |
| Db | 1621 | AACCGATTGACATATGAAAAAGAGTACTCTCCCAACACAGCTTTGTTGAGATCCGT       | 1680 |
| Qy | 1681 | GGCTCCCTATTTTCACCAAGGCGAAATATGAGAAACAAGCCTTTACGCTTAGAGGGCGA    | 1740 |
| Db | 1681 | GGCTCCCTATTTTCACCAAGGCGAAATATGAGAAACAAGCCTTTACGCTTAGAGGGCGA    | 1740 |
| Qy | 1741 | GCAAGAGATGTGGGATCTGAGAAAGCACTTCGAGATGATGAGCAGACACCTTTGAGAT     | 1800 |
| Db | 1741 | GCAAGAGATGTGGGATCTGAGAAAGCACTTCGAGATGATGAGCAGACACCTTTGAGAT     | 1800 |
| Qy | 1801 | AACGAGAGCGGTAGAGATTCCTGTTTGTCGCCCGACGACAGAGAGAAACCCAAAGC       | 1860 |
| Db | 1801 | AACGAGAGCGGTAGAGATTCCTGTTTGTCGCCCGACGACAGAGAGAAACCCAAAGC       | 1860 |
| Qy | 1861 | AACCTGAGTCAGACCAGTAGTGTCATCCCGGATCTGGCAGTGTTCACAGGAATGGGAG     | 1920 |
| Db | 1861 | AACCTGAGTCAGACCAGTAGTGTCATCCCGGATCTGGCAGTGTTCACAGGAATGGGAG     | 1920 |
| Qy | 1921 | ATGCACAGACAGTGTGGATTTGCAATGTGTGTGTTCTGTGGTGGTGAACCTTCAGTTCT    | 1980 |
| Db | 1921 | ATGCACAGACAGTGTGGATTTGCAATGTGTGTGTTCTGTGGTGGTGAACCTTCAGTTCT    | 1980 |
| Qy | 1981 | ACATCGCTCTGTTGAGACGCTTCGCGAGAGGTATATATGATATAGCAGCTACTGATGAC    | 2040 |
| Db | 1981 | ACATCGCTCTGTTGAGACGCTTCGCGAGAGGTATATATGATATAGCAGCTACTGATGAC    | 2040 |
| Qy | 2041 | AATGGAACACACACTGAAACTGAAATGAGAAAGAAAGTCAAGTCTTCCACGTTTCC       | 2100 |
| Db | 2011 | ---GGAAACACACACTGAAACTGAAATGAGAAAGAAAGTCAAGTCTTCCACGTTTCC      | 2067 |
| Qy | 2101 | ATGGAATTTCTGAAAGATCTTCCCAAAGGCAACGAGCATGTATPAGCCACATTTCTA      | 2160 |
| Db | 2068 | ATGGAATTTCTGAAAGATCTTCCCAAAGGCAACGAGCATGTATPAGCCACATTTCTA      | 2127 |
| Qy | 2161 | ACAATATACGTAGAGAACTGGAAGATCCAGGACAGAAATGCCACCTGTGTGTAA         | 2220 |
| Db | 2128 | ACAATATACGTAGAGAACTGGAAGATCCAGGACAGAAATGCCACCTGTGTGTAA         | 2187 |
| Qy | 2221 | TTTTCAACATATTTCTAATCTGGGAGCTTCTCCCATTTGGTTAAAGGAACATGTT        | 2280 |
| Db | 2188 | TTTTCAACATATTTCTAATCTGGGAGCTTCTCCCATTTGGTTAAAGGAACATGTT        | 2247 |
| Qy | 2281 | GTCACACTGGTGTGTATGAGACCACTTGTGTGACCTGGCCATCCATCTGATTTGCTTA     | 2340 |
| Db | 2248 | GTCACACTGGTGTGTATGAGACCACTTGTGTGACCTGGCCATCCATCTGATTTGCTTA     | 2307 |
| Qy | 2341 | AATACCTTTTATATGGCCATGTGAGACCTATCCAAATGACGACATTTCAATATGTGCTT    | 2400 |
| Db | 2308 | AATACCTTTTATATGGCCATGTGAGACCTATCCAAATGACGACATTTCAATATGTGCTT    | 2367 |
| Qy | 2401 | ACAGTAGGAACCTTGGTTTCTACTGGGATCTTACAGCAAGAAATGTTCTGAAAATTTAT    | 2460 |
| Db | 2368 | ACAGTAGGAACCTTGGTTTCTACTGGGATCTTACAGCAAGAAATGTTCTGAAAATTTAT    | 2427 |
| Qy | 2461 | GCCATAGGATCCCTTACTATTTATTTCCAAAGAGCGTGGAAATATCTTTGACGGTTTATGTG | 2520 |
| Db | 2428 | GCCATAGGATCCCTTACTATTTATTTCCAAAGAGCGTGGAAATATCTTTGACGGTTTATGTG | 2487 |

|    |      |  |      |
|----|------|--|------|
| QY | 2521 | ACGCTTACGCGGTGAGAACTTGGACATCCGCCAAATGTGGAAGATTATCTGTCCGTCA   | 2580 |
| Db | 2488 | ACGCTTACCGGTGAGAACTTGGACATCCGCCAAATGTGGAAGATTATCTGTCCGTCA    | 2547 |
| QY | 2581 | TTTCGATTGCTGCAGAGTTTCAAGTTGGCCAAATCTTGGCCACGTTAAATATGCTATA   | 2640 |
| Db | 2548 | TTTCGATTGCTGCAGAGTTTCAAGTTGGCCAAATCTTGGCCACGTTAAATATGCTATA   | 2607 |
| QY | 2641 | AAGATCATCGGCAATCCGTCGGGGGCTCTGGCAATTTAAACCTCGCTTGGCCATC      | 2700 |
| Db | 2608 | AAGATCATCGGCAATCCGTCGGGGGCTCTGGCAATTTAAACCTCGCTTGGCCATC      | 2665 |
| QY | 2701 | GTCCTCATTTTGGCCGTGTCGGGCAATGACCTTTGGTAAAGATACAAAGATTGTGTC    | 2760 |
| Db | 2668 | GTCCTCATTTTGGCCGTGTCGGGCAATGACCTTTGGTAAAGATACAAAGATTGTGTC    | 2727 |
| QY | 2761 | TGCAAGATCGCCAGTGTGATTTCAACTCCACGCTGGCAATGATGATCTTCCACATCC    | 2820 |
| Db | 2728 | TGCAAGATCGCCAGTGTGATTTCAACTCCACGCTGGCAATGATGATCTTCCACATCC    | 2787 |
| QY | 2821 | TTCCGATTGTGTTCGCCGTGCTGTGGGAGTGGATAGACACATGTGGACTGATG        | 2880 |
| Db | 2788 | TTCCGATTGTGTTCGCCGTGCTGTGGGAGTGGATAGACACATGTGGACTGATG        | 2847 |
| QY | 2881 | GAGGTGCTGTGTCAAAGCATGTGCTTACGCTTCATGCTTCATGATGGTATGTTGAAC    | 2940 |
| Db | 2848 | GAGGTGCTGTGTCAAAGCATGTGCTTACGCTTCATGCTTCATGATGGTATGTTGAAC    | 2907 |
| QY | 2941 | CTAGGTCCTGAATCTCTTCTTGCCCTTGCTTMTGAGCTCATTTAGTGCAGACACTT     | 3000 |
| Db | 2908 | CTAGGTCCTGAATCTCTTCTTGCCCTTGCTTMTGAGCTCATTTAGTGCAGACACTT     | 2967 |
| QY | 3001 | GCAGCACTGATGATGATATGATTAAGATTAATCTCCAAATTCGTGTGGATAGGATGAC   | 3060 |
| Db | 2968 | GCAGCACTGATGATGATTAAGATTAATCTCCAAATTCGTGTGGATAGGATGAC        | 3027 |
| QY | 3061 | AAAGAGTAGCTTATGTGAAAGAAAAATATGATTTATTCACACATCTTCATTAGG       | 3120 |
| Db | 3028 | AAAGAGTAGCTTATGTGAAAGAAAAATATGATTTATTCACACATCTTCATTAGG       | 3087 |
| QY | 3121 | AAACAAAAGTTTATGATGAAATTTAAACAATCTGATGATCTTAACACAGAAAGACGT    | 3180 |
| Db | 3088 | AAACAAAAGTTTATGATGAAATTTAAACAATCTGATGATCTTAACACAGAAAGACGT    | 3147 |
| QY | 3181 | TGTATGTCCATATATACARCAAGAAATTTGGAAAGATCTTGACTATCTTAAAGATGTAAT | 3240 |
| Db | 3148 | TGTATGTCCATATATACARCAAGAAATTTGGAAAGATCTTGACTATCTTAAAGATGTAAT | 3207 |
| QY | 3241 | GGAACCTCAAGTGTATAGAACTGGACAGCTGTTGAAAAATACATTTATGATGAAGT     | 3300 |
| Db | 3208 | GGAACCTCAAGTGTATAGAACTGGACAGCTGTTGAAAAATACATTTATGATGAAGT     | 3267 |
| QY | 3301 | GATTACATGTCATTCATTAACAAACCCCACTCTTACTGTGACGTGACCAATTCGTGAGA  | 3360 |
| Db | 3268 | GATTACATGTCATTCATTAACAAACCCCACTCTTACTGTGACGTGACCAATTCGTGAGA  | 3327 |
| QY | 3361 | GAATCTGACCTTGAATAATTTAAACACAGGAAGCTTTAGTAGTGAATCGGATCTGGAAG  | 3420 |
| Db | 3328 | GAATCTGACCTTGAATAATTTAAACACAGGAAGCTTTAGTAGTGAATCGGATCTGGAAG  | 3387 |
| QY | 3421 | AGCAAAAGAAATCGAATTAAGACAGTACTATCATGAAGGTAGCAGCTGTGGACATGGCC  | 3480 |
| Db | 3388 | AGCAAAAGAAATCGAATTAAGACAGTACTATCATGAAGGTAGCAGCTGTGGACATGGCC  | 3447 |
| QY | 3481 | GCACCTGTAGAAAGACGCCGTAGTGGAACTGTGAAGAACTTTGAACCGAAGCTTGT     | 3540 |
| Db | 3448 | GCACCTGTAGAAAGACGCCGTAGTGGAACTGTGAAGAACTTTGAACCGAAGCTTGT     | 3507 |
| QY | 3541 | TTTACGTGAAGGCTGTGTACAAAGATTCAAGTGTGTCAATCATGTGGAAGAAAGCAGA   | 3600 |
| Db | 3508 | TTTACGTGAAGGCTGTGTACAAAGATTCAAGTGTGTCAATCATGTGGAAGAAAGCAGA   | 3567 |





QY 955 CAGATTCAGATATCATTTCTGAGAGGTTTTAGATGACATAGTGAAT 1014  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
Db 1066 GAGGATTAAGTCACTTTTATTTTATAGAGGCGAAATATCTCTGTTTGGCAC 1125  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
QY 1015 AGCTGATGAGCGGCAATGTCAGAGGATATATGTGTGAAGCTGGTAGAAATCC 1074  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
Db 1126 AGCTGATGAGCGGCAATGTCAGAGGATATATGTGTGAAGCTGGTAGAAATCC 1185  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
QY 1075 AATATGCTACCAAGCTTTGATCTTACCTTACCTTGGGCTTTTGTCTGTTGACAT 1134  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
Db 1186 AACTATGCTACCAAGCTTTGATCTTACCTTGGGCTTTTGTCTGTTGACAT 1245  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
QY 1135 ATGACTGAGACTTCTGGGAAATTTTATCACTGACATCTAGCTGTGGGAAAG 1194  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
Db 1246 ATGACTGAGACTTCTGGGAAATTTTATCACTGACATCTAGCTGTGGGAAAG 1305  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
QY 1195 TACATGATATTTTGTGTTGTCATTTCTTGGGCTCATTTACCTAATTAATTTGATC 1254  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
Db 1306 TACATGATATTTTGTGTTGTCATTTCTTGGGCTCATTTACCTAATTAATTTGATC 1365  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
QY 1255 CTGGCTGTGTCGCTTGGCTTACGAGGAAACAAATCAGGCGCTTGGAAAGAGAA 1314  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
Db 1366 TTGGCTGTGTCGCTTGGCTTACGAGGAAACAAATCAGGCGCTTGGAAAGAGAA 1425  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
QY 1315 CAGAAAGAGCGGCAATTTACAGCATGATTAACAGCTTAAAGAACAGAGAGAGCT 1374  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
Db 1426 CAGAAAGAGCGGCAATTTACAGCATGATTAACAGCTTAAAGAACAGAGAGAGCT 1485  
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QY 1375 CAGCAGGACGACGAGG-----CACTGCTCAGAAACATTCAGAGAGCCCATGACGA 1428  
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Db 1486 CAGCAGGACGACGAGG-----CACTGCTCAGAAACATTCAGAGAGCCCATGACGA 1545  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
QY 1429 GGCAGGCTCTGAGACGCTCATCTGAAGCTTAAGTAACTTAACTTAACTTAACTTAA 1488  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
Db 1546 GGCAGGCTCTGAGACGCTCATCTGAAGCTTAAGTAACTTAACTTAACTTAACTTAA 1605  
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QY 1489 AGAAGAAATCGAG 1548  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
Db 1606 AGAAGAAATCGAG 1665  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
QY 1549 GAGGATGATTTCCAAAATCTGATTTGAGAGACATCAGAGAGAGAGAGAGAGAG 1608  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
Db 1666 GAGGATGATTTCCAAAATCTGATTTGAGAGACATCAGAGAGAGAGAGAGAGAG 1722  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
QY 1609 TCCATTTGAG 1668  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
Db 1723 TCCATTTGAG 1782  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
QY 1669 TTGAGCATCCGTGCTCCCTATTTTCCAGAGCGAATAGAGAGAGAGAGAGAGAG 1728  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
Db 1783 TTGAGCATCCGTGCTCCCTATTTTCCAGAGCGAATAGAGAGAGAGAGAGAGAG 1842  
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QY 1729 TTTAAGAGCGGAG 1788  
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Db 1843 TTTAAGAGCGGAG 1902  
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QY 1789 ACCTTTGAAGATTAAG 1848  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
Db 1903 ACCTTTGAAGATTAAG 1962  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
QY 1849 AGAGCAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGAC 1908  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
Db 1963 AGAGCAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGAC 2022  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
QY 1969 GCGATGAG 1968  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
Db 2023 GCGATGAG 2082  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
QY 1969 CTTTACATTTCTTACATTTCTTACATTTCTTACATTTCTTACATTTCTTACATTT 2028  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
Db 2083 CTTTACATTTCTTACATTTCTTACATTTCTTACATTTCTTACATTTCTTACATTT 2121  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
QY 2029 GCTACTGATGACATGACATGACATGACATGACATGACATGACATGACATGACAT 2088  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
Db 2122 -----GGCACAATCTAGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2166  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
QY 2089 TTCCAGCTTTCATGAGACTTTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2148  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
Db 2167 TTCCAGCTTTCATGAGACTTTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2226  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
QY 2149 GCCAGATTTCTAACAATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2208  
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Db 2227 GCCAGATTTCTAACAATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2286  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
QY 2209 TGTGGATTAATTTTCCAAATATTTTAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2268  
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Db 2287 TGTGGATTAATTTTCCAAATATTTTAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2346  
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QY 2269 GTGAACATGTTGTCACAGCTGTTGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2328  
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Db 2347 GTGAACATGTTGTCACAGCTGTTGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2406  
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QY 2329 TGTATGCTTAAATATCTTTTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2388  
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Db 2407 TGTATGCTTAAATATCTTTTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2466  
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QY 2389 AATATGCTTAAATATCTTTTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2448  
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Db 2467 AATATGCTTAAATATCTTTTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2526  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
QY 2449 CTGAATAATTTTCCATGAG 2508  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
Db 2527 CTGAATAATTTTCCATGAG 2586  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
QY 2509 GGTATATGTCAGAGCTTACAG 2568  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
Db 2587 GGTATATGTCAGAGCTTACAG 2646  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
QY 2569 GTTCTCCCTTCAATGAG 2628  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
Db 2647 GTTCTCCCTTCAATGAG 2706  
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QY 2629 AATATGCTAATTAATGAG 2688  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
Db 2707 AATATGCTAATTAATGAG 2766  
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QY 2689 TTGGCATATGCTTCAATTTTGGAG 2748  
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Db 2767 TTGGCATATGCTTCAATTTTGGAG 2826  
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QY 2749 AAGATTTGTCGAG 2808  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
Db 2827 AAGATTTGTCGAG 2886  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
QY 2809 TTCTTCACTCTTCTGATTTGTTCCGCTGCTGTGTGGAGAGAGAGAGAGAGAGAGAGAG 2868  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
Db 2887 TTCTTCACTCTTCTGATTTGTTCCGCTGCTGTGTGGAGAGAGAGAGAGAGAGAGAGAG 2946  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
QY 2869 TGGGATGATGAG 2928  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
Db 2947 TGGGATGATGAG 3006  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
QY 2929 GTGATTTGAG 2988  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
Db 3007 GTGATTTGAG 3066  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
QY 2989 GCGAGACATTTGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 3048  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
Db 3067 GCGAGACATTTGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 3126  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
QY 3049 GATAG 3108  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
Db 3127 GATAG 3186  
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QY 3109 TCCCTTATTTAG 3168  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111



Db 3187 GCCTTTGTAAGAGAGAAAGCTTTAGATGAATTAACCGCTGAGATCAATTAAT 3246  
Oy 3169 AAGAAGAGAGTGTATGTCACATCAATCAAC--AGAAATGGGAAGATCTGACTAT 3225  
Db 3247 AAAAAAGAGCGTGTATTTCAACCAATACCATAGAAATAGCAAGAGCTCAATTAAT 3306  
Oy 3226 CTTAAGATTAATGAACTACAAAGTGTATAGAACTGGACAGAGTGTGAAAAATAC 3285  
Db 3307 CTCAGAGAGGAATGGAATGAACTAGTGGCAT-----GGCAGAGTGTGAAAAATAT 3360  
Oy 3286 AATATGATGAAAGATGATTCATGATCAATCAATCAACCCAGCTTACTGTACTGTA 3345  
Db 3361 GTGCTGATGAAAGTATGATTCATGATTAATCAACCCAGCTTACTGTACTGTA 3420  
Oy 3346 CCAATGCTGTAGAGAAATGCTTGAATAATTTAAACAGGAACCTTACTGTA 3405  
Db 3421 CCAATGCTGTAGAGAAATGCTTGAATAATTTAAATCAAGAAATTCACACAGGAG 3480  
Oy 3406 TCGGATCTGGAAGAAAGAAAGAAATGAAAGAGTACTCATCAGAAAGTAC 3465  
Db 3481 TCGATATGAGAGAAAGAAAGAAAGAAAGTAAATGCA---ACTATGCTCATGAGGAGC 3537  
Oy 3466 ACTGTGACATCGCGCCACTGTAGA--AGAACAGCCGCTAGTGTAGACCTGAAGAACT 3522  
Db 3538 ACGGTATATGAGAGCTCCCGGAGGAGAAACAGCTGAGGTGAGCTGAGAAATCC 3597  
Oy 3523 CTTGAACCAAGCTGTGTTCACTGAAAGCTGTGTACAAAGATTCAGAGTGTGCAATC 3582  
Db 3598 CTTGAACCTGAAAGCTGTGTTCACTGAAAGCTGTGTACAAAGTGTGTCAGATA 3657  
Oy 3583 AATGTGAAGAAAGAGAGAAAGAAAGAAAGTGTGAACTGAGAAAGAGCTGTTCCGATA 3642  
Db 3658 AGCATGAAAGAAAGAGAGAAAGAAAGAAAGTGTGAACTGAGAAAGAAAGCTGTAAGATA 3717  
Oy 3643 GTTGAACATGACTGTGTTAGAACCTCATGTTTTCATGATTCCTTATGATGCTGCT 3702  
Db 3718 GTGAGACCAATGTTGTTCAACCTCATGTTTTCATGATTCCTTATGATGCTGCT 3777  
Oy 3703 CTGGCAATTAAGATTAATTAATGATTCAGCGAAAGAGATTAAGCAATGTTGAAATAT 3762  
Db 3778 CTGGCAATTAAGATTAATTAATGATTCAGCGAAAGAGATTAAGCAATGTTGAAATAT 3837  
Oy 3763 GCTGACAAAGTGTGTTCACTTACATTTTCACTTGAAGATGCTTCAAAATGGTGGCATAT 3822  
Db 3838 GCTGACAAAGTGTGTTCACTTACATTTTCACTTGAAGATGCTTCAAAATGGTGGCATAT 3897  
Oy 3823 GCTGATCAAAATTAATTCACCAATGCTGTGTGCTGAGCTTCTTAATTTGATGTT 3882  
Db 3898 GCTGATCAAAATTAATTCACCAATGCTGTGTGCTGAGCTTCTTAATTTGATGTT 3957  
Oy 3883 TCATGCTGATTAATTAATTCACCAATGCTGTGTGCTGAGCTTCTTAATTTGATGTT 3942  
Db 3958 TCATGCTGATTAATTAATTCACCAATGCTGTGTGCTGAGCTTCTTAATTTGATGTT 4017  
Oy 3943 CTCAGAGACTAAGAGCTGTAGAGCTTGAAGAGCTTATCTGATTTGAAGAGATGAGG 4002  
Db 4018 CTCAGAGACTAAGAGCTGTAGAGCTTGAAGAGCTTATCTGATTTGAAGAGATGAGG 4077  
Oy 4003 GTGCTGTGATGCTGTTTGAAGAGAAATTCATCATCAGTAATGTGCTGCTGCTGCT 4062  
Db 4078 GCTGCTGTGATGCTGTTTGAAGAGAAATTCATCATCAGTAATGTGCTGCTGCTGCT 4137  
Oy 4063 CTTATATGCTGCTAATTTTGAAGAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCT 4122  
Db 4138 CTTATATGCTGCTAATTTTGAAGAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCT 4197  
Oy 4123 CACTGATTAACACCACTGCTGATAGAGTGTGATGATGAAAGAGCTGATTAATCATACT 4182  
Db 4198 CACTGATTAATTAACACCACTGATAGAGTGTGATGATGAAAGAGCTGATTAATCATACT 4257  
Oy 4183 GATTCCTTAACCACTGATAGAGTGTGATGATGAAAGAGCTGATTAATCATACT 4242  
Db 4258 GATTCCTTAACCACTGATAGAGTGTGATGATGAAAGAGCTGATTAATCATACT 4317  
  
Oy 4243 TTGATATATGATGATTTGGTATCTCTTCTGTTGCTTCAAGTGTGCAATTCAGAGATG 4302  
Db 4318 TTGATATATGATGATTTGGTATCTCTTCTGTTGCTTCAAGTGTGCAATTCAGAGATG 4377  
Oy 4303 ATGATATATATGATGATGATGATTTGATGATGATGATGATGATGATGATGATGATGAT 4362  
Db 4378 ATGATATATATGATGATGATGATTTGATGATGATGATGATGATGATGATGATGATGAT 4437  
Oy 4363 GAAAGTGTGATGATGATGATTTGATGATGATGATGATGATGATGATGATGATGATGAT 4422  
Db 4438 GAAAGTGTGATGATGATGATTTGATGATGATGATGATGATGATGATGATGATGATGAT 4497  
Oy 4423 TTGATATATGATGATGATTTGATGATGATGATGATGATGATGATGATGATGATGAT 4482  
Db 4498 TTGATATATGATGATGATTTGATGATGATGATGATGATGATGATGATGATGATGAT 4557  
Oy 4483 GGTCAAGATGATGATGATTTGATGATGATGATGATGATGATGATGATGATGATGAT 4542  
Db 4558 GGTCAAGATGATGATGATTTGATGATGATGATGATGATGATGATGATGATGATGAT 4617  
Oy 4543 GGTCAAGATGATGATGATTTGATGATGATGATGATGATGATGATGATGATGATGAT 4602  
Db 4618 GGTCAAGATGATGATGATTTGATGATGATGATGATGATGATGATGATGATGATGAT 4677  
Oy 4603 TTGATATATGATGATGATTTGATGATGATGATGATGATGATGATGATGATGATGAT 4662  
Db 4678 TTGATATATGATGATGATTTGATGATGATGATGATGATGATGATGATGATGATGAT 4737  
Oy 4663 ATGATATATGATGATGATTTGATGATGATGATGATGATGATGATGATGATGATGAT 4722  
Db 4738 ATGATATATGATGATGATTTGATGATGATGATGATGATGATGATGATGATGATGAT 4797  
Oy 4723 GGTCAAGATGATGATGATTTGATGATGATGATGATGATGATGATGATGATGATGAT 4782  
Db 4798 GGTCAAGATGATGATGATTTGATGATGATGATGATGATGATGATGATGATGATGAT 4857  
Oy 4783 CTAGCATATATGATGATGATTTGATGATGATGATGATGATGATGATGATGATGATGAT 4842  
Db 4858 CTAGCATATATGATGATGATTTGATGATGATGATGATGATGATGATGATGATGATGAT 4917  
Oy 4843 TCCATGATGATGATGATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 4902  
Db 4918 TCCATGATGATGATGATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 4977  
Oy 4903 TTCCAGATGATGATGATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 4962  
Db 4978 TTCCAGATGATGATGATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 5037  
Oy 4963 GGTCAAGATGATGATGATTTGATGATGATGATGATGATGATGATGATGATGATGAT 5022  
Db 5038 GGTCAAGATGATGATGATTTGATGATGATGATGATGATGATGATGATGATGATGAT 5097  
Oy 5023 CTCATGATGATGATGATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 5082  
Db 5098 CTCATGATGATGATGATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 5157  
Oy 5083 GTTAAAGAGAGATGATGATGATTTGATGATGATGATGATGATGATGATGATGATGATGAT 5142  
Db 5158 GTTAAAGAGAGATGATGATGATTTGATGATGATGATGATGATGATGATGATGATGATGAT 5217  
Oy 5143 ATCTGCTATTTGATGATGATTTGATGATGATGATGATGATGATGATGATGATGATGAT 5202  
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Oy 5203 AACAGTAAAGAGAGATGATGATTTGATGATGATGATGATGATGATGATGATGATGATGAT 5262  
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Oy 5263 GATCTGGAAGAGATGATGATTTGATGATGATGATGATGATGATGATGATGATGATGAT 5322  
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QY 5323 CTGGTGTGGAGACATGATGATCGGTCATCTGGAGAACTTCACTGTTGCTACTGAA 5382  
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 ACCESSION AX164204  
 VERSION AX164204.1 GI:14545142  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens  
 human.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
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 Ragsdale, D.  
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 method using same to assess, diagnose, prognosis or treat epilepsy  
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 McGill University (Ca)  
 Location/Qualifiers  
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 BASE COUNT 2496 a 1591 c 1775 g 2487 t  
 ORIGIN

TITLE  
 JOURNAL  
 FEATURES  
 source

Query Match 70.0%; Score 4219; DB 6; Length 8349;  
 Best Local Similarity 82.5%; Pred. No. 0;  
 Matches 4989; Conservative 2; Mismatches 987; Indels 69; Gaps 11;

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 Db 106 ATGAGCAAAACAGTGTGTTGACACAGGACGATGATGATGATGATGATGATGATGATGAT 165  
 QY 61 TCTCTGCGGCTATGTAAGAGCAGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 119  
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 Db 166 TCTCTGCGGCTATGTAAGAGCAGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 225  
 QY 120 -CAAAAAGATGACAGCAAAATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 177  
 |||||  
 Db 226 CGCAAGAGATGAGAGATGAG 285  
 QY 178 AACCTTCATTTATTTATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 237  
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 Db 286 TCTCTGCGGCTATGTAAGAGCAGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 345  
 QY 238 CTGAGACCCCT 297  
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 QY 298 TTTCCGTTAGGCGCAACCT 357  
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 QY 358 ATAGCTATTAAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 417  
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 Db 466 ATAGCTATTAAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 525  
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 Db 1006 GATGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1065  
 QY 955 CAAGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1014  
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 Db 1066 GAGGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1125

|    |      |   |       |
|----|------|---|-------|
| OY | 1015 | AGCTGATGAGGCGCAATGTCGACAGAGGATATATGTGTGTAAAGCTGTGTGAATATCC        | 1074  |
| OY | 1015 | AGCTGATGAGGCGCAATGTCGACAGAGGATATATGTGTGTAAAGCTGTGTGAATATCC        | 1074  |
| Db | 1126 | AGCTGATGAGGCGCAATGTCGACAGAGGATATATGTGTGTAAAGCTGTGTGAATATCC        | 1185  |
| OY | 1075 | AATATGAGCTACACAACTTTGATTAACCTTACGTGGGCTTTTGTGCTTGTGTGACTA         | 11344 |
| Db | 1186 | AACATGAGCTACACAACTTTGATTAACCTTACGTGGGCTTTTGTGCTTGTGTGACTA         | 12455 |
| OY | 1135 | ATGACTCAGGACTTCTGGGAAAAATCTTTATCAACTGACATTAACGTGCTGTGGAAAAAG      | 11944 |
| Db | 1246 | ATGACTCAGGACTTCTGGGAAAAATCTTTATCAACTGACATTAACGTGCTGTGGAAAAAG      | 13050 |
| OY | 1195 | TACATGATATTTTGTGTGTGTGTCATTTTCTTGGGCTCATTTCTACTTAATTAATTTGTC      | 12344 |
| Db | 1306 | TACATGATATTTTGTGTGTGTGTCATTTTCTTGGGCTCATTTCTACTTAATTAATTTGTC      | 13655 |
| OY | 1255 | CTGGCTGTGGGCGCATGGGCTCTGAGAGGAAACAATTCAGGCCCACTGTGGAAGAACACAA     | 13144 |
| Db | 1366 | TTGGCTGTGGGCGCATGGGCTCTGAGAGGAAACAATTCAGGCCCACTGTGGAAGAACACAA     | 14255 |
| OY | 1315 | CAGAAAAGAGCCGGAATTTTCAGCAGATGATTTGAACAGCTTTAAAAAGCAACAGAGGAGCACT  | 13744 |
| Db | 1426 | CAGAAAAGAGCTGAATTTTCAGCAGATGATTTGAACAGCTTTAAAAAGCAACAGAGGAGCACT   | 14855 |
| OY | 1375 | CAGCAGGACGACGACG-----CACTGCTCTAGAACATTTCCAGAGAGCCCACTGACCA        | 1428  |
| Db | 1486 | CAGCAGGACGCTGACGCGCGCATCTGCTGATCAAGAGACATTCAGAGGCTGTGGGATTA       | 15455 |
| OY | 1429 | GGCAGGCTCTAGCAGCTCTCATCGAACCTCTAACTGATTTCCAAAGTGCTTAAGAA          | 1488  |
| Db | 1546 | GGAGTTTTTTCAGAGACTTCTTCAGTACGACTTCAATTAAGTATCCAAAAGTCAAAAAG       | 16055 |
| OY | 1489 | AGAGAAATCGAGAGAAAGAAAAGAAAAGAGAGACACTGTGTGGGAGAGAGAAAT            | 1548  |
| Db | 1606 | CTGAAAAACAGAAAGAAAAGAAAAGAAAAGAACATCTGTGAGAGAGAGAGAAAAT           | 16655 |
| OY | 1549 | GAGATGATATTTCCAAAAATCTGAATCTGAGAGACATCAGAGAGAAAGTTTTCGCTTC        | 1608  |
| Db | 1666 | GACAGAG---TCTTAAATATGGAATCTGAAGACAGCATTAAGAAAGGTTTCCGTTT          | 17222 |
| OY | 1609 | TCCATTTGAAGGAAACGATTTGACATTTGAAAAGAGGTACTCTCCCAACACAGCTTTG        | 1668  |
| Db | 1723 | TCTCTTGAGAGAACTAGCTGACATTTGAAAAGAGATTTTCTTCTCCACACAGCTTCTA        | 17822 |
| OY | 1669 | TTTGACATCCGTGGCTCCCTAATTTTTCACAGAGCGCAATTAAGAGAAACGCTTTTCAGC      | 1728  |
| Db | 1783 | CTGAGACATCCGTGGCTCCCTTCTCTCCCAAGACGCAACAGTAGAGGCGACCTTTTCAGC      | 1842  |
| OY | 1729 | TTTGAAGAGGCGAGCAAGATGTGGGATCTGAGAACGATTCGAGATGATGAGCACAGC         | 1788  |
| Db | 1843 | TTTCAAGAGGTGAGCAAAAGAGCAATTTGGCTCTGAAATTAAGCTTTGCTGATGATGAGCACAGC | 1902  |
| OY | 1789 | ACCTTGAAGATTAACGAGACCGGTAGAGATTCCTTGTGTGTCCCGCAGCACAGAGAG         | 1848  |
| Db | 1903 | ACCTTGAAGATTAACGAGACCGGTAGAGATTCCTTGTGTGTCCCGCAGCACAGAGAGAA       | 1962  |
| OY | 1849 | AGAGCAACAGCAACTGATCTAGACAGCAAGTAGGTATCCCGGATCTGTGAGTGTTTTCA       | 1908  |
| Db | 1963 | CGGGCGCAACAGCAATGTCAACGAGCGCAAGCGTCCCTCAAGGATCTGTCCCATCTGCC       | 2022  |
| OY | 1909 | GGCAATGGAGAGATGACAGCAGCTGTGATGTGCATGTGTGTGTTCTTGTGTGTGTGA         | 1968  |
| Db | 2023 | ATGAAATGGAGAGATGCAATGACGCTGTGTGATCTGCAATGATGTGTCTTCCGTGTGGGGGC    | 2082  |
| OY | 1969 | CTTTCAGTCTCTACATCCGCTGTGTGAGCAGCTTCTGCCAGAGGTATTAATAGATTAAGCA     | 2028  |
| Db | 2083 | CTTTCAGTCTCTACATCCGCTGTGTGAGCAGCTTCTGCCAGAGGTATTAATAGATTAAGCA     | 2121  |
| OY | 2029 | GCTACTGATGACATGAGCAACACACTGTAATGAAATGAGAAAGAGGCAAGTTCT            | 2088  |
| Db | 2122 | -----GGCACAACACTACTGAAACAGAAATTAAGAAAGAGCGGTCCAGTTCT              | 2166  |
| OY | 2089 | TTTCAAGTTTCCATGAGCTTCTTGAAGATCTTCCCAAGGCAACGAGCATGATGATTA         | 2148  |

|    |      |  |       |
|----|------|--|-------|
| Dd | 2167 | TATCATGTTTCCATGGATTTATATGGAAGATCTACATCAAGGCGAAGACCAATGAGTATA   | 22326 |
| Oy | 2149 | GCCAGCATCTTCAACAAATACAGTGAAGAACTTGAAGAAATCCGAGCAAAATGCCACCC    | 2208  |
| Dd | 2227 | GCGAGTATTTTGACCAACACATGGAAGAACTTGAAAGATCCAGACAAATGCCACCA       | 2286  |
| Oy | 2209 | TGTTGGTATAAATTTTCCACATATTTCTAATCTGGAGACTGTTCATATTTGGTTAAA      | 2266  |
| Dd | 2287 | TGCTGGTATAAATTTGCAATATATCTGTATTTGATTTGGAGCTGTGTAACCAATGTTTAAAG | 23446 |
| Oy | 2269 | GTTAAACATGTTCGAACCTGTGTGTGATGAGACCCATTTGTTCACCTGGCATTCACATC    | 24006 |
| Dd | 2347 | GTTAAACACCTTGTCAACCTGTGTGTATGAGACCCATTTGTTCACCTGGCATTCACATC    | 24006 |
| Oy | 2329 | TGTATGTCTTAAATACCTTTTCATGCGCCATGAGACACATATCCAAATGACGACATATTC   | 2386  |
| Dd | 2407 | TGCAATGTCTTAAATACCTTTTCATGCGCATGAGACACATATCCAAATGACGAGATTC     | 2466  |
| Oy | 2389 | AATATGTGCTTACAGTAGAAGAACTTGTTTACAGCGGATCTTTACACAGAAATGTTT      | 2448  |
| Dd | 2467 | AGCAGTGAAGTGTGTGGAAGACGTGTTTACAGGAGTCTTACACAGAAATGTTT          | 2528  |
| Oy | 2449 | CTGAATATTTATGCCATGATCCTTACTATATTTTCCAAAGAAAGCTGAATATCTTGAC     | 2508  |
| Dd | 2527 | CTCAAGATAAATGCCATGATGCATATTTATTTACTTCAAGAAAGCTGAATATTTTAT      | 2586  |
| Oy | 2509 | GTTTTATTTGAGAGCTTACCGTGAAGAACTTGAGACTGGCCAAATGTGAAGATATCT      | 2566  |
| Dd | 2587 | GTTTTATTTGAGAGCTTACCGTGAAGAACTTGAGACTGGCCAAATGTGAAGATATCTA     | 2646  |
| Oy | 2569 | GTTCCGCTTATATTCGATGTGCGAGTTTCAATTTGGCAAAATCTTGGCAGCATTA        | 2628  |
| Dd | 2647 | GTTCCGCAATATTCGCGGTCTCCAGTTTCAAGTTGGCAAAATCTTGGCAGCATTA        | 2706  |
| Oy | 2629 | AATATGCTAATAAAGATCATGGCAATTCGTTGGGGGCTCTGGGAATTTAACCTCTGC      | 2688  |
| Dd | 2707 | AATATGCTAATAAAGATCATGTCGCAATTCGTGGGGGCTCTGAGAAACCTCACCTTGTGA   | 2766  |
| Oy | 2689 | TTGCGCAATACGCTTCATTTTTCGCGTGTGCGCAATGCTGTTGGTAAAGCTAC          | 2748  |
| Dd | 2767 | TTTGCAATCATCGCTTCATTTTTCGCGTGTGCGCAATGCTGTTGGTAAAGCTAC         | 2826  |
| Oy | 2749 | AAAGATGTGTCTCAGATGCGCAAGTATTCACACTCCACGCTGGCAATGATATAC         | 2808  |
| Dd | 2827 | AAAGATGTGTCTCAGATGTTTCCATGATTTGGAACCTCCACGCTGGCAATGATATAC      | 2886  |
| Oy | 2809 | TTCTTCACCTCTCTGATTTGTTCGCGTGTCTGTGGGAGTGTGATGAGACATG           | 2868  |
| Dd | 2887 | TTTTTTCACCTCTCTGATTTGTTCGCGTGTCTGTGGGAGTGTGATGAGACATG          | 2946  |
| Oy | 2869 | TGGGACGTATGAGAGTGTCTGTGTCGAACCATGTGCTTACTGTTCATGATGCTATG       | 2928  |
| Dd | 2947 | TGGGACGTATGAGAGTGTCTGTGTCGAACCATGTGCTTACTGTTCATGATGCTATG       | 3006  |
| Oy | 2929 | GTTGATTTGGAACCTGAGTGTCTGATATCTTTCGCTGTCTTMTGAGCATTTAGT         | 2988  |
| Dd | 3007 | GTTGATTTGGAACCTGAGTGTCTGATATCTTTCGCTGTCTTMTGAGCATTTAGT         | 3066  |
| Oy | 2989 | GCAGACAACCTTGCAGCACTGTATGATATGAATGAATATCTCCAAATTTGCTGTG        | 3048  |
| Dd | 3067 | TCTGACATCTTGTGCTGCACATGATGATGAATGAATGAATATCTCCAAATTTGCTGTG     | 3126  |
| Oy | 3049 | GATGAGATGCACAAAGGATGCTTATGTGGAAGAAAAATATGATATTTATTCACAG        | 3108  |
| Dd | 3127 | GGAAGATGCAGAAAGGAATCGATTTGTGTTAAAGAAAAATACGGAATTTATTCAGAA      | 3186  |
| Oy | 3109 | TCTCTCATTTAGGAACAAAGATTTAGATGAATTAACCACTGATGATCTATAACAC        | 3168  |
| Dd | 3187 | GCTTTGTGTAGGAAGCAAGAACTTTAGATGAATTAACCACTGATGATCTATAATAT       | 3246  |
| Oy | 3169 | AAGAAACAGGTGTATGTCCAAATCATACAC---AGAATTTGGGAAGATCTTGACAT       | 3225  |

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Db 3307 CTCAAAAGCAAGATGAGACATCAAGTGTATAGAACTGCGACAGCTTGAAATATAC 3360  
OY 3286 AATATGATGAAATGATATACATCTTCAATTAACAAACCCAGCTGATCTGATGTA 3345  
Db 3261 GTCTGATGAAATGATATACATCTTCAATTAACAAACCCAGCTGATCTGATGTA 3420  
OY 3346 CCAATCTCTAGAGAAATCTGATCTTGAATTAACCGAAGACTTATAGTGA 3405  
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Db 3481 TCGATCTGAGAAACAAAGAACTGAAATGAAAGACTGATCAATCAAGTATG 3540  
OY 3466 ACTGTGACATCGGCGACCTGTAGA--AGAACGCCCTGATGGAACCTGAAAGAACT 3522  
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OY 3643 GTTGAACATATGATGATGAGACCTGATCTGATGATGATCTGATGATGATGATGAT 3702  
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OY 3823 GGTATCAAAATATTTACCAATGCTGATGATGATGATGATGATGATGATGATGATGAT 3882  
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OY 3883 TCAATGCTGATTAAGACAAATGCTGATGATGATGATGATGATGATGATGATGATGAT 3942  
Db 3958 TCAATGCTGATTAAGACAAATGCTGATGATGATGATGATGATGATGATGATGATGAT 4017  
OY 3943 CTGAGGACATTAAGAGCTGAGACCTCTAAGAGCTTATCTGATTTGAAGAGATGAG 4002  
Db 4018 CTGAGGACATTAAGAGCTGAGACCTCTAAGAGCTTATCTGATTTGAAGAGATGAG 4077  
OY 4003 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4062  
Db 4078 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4137  
OY 4063 CTATATCTGCTGATTTTACAGATGATGATGATGATGATGATGATGATGATGATGAT 4122  
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Db 4198 CACTGATTAAC 4257  
OY 4183 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4242  
Db 4258 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4317  
OY 4243 TTTGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4302  
Db 4318 TTTGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4377

OY 4303 ATGATATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4362  
Db 4378 ATGATATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4437  
OY 4363 GAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4422  
Db 4438 GAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4497  
OY 4423 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4482  
Db 4498 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4557  
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Db 4558 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4617  
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OY 4663 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4722  
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Db 4798 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4857  
OY 4783 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4842  
Db 4858 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4917  
OY 4843 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4902  
Db 4918 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4977  
OY 4903 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4962  
Db 4978 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5037  
OY 4963 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5022  
Db 5038 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5097  
OY 5023 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5082  
Db 5098 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5157  
OY 5083 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5142  
Db 5158 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5217  
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OY 5203 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5262  
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OY 5263 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5322  
Db 5338 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5397  
OY 5323 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5382  
Db 5398 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5457





OY 298 TTCGGTTCAGTGCACCTCTGCCCTGTACATTTTAACCTCCCTCAACCTCTTAGAAA 357  
 DB 406 TCTCGATTCAGTGCACCTCCCTGCTTACATTTTAACCTCCCTCAACCTCTTAGAAA 465  
 OY 358 ATAGCTATTAAGATTTTGGTACATTCATTTTACAGATGCTAATTAATGCTAATTTG 417  
 DB 466 TTAGCTATTAAGATTTTGGTACATTCATTTTACAGATGCTAATTAATGCTAATTTG 525  
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 OY 598 TTTCGCTACGTCACAGAGTTTGGACCTGCGCAATGCTGCGCAATGCTGCGCAATGCTG 657  
 DB 706 TTTCGCTACGTCACAGAGTTTGGACCTGCGCAATGCTGCGCAATGCTGCGCAATGCTG 765  
 OY 658 GTTCCGAGCATTTGAAGAGATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 717  
 DB 766 GTTCCGAGCATTTGAAGAGATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 825  
 OY 718 CTGATCAGCTCTGTGAAGAGCTCTGATGATGATGATGATGATGATGATGATGATGATG 777  
 DB 826 CTGATCAGCTCTGTGAAGAGCTCTGATGATGATGATGATGATGATGATGATGATGATG 885  
 OY 778 GTATTTGCTCTAATTTGGGCTGCGAGCTGTGATGCGGCACTGCGGCAATTAATGATCAA 837  
 DB 886 GTATTTGCTCTAATTTGGGCTGCGAGCTGTGATGCGGCACTGCGGCAATTAATGATCAA 945  
 OY 838 TGGCTCCGACCAATGCTCTGCTGAGAGAACT---AGTATGAAGAAATTAATTAATTA 894  
 DB 946 TGGCTCCGACCAATGCTCTGCTGAGAGAACT---AGTATGAAGAAATTAATTAATTA 1005  
 OY 895 AATTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 954  
 DB 1006 AATTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1065  
 OY 955 CAAGATTCAGAGATTAATTTCTGAGAGGTTTTTATGATGATGATGATGATGATGATG 1014  
 DB 1066 CAAGATTCAGAGATTAATTTCTGAGAGGTTTTTATGATGATGATGATGATGATGATG 1125  
 OY 1015 AGCTCTGATGAGGCAATGCTGAGAGGATATGCTGAGAGGATGCTGAGAGGATGCTG 1074  
 DB 1126 AGCTCTGATGAGGCAATGCTGAGAGGATATGCTGAGAGGATGCTGAGAGGATGCTG 1185  
 OY 1075 AATTATGCTACAGAGCTTTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 1134  
 DB 1186 AATTATGCTACAGAGCTTTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 1245  
 OY 1135 ATGACTCAGAGCTTGGGAAAATCTTTATCACTGATGATGATGATGATGATGATGATG 1194  
 DB 1246 ATGACTCAGAGCTTGGGAAAATCTTTATCACTGATGATGATGATGATGATGATGATG 1305  
 OY 1195 TACATGATATTTTGTGTGCTATTTCTGAGGCTCATATTCATGATGATGATGATGATG 1254  
 DB 1306 TACATGATATTTTGTGTGCTATTTCTGAGGCTCATATTCATGATGATGATGATGATG 1365  
 OY 1255 CTGGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1314  
 DB 1366 CTGGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1425  
 OY 1315 CAGAAAGAGGCGAATTTTACAGGATGATGATGATGATGATGATGATGATGATGATGATG 1374  
 DB 1426 CAGAAAGAGGCGAATTTTACAGGATGATGATGATGATGATGATGATGATGATGATGATG 1485  
 OY 1375 CAGAGGAGGAGAGG-----CAACTGCTCAGAGCAATTCAGAGAGGAGGAGGAGGAGG 1428  
 DB 1486 CAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1545  
 OY 1429 GCGAGGCTCTCAGAGGCTGATGAGGCTGATGAGGCTGATGAGGCTGATGAGGCTGATGAG 1488  
 DB 1546 GCGAGGCTCTCAGAGGCTGATGAGGCTGATGAGGCTGATGAGGCTGATGAGGCTGATGAG 1605  
 OY 1489 AGAAGAAATCGGAG 1548  
 DB 1506 AGAAGAAATCGGAG 1665  
 OY 1549 GAGAGATGATTCAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1608  
 DB 1666 GAGAGATGATTCAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1722  
 OY 1609 TCCATTTAG 1668  
 DB 1723 TCCATTTAG 1782  
 OY 1669 TTGAGCATTCGCTGCTCTATTTTCAACAGAGGAGAAATGAGAGAGAGAGAGAGAGAG 1728  
 DB 1783 TTGAGCATTCGCTGCTCTATTTTCAACAGAGGAGAAATGAGAGAGAGAGAGAGAGAG 1842  
 OY 1729 TTTAGAGGAG 1788  
 DB 1843 TTTAGAGGAG 1902  
 OY 1789 ACCCTTGAAGATTAAG 1848  
 DB 1903 ACCCTTGAAGATTAAG 1962  
 OY 1849 AGAGCAAG 1908  
 DB 1963 AGAGCAAG 2022  
 OY 1909 GCGAATGAG 1968  
 DB 2023 GCGAATGAG 2082  
 OY 1969 CTTGAGTCTCAG 2028  
 DB 2083 CTTGAGTCTCAG 2121  
 OY 2029 GCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2088  
 DB 2122 GCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2166  
 OY 2089 TTTCAAGTCTCAG 2148  
 DB 2167 TTTCAAGTCTCAG 2226  
 OY 2149 GCGAGATTTCTAACAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2208  
 DB 2227 GCGAGATTTCTAACAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2286  
 OY 2209 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2268  
 DB 2287 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2346  
 OY 2269 GTGAAACATGTTGCAACCGGTGTGATGATGATGATGATGATGATGATGATGATGATG 2328  
 DB 2347 GTGAAACATGTTGCAACCGGTGTGATGATGATGATGATGATGATGATGATGATGATG 2406  
 OY 2329 TGTATGCTCTAATAATCTCTTTTATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2388  
 DB 2407 TGTATGCTCTAATAATCTCTTTTATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2466  
 OY 2389 AATATGCTGTTTACATGAG 2448  
 DB 2467 AATATGCTGTTTACATGAG 2526  
 OY 2449 CTGAAATTAATTTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2508





|    |      |  |       |
|----|------|--|-------|
| OY | 4653 | ATGGCAACAAAGAGGAGGGAACAGATGACACAGATATGTGACATCTTTGGCA               | 47222 |
| DB | 4738 | ATGGCAACCAAGATGGTGGAAACCGATGACACAGTCAAGAAATGCAAAACATTTGTGAC        | 47997 |
| OY | 4723 | CGCAATCATCTGGTGTTCATTTGGTGCATTTACTTGGAGAGTGTGTACGAACTATCTCT        | 47822 |
| DB | 4798 | TGGATTAATCTGGGTGTATTTGTTGTTCTGTCTCAGCGAGAAATGGTGTCTGAAACTGATCTCT   | 48572 |
| OY | 4783 | CTAGCCCATTTATTTTACCATTTGATGAGATATTTTGGATTTTGTGGTGTCTATCTC          | 48422 |
| DB | 4858 | CTTGTGTACTACATATTTCACTATTTGGATGGAAATATTTTGGATTTTGTGGTGTCTATCTC     | 49171 |
| OY | 4843 | TCCATTTAGGTATGTTTCTTGCCGAGCGATAGAAAATATTTGTGTGCCCTACCTCG           | 49022 |
| DB | 4918 | TCCATTTAGGAATGTTTCTTGCTGTGAACATGATGAAAATATTTTGTGTGCCCTACCTCG       | 49777 |
| OY | 4903 | TTCCGAGAGATCCGTTCTGTAGAGATTTGGCCGAATCTTCAGCTCATCAAGAGGAGCAAG       | 49632 |
| DB | 4978 | TTTCGAGAGATCCGTTCTGTGTCTGATGAGATTTGGCCGAATCTTCAGCTCATCAAGAGGAGCAAG | 50272 |

|    |      |  |      |
|----|------|--|------|
| OY | 5743 | GAGGAGATATGCTGCATTTATTCACCGCTGGTTACGAGCGCCACCTTTAAAGGAACT  | 5802 |
|    |      |  |      |
| Db | 5818 | GAGAGAGTGTCGTATTTATTTATTCAGAGGGCTTACAGAGCTTACTTTGAGCAGAAA  | 5877 |
| OY | 5803 | GTAACAAGTCTCCTTAGTCACATATAAAACAAAATCAAAAGTGGGGCTATCTTCTT   | 5862 |
|    |      |  |      |
| Db | 5878 | GTTAAAAAGGTATACAGTATATACAGAAAGACAAAGGCAAAAGATGTATGAAACACC  | 5937 |
| OY | 5863 | ATTAAGAAGCATGATATATGACAGATTAATGAAATCTATTAACAAATAAAGTAT     | 5922 |
|    |      |  |      |
| Db | 5938 | ATCAAGAAGTACTCTCATTTGATTAATCTGAATGAGAAATTCACCTCCAGAAACCAT  | 5997 |
| OY | 5923 | CTGACCATGTCACATGACGTTGTCCACCTTCCATGACCGGATGCAAGAGCAATTTGTG | 5982 |
|    |      |  |      |
| Db | 5988 | ATGACGCGCTTCCA---CCACGTCCTCACCCCTGTATGATGTGTGACCAACCGAAAA  | 6054 |
| OY | 5983 | GAAATACATGACGAAAGGCAAAAGTGAATGAATGAAACCAATGGGAAATA         | 6029 |
|    |      |  |      |
| Db | 6055 | GAAATTTTGAATAAGCAATACGAAATGAAAGGAAAGCAAAAGGGAGAA           | 6101 |

Search completed: April 22, 2003, 09:58:47  
Job time : 10048 secs

|    |      |  |      |
|----|------|--|------|
| Oy | 4963 | GGGATTCGCAAGCGTGCCTTGGTTGAGATGATCCCTTCGCGCTTTTAAACATCGC        | 5022 |
| Db | 5038 | GGGATTCGCAAGCGTGCCTTGGTTGAGATGATCCCTTCGCGCTTTTAAACATCGC        | 5097 |
| Oy | 5023 | CTCCACTCTCTCCTAGTCATGTTCACTACAGCCATCTTGGATGTCCAACTTGCCTAT      | 5082 |
| Db | 5098 | CTCCCTCTCTTCTCTGGTCATGTCATCTACGCCATCTTGGATGTCCAAATTTGCTCAT     | 5157 |
| Oy | 5083 | GTTAAGAGGGAACTGGGATCGATGTGACATGTCAACTTGTGAACTTGTGGCAACGATG     | 5142 |
| Db | 5158 | GTTAAGAGGGAAAGTGGGATCGATGTGACATGTTCACATTTGGAACCTTTGGCAACGATG   | 5217 |
| Oy | 5143 | ATTCGCTATTCCAAATTAACAACTCTGCTGGCTGGATGATGTCATGACACCATCTTC      | 5202 |
| Db | 5218 | ATTCGCTATTCCAAATTAACAACTCTGCTGGCTGGATGATGTCATGACACCTATCTT      | 5277 |
| Oy | 5203 | AACGTAAGCCACCCGACTGTGACCCCTTAATPAAAGTTAAACCTGGAAGCTCAGTTAAGGA  | 5262 |
| Db | 5278 | AATATGTGACCTCCAGACTGTGACCTCTGACAAAGATCAACCTCGAAGCTCAGTTAAGGA   | 5357 |
| Oy | 5263 | GACGTGGGAAACCATCTGTGGAAATTTTCTTTTGTCACTTACATCATATATCTTC        | 5322 |
| Db | 5338 | GACGTGGGAAACCATCTGTGGAAATTTTCTTTTGTCACTTACATCATATATCTTC        | 5397 |
| Oy | 5323 | CTGCTGTGTGTAACATGTACATCGCGGTCATCTCGGAGAACTTCAGTGTGACATCGAA     | 5382 |
| Db | 5398 | CTGCTGTGTGTAACATGTACATCGCGGTCATCTCGGAGAACTTCAGTGTGACATCGAA     | 5457 |
| Oy | 5383 | GAAAGTCAGAGCCCTCTGAGTGAAGATGATCTTGGATGATGTTCTATGAGATTTGGAGAA   | 5442 |
| Db | 5458 | GAAAGTCAGAGCCCTCTGAGTGAAGATGATCTTGGATGATGTTCTATGAGATTTGGAGAA   | 5517 |
| Oy | 5443 | TTTGTATCCCGATGCCAACTCAGTTTCATGGAATTTGAAAAATTAATCTCACTTGGACGTGC | 5502 |
| Db | 5518 | TTTGTATCCCGATGCCAACTCAGTTTATGAGATTTGGCAAACTTTCGATTTGGCAGATGCC  | 5577 |
| Oy | 5503 | CTTGAACCCGCTCTCAGTATGTGCAACAACCAACCAACACGACATTCGCATGGATTTG     | 5562 |
| Db | 5578 | CTTGATCTCTCTCTTCTCATAGCAAAAACCAACCAACCAACGATCATTCGCATGGATTTG   | 5637 |
| Oy | 5563 | CCCATGTGAGTGTGATACCGGATCCAGTCTGTGATCTATTAATTTGGCTTTACAAACGG    | 5622 |
| Db | 5638 | CCCATGTGAGTGTGATACCGGATCCAGTCTGTGATCTATTAATTTGGCTTTACAAACGT    | 5697 |
| Oy | 5623 | GTTCTAGAGAGATGTGAGAGATGATGCTCTTACGATATCAGATGGAAGACGATTCATG     | 5682 |
| Db | 5698 | GTTTGTGTGAGATGTGAGAGATGATGCTCTTCCAAATACAGATGGAAGACGATTCATG     | 5757 |
| Oy | 5683 | GCATTCAATCTTCCAAAGTCTCCATATACAGCAACATCACTACTCTTTAAACGAAACAA    | 5742 |
| Db | 5758 | GCATCAAAACCCCTCCAAATGCTCTTATGAGCCCATTTACGACACAGTGAACGCAACAA    | 5817 |

GenCore version 5.1.4 p5.4578  
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OW nucleic - nucleic search, using sw model

Run on: April 22, 2003, 05:50:48 ; Search time 767.Seconds

(without alignments)  
17704.759 Million cell updates/sec

Title: US-09-930-871-11

Perfect score: 6030

Sequence: 1 atggagcaaacgtgtctgt.....aaaagccaaggaataa 6030

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 212599159 residues 4370478

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N.Geneseq\_101002.\*

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- 2: /SID2/gcgdata/geneq/geneq-emb1/NA1981.DAT.\*
- 3: /SID2/gcgdata/geneq/geneq-emb1/NA1982.DAT.\*
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- 23: /SID2/gcgdata/geneq/geneq-emb1/NA2001B.DAT.\*
- 24: /SID2/gcgdata/geneq/geneq-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score  | Query Match Length | ID   | Description                    |
|------------|--------|--------------------|------|--------------------------------|
| 1          | 6028.8 | 100.0              | 6030 | 24 AAD32844 Human ion channel  |
| 2          | 6015.2 | 99.8               | 8378 | 22 AAH55763 Human adult form o |
| 3          | 6006.6 | 99.6               | 6027 | 24 AAD27266 Human transporter  |
| 4          | 5963.2 | 98.9               | 8378 | 22 AAH55766 Human neonatal for |
| 5          | 5952.8 | 98.7               | 5997 | 24 AAD32839 Human ion channel  |
| 6          | 5917.4 | 98.1               | 8131 | 24 ABL39689 Human sodium chann |
| 7          | 5915.8 | 98.1               | 5922 | 24 AAD32845 Human ion channel  |
| 8          | 5839.8 | 96.8               | 5889 | 24 AAD32840 Human ion channel  |
| 9          | 4336.8 | 71.9               | 4362 | 24 AAD32846 Human ion channel  |

|    |        |      |      |                                 |
|----|--------|------|------|---------------------------------|
| 10 | 4260.8 | 70.7 | 4329 | 24 AAD32841 Human ion channel   |
| 11 | 4219   | 70.0 | 8349 | 22 AAH55793 Human adult form o  |
| 12 | 4219   | 70.0 | 8349 | 22 AAH55793 Human neonatal for  |
| 13 | 4150.8 | 68.8 | 4179 | 24 AAD32847 Human ion channel   |
| 14 | 4074.8 | 67.6 | 4146 | 24 AAD32842 Human ion channel   |
| 15 | 4057.8 | 67.3 | 4197 | 24 AAD32848 Human ion channel   |
| 16 | 4045   | 67.1 | 9123 | 24 ABL29690 Human sodium chann  |
| 17 | 3981.8 | 66.0 | 4164 | 24 AAD32843 Human ion channel   |
| 18 | 3785.4 | 62.8 | 9112 | 22 AAH55823 Human adult form o  |
| 19 | 3758.2 | 62.3 | 9112 | 22 AAH55824 Human neonatal for  |
| 20 | 3563.8 | 59.1 | 6822 | 24 ABL63697 Rat sequence diffe  |
| 21 | 3541.6 | 58.7 | 6404 | 17 AAT30195 Peripheral nervous  |
| 22 | 3476.8 | 57.7 | 6371 | 17 AAT30194 Peripheral nervous  |
| 23 | 3397.6 | 56.3 | 6452 | 17 AAT30193 Peripheral nervous  |
| 24 | 2807   | 46.6 | 7053 | 21 AA93791 Human CDNA encodin   |
| 25 | 2807   | 46.6 | 7053 | 24 ABL42751 Human sodium chann  |
| 26 | 2787.6 | 46.2 | 6007 | 19 AAH58421 Tetrodotoxin-sensl  |
| 27 | 2758.2 | 45.7 | 5977 | 19 AAH58420 Tetrodotoxin-sensl  |
| 28 | 2738.8 | 45.4 | 6556 | 19 AAH58419 PN4 sodium channel  |
| 29 | 2738.8 | 45.4 | 6556 | 19 AAH58419 PN4 sodium channel  |
| 30 | 1962.4 | 32.5 | 6021 | 24 ABL42420 Rat voltage-gated   |
| 31 | 1907.2 | 31.6 | 6048 | 19 AAH9029 Human hml sodium c   |
| 32 | 1907.2 | 31.6 | 6048 | 19 AAH9029 Human hml sodium c   |
| 33 | 1890.6 | 31.4 | 7555 | 16 AAQ81328 Cardiac sodium cha  |
| 34 | 1865   | 30.9 | 7555 | 11 AAQ05831 Cardiac sodium cha  |
| 35 | 1828.6 | 30.3 | 8530 | 12 AAS31089 Human diagnostic a  |
| 36 | 1789.8 | 29.7 | 3033 | 17 AAT30192 Peripheral nervous  |
| 37 | 1590   | 26.4 | 6606 | 20 AAH60872 Human SNTS1 ion cha |
| 38 | 1544.4 | 25.6 | 5874 | 22 AAH6961 Human hpn3 CDNA se   |
| 39 | 1542.8 | 25.6 | 5874 | 22 AAH6961 Human hpn3 CDNA se   |
| 40 | 1494.6 | 24.8 | 6373 | 22 AAH6960 Mouse SNTS1 ion cha  |
| 41 | 1474.8 | 24.5 | 6527 | 18 AAT77806 CDNA encoding vari  |
| 42 | 1469   | 24.4 | 6524 | 18 AAT77803 CDNA encoding wild  |
| 43 | 1468.4 | 24.4 | 6344 | 22 AAH6959 Rat SNTS1 ion chann  |
| 44 | 1468.4 | 24.4 | 6344 | 22 AAH6959 Rat SNTS1 ion chann  |
| 45 | 1361.4 | 22.6 | 7052 | 18 AAT77805 CDNA encoding vari  |

## ALIGNMENTS

RESULT 1  
ID AAD32844 standard; CDNA; 6030 BP.

XX AAD32844:

XX 01-JUL-2002 (first entry)

XX Human ion channel CDNA #6.

XX Human; novel human protein; NHP; voltage-gated sodium channel;

KW gene therapy; bioreactor; mental disorder; biological disorder;

KW gene; medical disorder; ss.

XX Homo sapiens.

XX Key

XX CDS

XX W0200214498-A2.

XX 21-FEB-2002.

XX 15-AUG-2001; 2001MO-US25656.

XX 16-AUG-2000; 2000US-225989P.

Location/Qualifiers  
1..6030  
/\*tag-  
/\*product- "Human ion channel protein #6"  
/\*transl\_except- (pos:2974..2976, aa:Xaa)  
/\*transl\_except- (pos:3199..3201, aa:Xaa)  
/\*note- "Xaa - any amino acid"

PA (LEXI-) LEXICON GENETICS INC.

XX Turner CA, Mathur B, Mathur D.

XX WPI, 2002-280757/32.

DR P-PSDB; AAE20515.

PT Novel polynucleotides encoding human sodium channel proteins,  
 particularly voltage-gated sodium channel proteins useful for drug  
 screening, diagnosis and in gene therapy of biological disorders

XX Claim 2: Page 55-57: 83pp: English.

XX The present sequence is a cDNA encoding novel human protein (NHP), ion  
 CC channel protein. NHP share structural similarity with mammalian sodium  
 CC channel proteins particularly voltage-gated sodium channel proteins.  
 CC NHP oligonucleotides are useful as hybridisation probes for screening  
 CC libraries and assessing gene expression patterns. Sequences derived  
 CC from regions adjacent to the intron/exon boundaries of NHP gene can be  
 CC used to design primers for use in amplification assays to detect  
 CC mutations within the exons, splice sites, introns that can be used in  
 CC diagnostics and pharmacogenomics. NHP nucleotide sequences are useful  
 CC for drug screening effective in the treatment of symptomatic or  
 CC phenotypic manifestations of perturbing the normal function of NHP in  
 CC the body, and nucleotide constructs encoding NHP products are useful to  
 CC genetically engineer host cells to express NHP products in vivo. These  
 CC genetically engineered cells function as bioreactors in the body  
 CC delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion  
 CC protein to the body. Nucleotide construct encoding NHP products are  
 CC also useful in gene therapy for modulating NHP expression and to  
 CC produce genetically engineered host cells to express NHP products in  
 CC vivo. NHP nucleotide sequences may also be used as part of ribozyme  
 CC and/or triple helix sequences that are useful for NHP gene regulation.  
 CC The NHP polypeptides are useful for generating antibodies, as  
 CC reagents in diagnostic assays, for identifying other cellular gene  
 CC products related to NHP and as reagents in assays for screening for  
 CC compounds that are useful in the treatment of mental, biological or  
 CC medical disorders and diseases.

XX Sequence 6030 BP: 1786 A; 1190 C; 1345 G; 1706 T; 3 other:

Query Match 100.0%; Score 6028.8; DB 24; Length 6030;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 6030; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 ATGAGCAACAGTGTCTTACACAGGAGCTGACAGCTTCACTTCCACACAGAA 60  
 Db 1 ATGAGCAACAGTGTCTTACACAGGAGCTGACAGCTTCACTTCCACACAGAA 60  
 XX 61 TCTCTTGGGCTATTTGAAAGAGCATTGCAAGAAAGCAAGATCCCAACAGAC 120  
 Db 61 TCTCTTGGGCTATTTGAAAGAGCATTGCAAGAAAGCAAGATCCCAACAGAC 120  
 XX 121 AAAAAAGATACGACGAAATATGCCCCAAGCAATATGACTTGGAGAGTGAAGAAC 180  
 Db 121 AAAAAAGATACGACGAAATATGCCCCAAGCAATATGACTTGGAGAGTGAAGAAC 180  
 XX 121 AAAAAAGATACGACGAAATATGCCCCAAGCAATATGACTTGGAGAGTGAAGAAC 180  
 Db 121 AAAAAAGATACGACGAAATATGCCCCAAGCAATATGACTTGGAGAGTGAAGAAC 180  
 XX 181 CTTCATTTATTTATGAGAGCATTTCTCCAGAGTGTGTCAGAGGCCCTGGAGGACCTG 240  
 Db 181 CTTCATTTATTTATGAGAGCATTTCTCCAGAGTGTGTCAGAGGCCCTGGAGGACCTG 240  
 XX 241 GACCCCTACTATATCAATAAGAAACTTTATATGATATGAAATGAAGAGGACCTTTC 300  
 Db 241 GACCCCTACTATATCAATAAGAAACTTTATATGATATGAAATGAAGAGGACCTTTC 300  
 XX 301 CGGTTAGTGCACCTTGGCCCTGTACATTTTAACCTCCCTCAATCTCTTGAAGAAATA 360  
 Db 301 CGGTTAGTGCACCTTGGCCCTGTACATTTTAACCTCCCTCAATCTCTTGAAGAAATA 360  
 XX 361 GCTATTTAGATTTTGGTACATTTATTCAGATGCTATTTATGTCACCTATTTTGACA 420  
 Db 361 GCTATTTAGATTTTGGTACATTTATTCAGATGCTATTTATGTCACCTATTTTGACA 420

XX 421 AACTGTGTTTATGACAAATAGATACCTCCCTGATTTGACAAAGATATGATATACCC 480  
 Db 421 AACTGTGTTTATGACAAATAGATACCTCCCTGATTTGACAAAGATATGATATACCC 480  
 XX 481 TTCCAGAGAAATATATCTTTTGAATCACTTATTAATAATATGCAAGGGATCTGTTTA 540  
 Db 481 TTCCAGAGAAATATATCTTTTGAATCACTTATTAATAATATGCAAGGGATCTGTTTA 540  
 XX 541 GAAGATTTTCTTTTCTCCGAGATCCATGAGAACCTGCGATTTCACTGCTATTAATTT 600  
 Db 541 GAAGATTTTCTTTTCTCCGAGATCCATGAGAACCTGCGATTTCACTGCTATTAATTT 600  
 XX 601 GCGTACGTCACAGAGTTTGGACCTGGCAATCTCCGCAATGAGAACCTTACAGATT 660  
 Db 601 GCGTACGTCACAGAGTTTGGACCTGGCAATCTCCGCAATGAGAACCTTACAGATT 660  
 XX 661 CTCCGAGCATTTGAAGAGATTTCACTATTCAGAGCTGAAACCATTTGGAGGACCTG 720  
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 XX 721 ATCCAGCTGTGAAGAGCTCTCAGAGTATATGATCTGATCTGCTCTGACGCTA 780  
 Db 721 ATCCAGCTGTGAAGAGCTCTCAGAGTATATGATCTGATCTGCTCTGACGCTA 780  
 XX 781 TTGCTCTAATTTGGGCTGACAGCTGTTTCATGAGGCACTGAGAAATATATATCAATG 840  
 Db 781 TTGCTCTAATTTGGGCTGACAGCTGTTTCATGAGGCACTGAGAAATATATATCAATG 840  
 XX 841 CTTCACCAATCTCTCTTGGAGAAACATATATGAAAGAAATATATATATATAT 900  
 Db 841 CTTCACCAATCTCTCTTGGAGAAACATATATGAAAGAAATATATATATATAT 900  
 XX 901 AATGATACCTTTTAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAAT 960  
 Db 901 AATGATACCTTTTAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAAT 960  
 XX 961 TCAAGATATATATTTTCTGAGAGGTTTATGATGATGATGATGATGATGATGATGAT 1020  
 Db 961 TCAAGATATATATTTTCTGAGAGGTTTATGATGATGATGATGATGATGATGATGAT 1020  
 XX 1021 GATGAGGCCAATGCTCAGAGGATATATGATGATGATGATGATGATGATGATGATGAT 1080  
 Db 1021 GATGAGGCCAATGCTCAGAGGATATATGATGATGATGATGATGATGATGATGATGAT 1080  
 XX 1081 GGTACACAACTTTGATACCTCAGTGGGCTTTTGTGCTGCTGCTGCTGCTGCTGCTGCT 1140  
 Db 1081 GGTACACAACTTTGATACCTCAGTGGGCTTTTGTGCTGCTGCTGCTGCTGCTGCTGCT 1140  
 XX 1141 CAGGACTTCTGGGAAATCTTTATCACTGATATGATGATGATGATGATGATGATGATGAT 1200  
 Db 1141 CAGGACTTCTGGGAAATCTTTATCACTGATATGATGATGATGATGATGATGATGATGAT 1200  
 XX 1201 ATATTTTGTGTGTTGCTATTTCTTGGGCTCAATTTCACTTAATTAATTTGATCTGGCT 1260  
 Db 1201 ATATTTTGTGTGTTGCTATTTCTTGGGCTCAATTTCACTTAATTAATTTGATCTGGCT 1260  
 XX 1261 GTGGTGGCCATGAGCTTACAGAGAAAGAAATCAGGCACTTGAAGAAAGAAAGAAAGAA 1320  
 Db 1261 GTGGTGGCCATGAGCTTACAGAGAAAGAAATCAGGCACTTGAAGAAAGAAAGAAAGAA 1320  
 XX 1321 GAGGCCGAATTTAGCAGATGATGAAACAGCTTAAAGAGCAAGAGAGGAGCTCAGAC 1380  
 Db 1321 GAGGCCGAATTTAGCAGATGATGAAACAGCTTAAAGAGCAAGAGAGGAGCTCAGAC 1380  
 XX 1381 GAGGCAAGGCAATGCTCTCAGAGAACTTCCAGAGAGGCTCAGAGAGGAGGCTCTCA 1440  
 Db 1381 GAGGCAAGGCAATGCTCTCAGAGAACTTCCAGAGAGGCTCAGAGAGGAGGCTCTCA 1440  
 XX 1441 GACAGCTCATCTGAGAGCTTAAAGTTGATTTCAAGAGGCTTAAAGAGGCTTAAAGAGG 1500  
 Db 1441 GACAGCTCATCTGAGAGCTTAAAGTTGATTTCAAGAGGCTTAAAGAGGCTTAAAGAGG 1500  
 XX 1501 AGGAGAGAAAGAAAGAAAGAGAGAGCTGTGGGGAGAGAGAGAGAGAGAGAGAGATTC 1560

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|---|------|---|------|
| D | 1501 | AGGAAGAAAGAAAAAGAAAGACAGCTCGGTGGGGAAGAAAGATGAGATGAATTC      | 1560 |
| Q | 1561 | CAAAAATCTGAATCTGAGAGACAGCATAGAGAGAAAGTTTTGCTTCTCCATTGAAGG   | 1620 |
| D | 1561 | CAAAATCTGATCTGAGAGACAGCATAGAGAGAAAGTTTTGCTTCTCCATTGAAGG     | 1620 |
| Q | 1621 | AACCGATTGACATATGAAAAGAGGTACTCTCCCGCACCAAGCTTTGTGTAGCATCCGT  | 1680 |
| D | 1621 | AACCGATTGACATATGAAAAGAGGTACTCTCCCGCACCAAGCTTTGTGTAGCATCCGT  | 1680 |
| Q | 1681 | GGCCTCCCAATTTTCCACCAAGCGCAAAATAGCAAGCAAGCTTTGAGTTGAGAGGGA   | 1740 |
| D | 1681 | GGCCTCCCAATTTTCCACCAAGCGCAAAATAGCAAGCAAGCTTTGAGTTGAGAGGGA   | 1740 |
| Q | 1741 | GCAAAAGATGTGGGATCTGAGAACAGACTTCGAGATGATAGACACAGCACTTTGAGAT  | 1800 |
| D | 1741 | GCAAAAGATGTGGGATCTGAGAACAGACTTCGAGATGATAGACACAGCACTTTGAGAT  | 1800 |
| Q | 1801 | AACGAGAGCCGTAAAGATTCCTTGTGTGCCCGACAGACGGAGAGAGACGCAAGC      | 1860 |
| D | 1801 | AACGAGAGCCGTAAAGATTCCTTGTGTGCCCGACAGACGGAGAGAGAGCCAACAGC    | 1860 |
| Q | 1861 | AACCGAGTCTGACAGCAGTAGGTCAATCCGGATCTGTGGAGTGTTCACGSAATGGGAG  | 1920 |
| D | 1861 | AACCGAGTCTGACAGCAGTAGGTCAATCCGGATCTGTGGAGTGTTCACGSAATGGGAG  | 1920 |
| Q | 1921 | ATGCACAGCACTGTGGAATTCGCAATGGTGTTGTTCCCTGTTGGTGGACCTTCAAGTCT | 1980 |
| D | 1921 | ATGCACAGCACTGTGGAATTCGCAATGGTGTTGTTCCCTGTTGGTGGACCTTCAAGTCT | 1980 |
| Q | 1981 | ACATGCGCTGTGGACAGCTTCTGCCAGAGTGATTAATGATAGCCAGCTACTGATAC    | 2040 |
| D | 1981 | ACATGCGCTGTGGACAGCTTCTGCCAGAGTGATTAATGATAGCCAGCTACTGATAC    | 2040 |
| Q | 2041 | AATGGAACAACCACTGAAACTGAAATGAGAAAGAGGTCAAGTCTTCCAGCTTCC      | 2100 |
| D | 2041 | AATGGAACAACCACTGAAACTGAAATGAGAAAGAGGTCAAGTCTTCCAGCTTCC      | 2100 |
| Q | 2101 | ATGCACTTCTAGAAAGATTCCTTCCCAAAGCAACGACAAATGATAGCCAGCACTTCTA  | 2160 |
| D | 2101 | ATGCACTTCTAGAAAGATTCCTTCCCAAAGCAACGACAAATGATAGCCAGCACTTCTA  | 2160 |
| Q | 2161 | ACAAATACAGTAGAAGAACTTGAAGATCCAGGACAGAAATGCCACCTGTGTGTAA     | 2220 |
| D | 2161 | ACAAATACAGTAGAAGAACTTGAAGATCCAGGACAGAAATGCCACCTGTGTGTAA     | 2220 |
| Q | 2221 | TTTTTCCAAACATATCTTAATCTGGGACGTCTCCATATTTGTTAAAGTGAACATGTT   | 2280 |
| D | 2221 | TTTTTCCAAACATATCTTAATCTGGGACGTCTCCATATTTGTTAAAGTGAACATGTT   | 2280 |
| Q | 2281 | GTCACACCGTGTGATGAGGACCACTTGTGTGACCTGCCATCACATCTGATATGTCTTA  | 2340 |
| D | 2281 | GTCACACCGTGTGATGAGGACCACTTGTGTGACCTGCCATCACATCTGATATGTCTTA  | 2340 |
| Q | 2341 | AATACTTTTTCATGGCATGAGGACACTATCCATGACGAGCCATTTCAATATGTGCTT   | 2400 |
| D | 2341 | AATACTTTTTCATGGCATGAGGACACTATCCATGACGAGCCATTTCAATATGTGCTT   | 2400 |
| Q | 2401 | ACATAGAGAAACTGTGTTTCACTGCGGATCTTACACGAGAAATGTTCTCAAAATATTT  | 2460 |
| D | 2401 | ACATAGAGAAACTGTGTTTCACTGCGGATCTTACACGAGAAATGTTCTCAAAATATTT  | 2460 |
| Q | 2461 | GCCATGATCCTTACATTTATTTTCCAAAGAGCGTGSAAATATCTTACAGCGTTTATGTG | 2520 |
| D | 2461 | GCCATGATCCTTACATTTATTTTCCAAAGAGCGTGSAAATATCTTACAGCGTTTATGTG | 2520 |
| Q | 2521 | ACGCTTACCGTGTAGAACTTGACCTGGCAATGTGGAAGATTATCTGTCTCCGTCA     | 2580 |
| D | 2521 | ACGCTTACCGTGTAGAACTTGACCTGGCAATGTGGAAGATTATCTGTCTCCGTCA     | 2580 |
| Q | 2581 | TTTGATTTGCTGGAGTTTCAAGTTGGCAAAATCTTGGCCAAAGTTAAATATGCTAATA  | 2640 |
| D | 2581 | TTTGATTTGCTGGAGTTTCAAGTTGGCAAAATCTTGGCCAAAGTTAAATATGCTAATA  | 2640 |

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|----|------|---|------|
| Db | 2581 | TTTGATTCGCGGAGAGTTTCAAGTTGGCAAAATCTTGGCCAAAGTTAAATTCGTATA     | 2641 |
| OY | 2641 | AAGATCATCGGCAATTCCTGGGGGGCTCTGGAAATTTAAACCTGCTTGGCCATCATC     | 2700 |
| Db | 2641 | AAGATCATCGGCAATTCCTGGGGGGCTCTGGAAATTTAAACCTGCTTGGCCATCATC     | 2700 |
| OY | 2701 | GCTCTCAATTTTGGCCGGTGGGCGGATGCGAGCTCTTGGTAAAGTACAAAGATTGTGTC   | 2760 |
| Db | 2701 | GCTCTCAATTTTGGCCGGTGGGCGGATGCGAGCTCTTGGTAAAGTACAAAGATTGTGTC   | 2760 |
| OY | 2761 | TGCAGAATCGGCAGTGAATTTCAACTCCACAGCTGGCAATGAAGACTCTTCCACACC     | 2820 |
| Db | 2761 | TGCAGAATCGGCAGTGAATTTCAACTCCACAGCTGGCAATGAAGACTCTTCCACACC     | 2820 |
| OY | 2821 | TTCTCGATTGGTTCGCGGCTGTGTGGGAGTGATAGAGACCATTGGGAGCTGTATG       | 2880 |
| Db | 2821 | TTCTCGATTGGTTCGCGGCTGTGTGGGAGTGATAGAGACCATTGGGAGCTGTATG       | 2880 |
| OY | 2881 | GAGTTGCTGTGTCAAGCATGTGCTTACTGTCTCATGATGTGTATGGTATTGGAAC       | 2940 |
| Db | 2881 | GAGTTGCTGTGTCAAGCATGTGCTTACTGTCTCATGATGTGTATGGTATTGGAAC       | 2940 |
| OY | 2941 | CTAGGTCGCGGATCTCTTTCGGGCTTGGGCTTMTAGCTCATTTAGTGGACAAACCTT     | 3000 |
| Db | 2941 | CTAGGTCGCGGATCTCTTTCGGGCTTGGGCTTMTAGCTCATTTAGTGGACAAACCTT     | 3000 |
| OY | 3001 | GCAGCCACTGATGATGATTAATGAATTAATCTCAAAATGCTGTGGATAGATGCAC       | 3060 |
| Db | 3001 | GCAGCCACTGATGATGATTAATGAATTAATCTCAAAATGCTGTGGATAGATGCAC       | 3060 |
| OY | 3061 | AAAGAGTAGCTTATGTGAAAGAAAAATATGAAATTTATCAACAGTCTTCATTAGG       | 3120 |
| Db | 3061 | AAAGAGTAGCTTATGTGAAAGAAAAATATGAAATTTATCAACAGTCTTCATTAGG       | 3120 |
| OY | 3121 | AAACAAAAGATTTTATGATGAAATTAACACACTGATGATCTTAACAACAAGAAAGACGT   | 3180 |
| Db | 3121 | AAACAAAAGATTTTATGATGAAATTAACACACTGATGATCTTAACAACAAGAAAGACGT   | 3180 |
| OY | 3181 | TGTATGTCCATCATATACARCAAGAAATTTGGGAAGATCTTGAATCTTAAAGATGTAAAT  | 3240 |
| Db | 3181 | TGTATGTCCATCATATACARCAAGAAATTTGGGAAGATCTTGAATCTTAAAGATGTAAAT  | 3240 |
| OY | 3241 | GGAACCTCAAGTGGTATAGGAAGCTGGCAGACAGTGTGAAAAATACATTATTGATGAAAGT | 3300 |
| Db | 3241 | GGAACCTCAAGTGGTATAGGAAGCTGGCAGACAGTGTGAAAAATACATTATTGATGAAAGT | 3300 |
| OY | 3301 | GATTACATGTCAATTCATTAACAACCCCACTTACTGTGACGTACACAAATGTCTGTAGGA  | 3360 |
| Db | 3301 | GATTACATGTCAATTCATTAACAACCCCACTTACTGTGACGTACACAAATGTCTGTAGGA  | 3360 |
| OY | 3361 | GAATCTACTTTGAATAATTTAAACACAGGAAGCTTATGATGAAATCGGATCTGGAAGAA   | 3420 |
| Db | 3361 | GAATCTACTTTGAATAATTTAAACACAGGAAGCTTATGATGAAATCGGATCTGGAAGAA   | 3420 |
| OY | 3421 | AGCAAAAGAACTGATTAAGAAAGCAGTACCTCATCAGAAAGTAGACACTGTGGACATCGGC | 3480 |
| Db | 3421 | AGCAAAAGAACTGATTAAGAAAGCAGTACCTCATCAGAAAGTAGACACTGTGGACATCGGC | 3480 |
| OY | 3481 | GCACCTGTAAAGAACAGCCCTAGTGGAACTGGAAGAACTCTTGAACCAGAAAGCTTGT    | 3540 |
| Db | 3481 | GCACCTGTAAAGAACAGCCCTAGTGGAACTGGAAGAACTCTTGAACCAGAAAGCTTGT    | 3540 |
| OY | 3541 | TTTCACTGAAGGCTGTGTACAAAGATTTCAAGTTTGTCAAAATCAATGGGAAGAGGAGA   | 3600 |
| Db | 3541 | TTTCACTGAAGGCTGTGTACAAAGATTTCAAGTTTGTCAAAATCAATGGGAAGAGGAGA   | 3600 |
| OY | 3601 | GGAAAACAATGTGTGAACCTGAGAAAGAGCTGTTCGAAATAGTTGAACATTAAGCTTTT   | 3660 |
| Db | 3601 | GGAAAACAATGTGTGTGAACCTGAGAAAGAGCTGTTCGAAATAGTTGAACATTAAGCTTTT | 3660 |
| OY | 3661 | GAGACCTCAATGTTTATTAATGATTTCTCTTATGATGTGTCTGCGCATTTGGAAGATATA  | 3720 |
| Db | 3661 | GAGACCTCAATGTTTATTAATGATTTCTCTTATGATGTGTCTGCGCATTTGGAAGATATA  | 3720 |

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|----|------|---|------|
| OY | 3721 | TATATTGATGACGAAAGACGATTAGACAGATGTTGGAAATATGCTGCAGAAAGTTTCACT  | 3780 |
| Db | 3721 | TATATTGATGACGAAAGACGATTAGACAGATGTTGGAAATATGCTGCAGAAAGTTTCACT  | 3780 |
| OY | 3781 | TATATTTCATTTCTGGAAATGCTCTTAAATNAGGTGGCAATGSGCTATCAAACTATTTC   | 3840 |
| Db | 3781 | TATATTTCATTTCTGGAAATGCTCTTAAATNAGGTGGCAATGSGCTATCAAACTATTTC   | 3840 |
| OY | 3841 | ACCAATGCCCTGATGTTGGCTGGACCTCTTAATTTGGATGTTTCATTTGCTGAGTTTACA  | 3900 |
| Db | 3841 | ACCAATGCCCTGATGTTGGCTGGACCTCTTAATTTGGATGTTTCATTTGCTGAGTTTACA  | 3900 |
| OY | 3901 | GCAAAATGCCCTGGGTTACACAGAACTGGAGCCATCAAACTCTCAGAGACACTAAGAGCT  | 3960 |
| Db | 3901 | GCAAAATGCCCTGGGTTACACAGAACTGGAGCCATCAAACTCTCAGAGACACTAAGAGCT  | 3960 |
| OY | 3961 | CTGAGACCTCTAAGACCCCTATCTCGATTTGAAGGGATGAGGGTGTTGTAATGGCCCT    | 4020 |
| Db | 3961 | CTGAGACCTCTAAGACCCCTATCTCGATTTGAAGGGATGAGGGTGTTGTAATGGCCCT    | 4020 |
| OY | 4021 | TTTGGAGCAATTTCATCCATCATGAAATGTCCTTGCTTGTATTAATTCGGCTAAT       | 4080 |
| Db | 4021 | TTTGGAGCAATTTCATCCATCATGAAATGTCCTTGCTTGTATTAATTCGGCTAAT       | 4080 |
| OY | 4081 | TTTCAGATCATGGGCGTAAATTTGTTTGGCGGAATTTACACAGTGTATTAACACCACA    | 4140 |
| Db | 4081 | TTTCAGATCATGGGCGTAAATTTGTTTGGCGGAATTTACACAGTGTATTAACACCACA    | 4140 |
| OY | 4141 | ACTGCTGACAGGTTTGACATCGAAGACGTGAATTAATCACTAGTTGCCCTAAACTAATA   | 4200 |
| Db | 4141 | ACTGCTGACAGGTTTGACATCGAAGACGTGAATTAATCACTAGTTGCCCTAAACTAATA   | 4200 |
| OY | 4201 | GAAAGAAATGAGACCTCGATGAGGAAAAATGTAAGTAACCTTGATTAATGTAGAGTTT    | 4260 |
| Db | 4201 | GAAAGAAATGAGACCTCGATGAGGAAAAATGTAAGTAACCTTGATTAATGTAGAGTTT    | 4260 |
| OY | 4261 | GGGTATCTCTCTTGGCTTCAGAGTTGGCACATTTAAAGATGAGTGAATTAATGATGCA    | 4320 |
| Db | 4261 | GGGTATCTCTCTTGGCTTCAGAGTTGGCACATTTAAAGATGAGTGAATTAATGATGCA    | 4320 |
| OY | 4321 | GCAGTGGATTCCAGAAATGTGGAACTCCAGCCCTAATATGAGAAAGTCTGTACATGAT    | 4380 |
| Db | 4321 | GCAGTGGATTCCAGAAATGTGGAACTCCAGCCCTAATATGAGAAAGTCTGTACATGAT    | 4380 |
| OY | 4381 | CTTTACTTGGTATTTTCAATCACTTTGGGCTCTTCACTGTAACCGTTTATTTGGT       | 4440 |
| Db | 4381 | CTTTACTTGGTATTTTCAATCACTTTGGGCTCTTCACTGTAACCGTTTATTTGGT       | 4440 |
| OY | 4441 | GTTCATCATGATTAATTTCAACGACGAGAAAAGAGGTTTGGAGCTCAAGCATCTTTATG   | 4500 |
| Db | 4441 | GTTCATCATGATTAATTTCAACGACGAGAAAAGAGGTTTGGAGCTCAAGCATCTTTATG   | 4500 |
| OY | 4501 | ACAGAAAGACAGAAAGAAATCTATATGCAATGAAAAATTTNAGATCGAAAAAACCAGCA   | 4560 |
| Db | 4501 | ACAGAAAGACAGAAAGAAATCTATATGCAATGAAAAATTTNAGATCGAAAAAACCAGCA   | 4560 |
| OY | 4561 | AAGCCTATACCTCGACCAGAAAACAAATTTCAAGGAATGGCTTTTACTTCGTAAACGAGA  | 4620 |
| Db | 4561 | AAGCCTATACCTCGACCAGAAAACAAATTTCAAGGAATGGCTTTTACTTCGTAAACGAGA  | 4620 |
| OY | 4621 | CAGGTTTTTGACATAAGCAATCATGATTTCTCATCTGCTTAACATGGTCAACATGATGATG | 4680 |
| Db | 4621 | CAGGTTTTTGACATAAGCAATCATGATTTCTCATCTGCTTAACATGATGATGATG       | 4680 |
| OY | 4681 | GAAACAGATGACAGAGTAAATGTGATACATTTTTCACAGCATCATCTGGGTGTC        | 4740 |
| Db | 4681 | GAAACAGATGACAGAGTAAATGTGATACATTTTTCACAGCATCATCTGGGTGTC        | 4740 |
| OY | 4741 | ATTGTGCTATTTTACTGAGAGTGTGTACTGAACCTCATCTCTACGCCATTAATATTTT    | 4800 |
| Db | 4741 | ATTGTGCTATTTTACTGAGAGTGTGTACTGAACCTCATCTCTACGCCATTAATATTTT    | 4800 |

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| QY | 4801 | ACCAATGATGAAATATTTTGAATTTTGCGTGTCAATTCCTCCAAATGATAGATGTTT     | 4860 |
| Db | 4801 | ACCAATGATGAAATATTTTGAATTTTGCGTGTCAATTCCTCCAAATGATAGATGTTT     | 4860 |
| QY | 4861 | CTTGCCGAGCGATATGAAAGATATTTGCTGCCCAACCTGTGCGAGTGATGCCGTTT      | 4920 |
| Db | 4861 | CTTGCCGAGCGATATGAAAGATATTTGCTGTCCCTTAACCTGTGCGAGTGATGCCGTTT   | 4920 |
| QY | 4921 | GCTAGGATTTGGCCGAATCCTACGCTCATCAAGAGACAAAGGGAGATGCCAGCGCTGC    | 4980 |
| Db | 4921 | GCTAGGATTTGGCCGAATCCTACGCTCATCAAGAGAGCAAAAGGGATTCGGACGCTGC    | 4980 |
| QY | 4981 | TTTTGCTTTGATGATGTCCTCTCTCGGTGTTTAAACATGCGCCTCCTACTCTTCTAGTC   | 5040 |
| Db | 4981 | TTTTGCTTTGATGATGTCCTCTCTCGGTGTTTAAACATGCGCCTCCTACTCTTCTAGTC   | 5040 |
| QY | 5041 | ATGTCATCTACGCAATCTTTGGGATGTCACATTTTGCTATGTTAAAGGGAATGTGGG     | 5100 |
| Db | 5041 | ATGTCATCTACGCAATCTTTGGGATGTCACATTTTGCTATGTTAAAGGGAATGTGGG     | 5100 |
| QY | 5101 | ATCGATGACATGTTCAACTTTTGAGACCTTTGGCAACAGATGATGTCGCTATTTCCAAAT  | 5160 |
| Db | 5101 | ATCGATGACATGTTCAACTTTTGAGACCTTTGGCAACAGATGATGTCGCTATTTCCAAAT  | 5160 |
| QY | 5161 | ACAACCTCTGCTGCGTGGATGATGATGCTAAGACCAATCTCTCAACAGTAAGCCACCGAC  | 5220 |
| Db | 5161 | ACAACCTCTGCTGCGTGGATGATGATGCTAAGACCAATCTCTCAACAGTAAGCCACCGAC  | 5220 |
| QY | 5221 | TGTGACCTATATAAGTTAAACCTCTGGAAAGCTCAAGTTAAAGGAGATGTGGAAACCATCT | 5280 |
| Db | 5221 | TGTGACCTATATAAGTTAAACCTCTGGAAAGCTCAAGTTAAAGGAGATGTGGAAACCATCT | 5280 |
| QY | 5281 | GTGGAATTTTCTTTTGTGACATGATCATATATCTCTCGTGGTGTGGTGAACATG        | 5340 |
| Db | 5281 | GTGGAATTTTCTTTTGTGACATGATCATATATCTCTCGTGGTGTGGTGAACATG        | 5340 |
| QY | 5341 | TACATCGCGGTCAATCTGGAGAACTTCAAGTGTCTACTGAAGAAAATGACAGGCTCTG    | 5400 |
| Db | 5341 | TACATCGCGGTCAATCTGGAGAACTTCAAGTGTCTACTGAAGAAAATGACAGGCTCTG    | 5400 |
| QY | 5401 | AGTGAAGATGACTTTGAGATGTTCTTANAGAGCTTTGGGAAATGTTGATCCGATGCAACT  | 5460 |
| Db | 5401 | AGTGAAGATGACTTTGAGATGTTCTTANAGAGCTTTGGGAAATGTTGATCCGATGCAACT  | 5460 |
| QY | 5461 | CAGTTCATGGAATTTGAAAAATATATGCAATTTGCGAGCTGCCCTTGAACCGCCTGCAT   | 5520 |
| Db | 5461 | CAGTTCATGGAATTTGAAAAATATATGCAATTTGCGAGCTGCCCTTGAACCGCCTGCAT   | 5520 |
| QY | 5521 | CTGCGACAACCAACAACTCAGCTCATTTGCCATGATTTGCCATGGTGGATGAGTGATC    | 5580 |
| Db | 5521 | CTGCGACAACCAACAACTCAGCTCATTTGCCATGATTTGCCATGGTGGATGAGTGATC    | 5580 |
| QY | 5581 | CGGATTCACCTCTGATATCTTATTTGCTTTTACAAAGCGGGTCTTAGAGAGAGTGGG     | 5640 |
| Db | 5581 | CGGATTCACCTCTGATATCTTATTTGCTTTTACAAAGCGGGTCTTAGAGAGAGTGGG     | 5640 |
| QY | 5641 | GAGATGATGCTCTACCAATACAGATGGAAGCGCTCATGGCTTCCAAATCCTTCCAG      | 5700 |
| Db | 5641 | GAGATGATGCTCTACCAATACAGATGGAAGCGCTCATGGCTTCCAAATCCTTCCAG      | 5700 |
| QY | 5701 | GTCTCTATACGCCAATCACTACTTATAACGAAAAACAAGAGAGTATCTGCTGC         | 5760 |
| Db | 5701 | GTCTCTATACGCCAATCACTACTTATAACGAAAAACAAGAGAGTATCTGCTGC         | 5760 |
| QY | 5761 | ATTATTCAGCGTGTCTACAGACCCCACTTTTAAAGCGAAGCTGTAACAAGCTTCTCTT    | 5820 |
| Db | 5761 | ATTATTCAGCGTGTCTACAGACCCCACTTTTAAAGCGAAGCTGTAACAAGCTTCTCTT    | 5820 |
| QY | 5821 | ACGTACATATAAACAACAAATCAAGGTGGGGCTATCTCTTATATAAGAGACATATATA    | 5880 |
| Db | 5821 | ACGTACATATAAACAACAAATCAAGGTGGGGCTATCTCTTATATAAGAGACATATATA    | 5880 |
| QY | 5881 | ATTACAGAAATTAATGAAACTCTATTAACAGAAAAACTGATGTGACATGTCCACTGCA    | 5940 |



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Db 5881 AATGACAAATTAATGAAACCTTATACAGAAAAACGATCTGACCATGTCCACTGCA 5940  
Oy 5941 GCTTGTCCACCTTCTATGACCGGCTGACAAAGCCATTGTGGAAAAACATGACGAA 6000  
Db 5941 GCTTGTCCACCTTCTATGACCGGCTGACAAAGCCATTGTGGAAAAACATGACGAA 6000  
Oy 6001 GGCAGATGAAAAAGCCAAAGGGAATTA 6030  
Db 6001 GGCAGATGAAAAAGCCAAAGGGAATTA 6030  
RESULT 2  
ID AAH55763 standard; cDNA: 8378 BP.  
XX AAH55763;  
AC AAH55763;  
XX  
DT 04-SEP-2001 (first entry)  
XX  
DE Human adult form of SCN1A nucleotide sequence SEQ ID NO:1.  
XX  
KW Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;  
KW diagnosis; mutation; chromosome 2q23-q31; neurological disorder;  
KW anticonvulsant; neuroprotective; ss.  
XX  
OS Homo sapiens.  
XX  
PN WC200138564-A2.  
XX  
PD 31-MAY-2001.  
XX  
PF 24-NOV-2000; 2000WO-CA014404.  
XX  
PR 26-NOV-1999; 99US-0167623.  
XX  
PA (UYMC-) UNIV MCGILL.  
XX  
PI Rouleau GA, LaFreniere RG, Rochefort D, Cossette P, Ragsdale D;  
DR WPI; 2001-355945/37.  
DR P-PSDB; AAB99674.  
XX  
PT Determining a predisposition to epilepsy and/or development of epilepsy  
PT comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a  
PT DNA variant, equivalent, or mutation which shows a linkage  
PT disequilibrium.  
XX  
PS Disclosure; Page 90-93; 268pp; English.  
XX  
CC The present invention describes a method (M1) of determining an  
CC individual's predisposition to epilepsy and/or development of epilepsy,  
CC as well as predicting the individual's response to medication. The  
CC method comprises determining the genotype of at least one gene selected  
CC from SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation  
CC which shows a linkage disequilibrium. SCN1A, SCN2A and SCN3A are all  
CC sodium channel genes located on chromosome 2. The idiopathic generalised  
CC epilepsy (IGE) gene is more specifically localised on chromosome  
CC 2q23-q31. Compounds identified as modulators of the biological activity  
CC of SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating  
CC epilepsy or other neurological disorders. They have anticonvulsant and  
CC neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to  
CC AAB99679 represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR  
CC primers, oligonucleotides and proteins given in the exemplification of  
CC the present invention.  
XX  
XX  
SO Sequence 8378 BP; 2496 A; 1575 C; 1782 G; 2525 T; 0 other;  
Query Match 99.88; Score 6015.2; DB 22; Length 8378;  
Best Local Similarity 99.98; Pred. No. 0;  
Matches 6023; Conservative 3; Mismatches 1; Indels 1; Gaps 1;  
Oy 1 AATGACAAATGATGCTTGTACACACGACCTGACAGCTTCACTTCTTCACGAGAA 60

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Db 266 AATGACAAATGATGCTTGTACACACGACCTGACAGCTTCACTTCTTCACGAGAA 325  
Oy 61 TCTCTGCGGCTATTGAAAGAGCATTTGCAAGAAAGGCAAAAGATCCCAACCGAC 120  
Db 326 TCTCTGCGGCTATTGAAAGAGCATTTGCAAGAAAGGCAAAAGATCCCAACCGAC 385  
Oy 121 AAAAAAGATGACGAGAAAAATGGCCCAAGCCAAATAGTACTTGGAACTGGAAAGAAC 180  
Db 386 AAAAAAGATGACGAGAAAAATGGCCCAAGCCAAATAGTACTTGGAACTGGAAAGAAC 445  
Oy 181 CTTCATTTATTTATGAGACATTCCTCCAGAGATGGTGTGACAGGCCCTGGAGAGCTG 240  
Db 446 CTTCATTTATTTATGAGACATTCCTCCAGAGATGGTGTGACAGGCCCTGGAGAGCTG 505  
Oy 241 GACCCCTACTATATCATATGAAAACTTTATATGATTAATGAAATGAGGAGGCATCTTC 300  
Db 506 GACCCCTACTATATCATATGAAAACTTTATATGATTAATGAAATGAGGAGGCATCTTC 565  
Oy 301 CGGTTCAGTCCACCTCTGCTGTCATTTTAACTCCCTCAATCTCTTAGGAAAAAT 360  
Db 566 CGGTTCAGTCCACCTCTGCTGTCATTTTAACTCCCTCAATCTCTTAGGAAAAAT 625  
Oy 361 GCTATTAAATTTGGTACATTCATTTATGAGATGCTATTTATGTCATTTTGGACA 420  
Db 626 GCTATTAAATTTGGTACATTCATTTATGAGATGCTATTTATGTCATTTTGGACA 685  
Oy 421 AACTGTGTGTTATGACAAATGAGTAACCTCCTGATTTGACAAAGATAGATACACC 480  
Db 686 AACTGTGTGTTATGACAAATGAGTAACCTCCTGATTTGACAAAGATAGATACACC 745  
Oy 481 TTCACAGGAATATATCTTTTGAATCATCTTATTAATTAATTTGCAAGGGGATCTGTTA 540  
Db 746 TTCACAGGAATATATCTTTTGAATCATCTTATTAATTAATTTGCAAGGGGATCTGTTA 805  
Oy 541 GAAGATTTTACTTTCCTCGGATCCAGATGGAATGCTGCTGATTCACCTGATTCATTT 600  
Db 806 GAAGATTTTACTTTCCTCGGATCCAGATGGAATGCTGCTGATTCACCTGATTCATTT 865  
Oy 601 GCGTACGTACAGAGTTGTGAGACCTGGGCAATGTCGCGCATTTGAAACATTCAGAGTT 660  
Db 866 GCGTACGTACAGAGTTGTGAGACCTGGGCAATGTCGCGCATTTGAAACATTCAGAGTT 925  
Oy 661 CTCGAGCATTTGAACAGATTTTCAGTATTCAGAGCTGTAACCATTTGGAGCCCTG 720  
Db 926 CTCGAGCATTTGAACAGATTTTCAGTATTCAGAGCTGTAACCATTTGGAGCCCTG 985  
Oy 721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGCTGTCTGAGACCTA 780  
Db 986 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGCTGTCTGAGACCTA 1045  
Oy 781 TTGCTCTAATTTGGCTGACGCTGTTCATGAGCAACCTGAGAAATATATATACAAATG 840  
Db 1046 TTGCTCTAATTTGGCTGACGCTGTTCATGAGCAACCTGAGAAATATATATACAAATG 1105  
Oy 841 CTTCCACCAAGCTCTCTGAGAGAACATATATATATATATATATATATATATATAT 900  
Db 1106 CTTCCACCAAGCTCTCTGAGAGAACATATATATATATATATATATATATATATAT 1165  
Oy 901 AATGTACACTATTAATGAAGAACTGCTTTGATTTGATGAGAGCATATATATATAT 960  
Db 1166 AATGTACACTATTAATGAAGAACTGCTTTGATTTGATGAGAGCATATATATATAT 1225  
Oy 961 TCAGATATCATTAATTTCTGAGAGGTTTTTATGATGCACTATATGAGAAATAGCTCT 1020  
Db 1226 TCAGATATCATTAATTTCTGAGAGGTTTTTATGATGCACTATATGAGAAATAGCTCT 1285  
Oy 1021 GATGAGGCAATGTCAGAGAGGATATATGTTGTAAGTGTGTAAGTATCCCAATAT 1080  
Db 1286 GATGAGGCAATGTCAGAGAGGATATATGTTGTAAGTGTGTAAGTATCCCAATAT 1345  
Oy 1081 GGTTCACAGAGTTGATACCTTCAGTGGGGTTTTTTTGTCTTTCGATTAATGACT 1140

Db 1346 GGCATACACAGCTTGTATACCTTCAGTTGGGCTTTTTCCTGTTGATGACTAATGACT 1405  
QY 1141 CAGAGCTTCTGGGAAAACTTTATCACTGACATTAAGTCTGCTGGGAAAAAGTACATG 1200  
Db 1406 CAGAGCTTCTGGGAAAACTTTATCACTGACATTAAGTCTGCTGGGAAAAAGTACATG 1465  
QY 1201 AATATTTTGTGTTGATGATTTTCTGGGCTTATCTACCTAATTAATTTGATCTGCTG 1260  
Db 1466 AATATTTTGTGTTGATGATTTTCTGGGCTTATCTACCTAATTAATTTGATCTGCTG 1525  
QY 1261 GTGTGGCCATGGCTTACAGAGAACAGATCAGGCCACTTGGAGAGAACAGAGAAA 1320  
Db 1526 GTGTGGCCATGGCTTACAGAGAACAGATCAGGCCACTTGGAGAGAACAGAGAAA 1585  
QY 1321 GAGGCCGAATTTACAGAGATGATGAAGCTTTAAAAAGCAACAGAGAGAGCTACAGAG 1380  
Db 1586 GAGGCCGAATTTACAGAGATGATGAAGCTTTAAAAAGCAACAGAGAGAGCTACAGAG 1645  
QY 1381 GCAGCAAGGAGAGCTGCTGAGAACATTCAGAGAGCCAGCTGAGAGAGAGCTCTCA 1440  
Db 1646 GCAGCAAGGAGAGCTGCTGAGAACATTCAGAGAGCCAGCTGAGAGAGAGCTCTCA 1705  
QY 1441 GACAGCTCATGTAAGCTCTAAGTTGAGTTCCAGAGTGTCTAAGAGAGAGAAATGCG 1500  
Db 1706 GACAGCTCATGTAAGCTCTAAGTTGAGTTCCAGAGTGTCTAAGAGAGAGAAATGCG 1765  
QY 1501 AGAGAGAAAAAGAAACAG 1560  
Db 1766 AGAGAGAAAAAGAAACAG 1825  
QY 1561 CAAAAATCTGAATCTGAG 1620  
Db 1826 CAAAAATCTGAATCTGAG 1885  
QY 1621 AACCAGTTGACATATGAAAAAGAGTACTCTCCACACAGAGCTTTGTTGAGACATCCG 1680  
Db 1886 AACCAGTTGACATATGAAAAAGAGTACTCTCCACACAGAGCTTTGTTGAGACATCCG 1945  
QY 1881 GGGTCCCATTTTTCACCAAGGCGAAATAGCAGAACAGCCCTTTTCAAGTTTAAAGGGGA 1740  
Db 1946 GGGTCCCATTTTTCACCAAGGCGAAATAGCAGAACAGCCCTTTTCAAGTTTAAAGGGGA 2005  
QY 1741 GCAAGAGATGAGAGATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800  
Db 2006 GCAAGAGATGAGAGATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2065  
QY 1801 AAGCAGAGCCGTAGAGATCTCTGTTGTGCTCCGAGAGACAGAGAGAGAGAGAGAG 1860  
Db 2066 AAGCAGAGCCGTAGAGATCTCTGTTGTGCTCCGAGAGACAGAGAGAGAGAGAGAG 2125  
QY 1861 AACCTGATGACAGCAGTATGATCCCGGATGCTGGGAGAGTTTCCAGAGCAATGGGAG 1920  
Db 2126 AACCTGATGACAGCAGTATGATCCCGGATGCTGGGAGAGTTTCCAGAGCAATGGGAG 2185  
QY 1921 ATGACAGAGACTGTGATGATGCAATGATGTTGCTTTGTTGGTGAAGCTTCACTTCT 1980  
Db 2186 ATGACAGAGACTGTGATGATGCAATGATGTTGCTTTGTTGGTGAAGCTTCACTTCT 2245  
QY 1981 ACATGCTCTGTGGAGAGCTTCTCCAGAGAGTAAATAGATTAAGCAGCTACTGATGAC 2040  
Db 2246 ACATGCTCTGTGGAGAGCTTCTCCAGAGAGTAAATAGATTAAGCAGCTACTGATGAC 2305  
QY 2041 AATGAGCAACCACTGAAACTGAATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2100  
Db 2306 AATGAGCAACCACTGAAACTGAATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2365  
QY 2101 ATGAGCACTTCTAGAGAGCTTCTCCAAAGGCAACGAGCAATGAGTATAGCCAGCATCTA 2160  
Db 2366 ATGAGCACTTCTAGAGAGCTTCTCCAAAGGCAACGAGCAATGAGTATAGCCAGCATCTA 2425  
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Db 2426 ACAAAATCAGTAGAGAGAACTTGAAGATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2485  
QY 2221 TTTTCCAAACATATTTCTTAATCTGGGAGCTGTTCTCCATATTTGGTTAAAGTAAACATGTT 2280  
Db 2486 TTTTCCAAACATATTTCTTAATCTGGGAGCTGTTCTCCATATTTGGTTAAAGTAAACATGTT 2545  
QY 2281 GTCAACCTGGTGTGATGAG 2340  
Db 2546 GTCAACCTGGTGTGATGAG 2605  
QY 2341 AATACCTTTTTCATAGGAG 2400  
Db 2606 AATACCTTTTTCATAGGAG 2665  
QY 2401 ACAGTAGAGAACTTGTTTCACTGGAGATCTTACAGAGAGAGAGAGAGAGAGAGAGAG 2460  
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QY 2461 GGCATGATCTCTTACTATATTTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2520  
Db 2726 GGCATGATCTCTTACTATATTTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2785  
QY 2521 AAGCTTACCTGTTAG 2580  
Db 2786 AAGCTTACCTGTTAG 2845  
QY 2581 TTTGATTTGCTGAG 2640  
Db 2846 TTTGATTTGCTGAG 2905  
QY 2641 AAGATCATCGGCATATTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2700  
Db 2906 AAGATCATCGGCATATTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2965  
QY 2701 GTCCTCATTTTGGCGGTGCTGGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2760  
Db 2966 GTCCTCATTTTGGCGGTGCTGGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3025  
QY 2761 TGCAAGATCGGCATATTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2820  
Db 3026 TGCAAGATCGGCATATTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3085  
QY 2821 TTTCTGATTTGTTCCGAGTCTGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2880  
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QY 2881 GAGGTGCTGTCAAGCAGATGAGTCTTACTGTTCTTCAATGATGATGATGATGATGATG 2940  
Db 3146 GAGGTGCTGTCAAGCAGATGAGTCTTACTGTTCTTCAATGATGATGATGATGATGATG 3205  
QY 2941 CTAGTGTCTCTGAAATCTTCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3000  
Db 3206 CTAGTGTCTCTGAAATCTTCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3265  
QY 3001 GCAGCCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3060  
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QY 3061 AAAGAGTAGCTTATGTAAG 3120  
Db 3326 AAAGAGTAGCTTATGTAAG 3385  
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Db 3386 AAACAAAAGATTTAGATGAAATTAACCACTGATGATGATGATGATGATGATGATGATG 3445  
QY 3181 TGTATGTCCATATCAG 3240  
Db 3446 TGTATGTCCATATCAG 3505  
QY 3241 GGAATCTCAAGTGTATGAG 3300  
Db 3506 GGAATCTCAAGTGTATGAG 3565

3301 GATTACATGTCATTCATTAACACACCCAGTCTTACTGTAGTACCAATTCGTGTAGA 3360  
3566 GATTACATGTCATTCATTAACACACCCAGTCTTACTGTAGTACCAATTCGTGTAGA 3625  
3361 GATTCGCTTGAATTAATTAACACGAGACCTTACTGTAGTAAATTCGTGTAGA 3420  
3626 GATTCGCTTGAATTAATTAACACGAGACCTTACTGTAGTAAATTCGTGTAGA 3685  
3421 AGCAAGAGAAACGTAAGAAAGCAAGTCTGATGAGAGAGTGTAGTACGACATCCGC 3480  
3666 AGCAAGAGAAACGTAAGAAAGCAAGTCTGATGAGAGAGTGTAGTACGACATCCGC 3745  
3481 GCACCTGTAGAAGAACACCCGCTAGTGTAGTACGAGACCTTGTGAACGAGACTGT 3540  
3746 GCACCTGTAGAAGAACACCCGCTAGTGTAGTACGAGACCTTGTGAACGAGACTGT 3805  
3541 TTCCTGAGGCTGTGTACAAAGATTCAGTGTGTCAATTCATGTGGAAGAGCAGA 3600  
3806 TTCCTGAGGCTGTGTACAAAGATTCAGTGTGTCAATTCATGTGGAAGAGCAGA 3865  
3601 GGAAGAACATGCTGAGACCTGAGAGAGCTGTCCGAAATAGTTGAACATACGCTTT 3660  
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3721 TATATGATCAGCGAAGACATTAAGACATGTTGGAATATGCTGACAGGTTTCTACT 3780  
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3781 TACATTTTCATTTGTTTCATGATTCCTCTAGTGTGTGTGTGTGTGTGTGTGTGT 3840  
4045 TACATTTTCATTTGTTTCATGATTCCTCTAGTGTGTGTGTGTGTGTGTGTGTGT 4104  
3841 ACCAATGCTGT 3900  
4105 ACCAATGCTGT 4164  
3901 GCAATGCTGT 3960  
4165 GCAATGCTGT 4224  
3961 CTGAGACCTCCTAAGAGCTTATCTGATGAGAGGATGAGGAGGTTGTGAACCTT 4020  
4225 CTGAGACCTCCTAAGAGCTTATCTGATGAGAGGATGAGGAGGTTGTGAACCTT 4284  
4021 TTAGAGCAATTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 4080  
4285 TTAGAGCAATTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 4344  
4081 TTGACGATCATGGCGTAATTTGTTGCTGGCAATTTCAACACTGTATTAACACACA 4140  
4345 TTGACGATCATGGCGTAATTTGTTGCTGGCAATTTCAACACTGTATTAACACACA 4404  
4141 ACTGAGTACAGGTTGATGATGAGAGTGTGAATATCATCATCATCATCATCATCAT 4200  
4405 ACTGAGTACAGGTTGATGATGAGAGTGTGAATATCATCATCATCATCATCATCAT 4464  
4201 GAAAGAAATGAGCTGCTGATGAGAGTGTGAATATCATCATCATCATCATCATCAT 4260  
4465 GAAAGAAATGAGCTGCTGATGAGAGTGTGAATATCATCATCATCATCATCATCAT 4524  
4261 GGGATATCTCTTGTCTCAAGTTGCCAATTCAGAGAGATGATATATATATATATGA 4320  
4525 GGGATATCTCTTGTCTCAAGTTGCCAATTCAGAGAGATGATATATATATATATGA 4584  
4321 GCAGTTGATCCAGAAATGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGT 4380  
4585 GCAGTTGATCCAGAAATGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGT 4644  
4381 CTTCATCTTGTATTTATCATCATCATCATCATCATCATCATCATCATCATCATCAT 4440  
4645 CTTCATCTTGTATTTATCATCATCATCATCATCATCATCATCATCATCATCATCAT 4704  
4441 GTCATCATGATTAATTTCAACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4500  
4705 GTCATCATGATTAATTTCAACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4764  
4501 ACAG 4560  
4765 ACAG 4824  
4561 AAGCTTAACCTGAGACAG 4620  
4825 AAGCTTAACCTGAGACAG 4884  
4621 CAAGTTTGTACATTAAGATCATGATTCATCTGATTCATCATGATGATGATGATG 4680  
4885 CAAGTTTGTACATTAAGATCATGATTCATCTGATTCATCATGATGATGATGATG 4944  
4681 GAAACAGATGACAG 4740  
4945 GAAACAGATGACAG 5004  
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5005 ATTGCTATTTACTGAG 5064  
4801 ACCATGATGAG 4860  
5065 ACCATGATGAG 5124  
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5125 CTTCGCGAGCTGATGAG 5184  
4921 GCTAGAGATGAG 4980  
5185 GCTAGAGATGAG 5244  
4981 TTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5040  
5245 TTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5304  
5041 ATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5100  
5305 ATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5364  
5101 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5160  
5365 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5424  
5161 ACAACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5220  
5425 ACAACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5484  
5221 TGTGACCTTAATAAGTTAAACCTGGAAGCTCAGTTAAGGAGAGCTGTGGAAACCATCT 5280  
5485 TGTGACCTTAATAAGTTAAACCTGGAAGCTCAGTTAAGGAGAGCTGTGGAAACCATCT 5544  
5281 GTTGAATTTCTTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 5340  
5545 GTTGAATTTCTTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 5604  
5341 TACATGCGGCTGATCTGAG 5400  
5605 TACATGCGGCTGATCTGAG 5664  
5401 AGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5460  
5665 AGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5724  
5461 CAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5520

PR 26-MAY-2000; 2000US-208424P.  
PR 01-JUN-2000; 2000US-209001P.  
PR 08-JUN-2000; 2000US-210588P.  
PR 16-JUN-2000; 2000US-212335P.  
PR 22-JUN-2000; 2000US-213747P.  
PR 29-JUN-2000; 2000US-215391P.  
  
XX (INCYTE-) INCYTE GENOMICS INC.  
XX  
PI Thornton M, Wallia NK, Yue H, Nguyen DB, Lai P, Gandhi AR;  
PI Tibzonley CM, Yao MG, Ramkumar J, Au-Young J, Lu Y, Tang YT;  
PI Azimwazi Y, Bruns EM, Griffith JA, Yang J, Sanjanwalla MS;  
PI Rammann BE, Lee EA, Hatalla A, Baughn MR, Green BD, Khan FA;  
PI Kearney L, Elliot VS, Seilheimer JJ, Pollock JL, Borowsky ML;  
PI Burford N, Ding L, Lu DAM, Hillman JL;  
XX  
DR WPI: 2002-122055/16.  
DR P-P-SDB; AAEL6776.  
XX  
PT New human transporters and ion channels (TRICH) polypeptides useful for  
PT diagnosing, treating or preventing disorders associated with aberrant  
PT expression of TRICH -  
XX  
PS Claim 11: Page 196-197; 210pp; English.  
XX  
XX The invention relates to human transporters and ion channels (TRICH)  
CC polypeptides and their cDNA molecules. The nucleic acid and polypeptide  
CC sequences are useful in the diagnosis, treatment, and prevention of  
CC disorders associated with transport (akinesia, cystic fibrosis), Bell's  
CC palsy, amyotrophic lateral sclerosis(s), neurological (Alzheimer's disease,  
CC amnesia, dementia); muscle (cardiomyopathy, myocarditis, Duchenne's  
CC muscular dystrophy); immunological (AIDS, Addison's disease, allergies,  
CC asthma); cell proliferative disorders (cancers, leukaemia, psoriasis);  
CC cardiac disease (angina, hypertension, or bradyarrhythmia); and in the  
CC assessment of the effects of exogenous compounds on the expression of  
CC nucleic acid and amino acid sequences of transporters and ion channels.  
CC The polynucleotides may be used to detect and quantify gene expression

XX genomic sequence, and in drug screening. The present sequence is human TRICH-13 cDNA.

| Model    | Best Local Similarity | Pred. No. 0; | Best Local Similarity | Pred. No. 0; |         |
|----------|-----------------------|--------------|-----------------------|--------------|---------|
| Model 1  | 99.88;                | 0000.0;      | Model 2               | 99.88;       | 0000.0; |
| Model 3  | 99.88;                | 0000.0;      | Model 4               | 99.88;       | 0000.0; |
| Model 5  | 99.88;                | 0000.0;      | Model 6               | 99.88;       | 0000.0; |
| Model 7  | 99.88;                | 0000.0;      | Model 8               | 99.88;       | 0000.0; |
| Model 9  | 99.88;                | 0000.0;      | Model 10              | 99.88;       | 0000.0; |
| Model 11 | 99.88;                | 0000.0;      | Model 12              | 99.88;       | 0000.0; |
| Model 13 | 99.88;                | 0000.0;      | Model 14              | 99.88;       | 0000.0; |
| Model 15 | 99.88;                | 0000.0;      | Model 16              | 99.88;       | 0000.0; |
| Model 17 | 99.88;                | 0000.0;      | Model 18              | 99.88;       | 0000.0; |
| Model 19 | 99.88;                | 0000.0;      | Model 20              | 99.88;       | 0000.0; |
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| Model 27 | 99.88;                | 0000.0;      | Model 28              | 99.88;       | 0000.0; |
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| Model 31 | 99.88;                | 0000.0;      | Model 32              | 99.88;       | 0000.0; |
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| Model 39 | 99.88;                | 0000.0;      | Model 40              | 99.88;       | 0000.0; |
| Model 41 | 99.88;                | 0000.0;      | Model 42              | 99.88;       | 0000.0; |
| Model 43 | 99.88;                | 0000.0;      | Model 44              | 99.88;       | 0000.0; |
| Model 45 | 99.88;                | 0000.0;      | Model 46              | 99.88;       | 0000.0; |
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| Model 49 | 99.88;                | 0000.0;      | Model 50              | 99.88;       | 0000.0; |
| Model 51 | 99.88;                | 0000.0;      | Model 52              | 99.88;       | 0000.0; |
| Model 53 | 99.88;                | 0000.0;      | Model 54              | 99.88;       | 0000.0; |
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| Model 59 | 99.88;                | 0000.0;      | Model 60              | 99.88;       | 0000.0; |
| Model 61 | 99.88;                | 0000.0;      | Model 62              | 99.88;       | 0000.0; |
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| Model 83 | 99.88;                | 0000.0;      | Model 84              | 99.88;       | 0000.0; |
| Model 85 | 99.88;                | 0000.0;      | Model 86              | 99.88;       | 0000.0; |
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| Model 99 | 99.88;                | 0000.0;      | Model 100             | 99.88;       | 0000.0; |

[illegible]

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| Db | 1   | ATGAGACAAACATGCTGTGTACCCACGAGCCGAAAGTTCAACCTTCCACCCAGAA       | 60  |
| Dy | 61  | TCCTCTGGCGGCTATTGAAAGACCATTTGCGAAGAAAGAAAGCAATCCCAACCAAC      | 120 |
| Dz | 61  | TCCTCTGGCGGCTATTGAAAGACCATTTGCGAAGAAAGAAAGCAATCCCAACCAAC      | 120 |
| Dy | 121 | AAAAAAGATACACACGCAAAATGGCCCAAAAGCCAAATATGCACTTGGAAAGCTGAAGAAC | 180 |

Db 121 AAAAAGATGACGACGAATAATGGCCCAAGCCCAATAGTACTTGGAGCTGGAAGAAC 180.

QY 181 CTTCAATTTTATATGAGACATCTCCAGAGATGTTCTCAGACCCCTGGAGACTG 240

Db 181 CTTCCATTTTATATGAGACATCTCCAGAGATGTTCTCAGACCCCTGGAGACTG 240

QY 241 GACCCCTACTATATCAATTAAGAAAACCTTTTATATGTTGAATTAAGGAGGCCACTTTC 300

[illegible][illegible][illegible]

XX

Db 361 GCTATTAGATTTGGTACATTCATTATTCACAGCATGTAATATATGCACTTTTGNAA 420  
Qy 421 AACGTGTGTTATATGACAAATGATTAACCTCTGATTTGACAAAGANTGATGATACCC 480  
Db 421 AACGTGTGTTATATGACAAATGATTAACCTCTGATTTGACAAAGANTGATGATACCC 480  
Qy 481 TTCACAGAAATATATGATTTGATATCACTTATATAAATATATGCAAGGGGATTCGTTTA 540  
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Qy 541 GAAATTTTACTTCTTCCTCGGATCCATGAACTGCTGATTCGATTCAGTCTATTCATTT 600  
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Qy 601 GCGTACGTACAGAGTGTGTGAGCTGGGCAATGTCTGGCAATGATGAAATTCAGAGTT 660  
Db 601 GCGTACGTACAGAGTGTGTGAGCTGGGCAATGTCTGGCAATGATGAAATTCAGAGTT 660  
Qy 661 CTCGAGGATTTGAAGCATTTCACTGATTCAGGCTGAAACCATTTGTGGAGCCCTG 720  
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Qy 841 CCTCCACCAATGCTCTCTGAGGACATATGTAAGAAATATATATCTGTAATAT 900  
Db 841 CCTCCACCAATGCTCTCTGAGGACATATGTAAGAAATATATATCTGTAATAT 900  
Qy 901 AATGTTACACTTATTAATGAAACTGTCTTGAATTTGATGATGCAATCAATATTCAGAT 960  
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Qy 961 TCAGATATCAATTTATTTCTGAGGAGGTTTATGATGCACTATATGTAAGAAATGCTCT 1020  
Db 961 TCAGATATCAATTTATTTCTGAGGAGGTTTATGATGCACTATATGTAAGAAATGCTCT 1020  
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Db 1141 CAGCACTTCTGGGAAATCTTATATCACTGATACCTGCTGGGAAACGTAATG 1200  
Qy 1201 ATATTTTGTGTTGTCATTTCTTGGGCTCATTTCTACATTAATTAATTTGATCTGCT 1260  
Db 1201 ATATTTTGTGTTGTCATTTCTTGGGCTCATTTCTACATTAATTAATTTGATCTGCT 1260  
Qy 1261 GTGTGTCATGTCAGAGCAATGATGAGCACTGAGCACTTGAAGAGCAAGAA 1320  
Db 1261 GTGTGTCATGTCAGAGCAATGATGAGCACTGAGCACTTGAAGAGCAAGAA 1320  
Qy 1321 GAGGCGCAATTTCAAGCAATGATGAGCACTTAAAAAGCAAGAGGAGCTCAGAG 1380  
Db 1321 GAGGCGCAATTTCAAGCAATGATGAGCACTTAAAAAGCAAGAGGAGCTCAGAG 1380  
Qy 1381 GCAGCAAGGCAAGCTCTGAGCAATTCAGAGGCGCACTGAGCAAGAGGCTCA 1440  
Db 1381 GCAGCAAGGCAAGCTCTGAGCAATTCAGAGGCGCACTGAGCAAGAGGCTCA 1440  
Qy 1441 GACAGCTCATGTGAAGCTCTGAGTTGAGTTCAAGAGTGTGAAGAGAAATGCG 1500  
Db 1441 GACAGCTCATGTGAAGCTCTGAGTTGAGTTCAAGAGTGTGAAGAGAAATGCG 1500  
Db 1501 AGGAAGAAAAAGAAACAGAAAGAGCACTGTGTGGGAAAGAGAAAGATGAGATTAATTC 1560  
Qy 1501 AGGAAGAAAAAGAAACAGAAAGAGCACTGTGTGGGAAAGAGAAAGATGAGATTAATTC 1560  
Db 1561 CAAAATCTGATTCGAGAGCAAGCATCAGAGAGAAAGTTTCGCTCTCCATTGAAGG 1620  
Qy 1561 CAAAATCTGATTCGAGAGCAAGCATCAGAGAGAAAGTTTCGCTCTCCATTGAAGG 1620  
Db 1561 CAAAATCTGATTCGAGAGCAAGCATCAGAGAGAAAGTTTCGCTCTCCATTGAAGG 1620  
Qy 1621 AACCATTTGATTAAGAAAGAGTACTCTCCCAACAGCACTTTGTTGAGCAATCCGT 1680  
Db 1621 AACCATTTGATTAAGAAAGAGTACTCTCCCAACAGCACTTTGTTGAGCAATCCGT 1680  
Qy 1681 GGTCTCTATTTTCAACAAAGCGGAAATAGCAGAAAGCTTTTCACTTTAGAGGCGA 1740  
Db 1681 GGTCTCTATTTTCAACAAAGCGGAAATAGCAGAAAGCTTTTCACTTTAGAGGCGA 1740  
Qy 1741 GCAAGAGTGTGGGATCTGAGAAAGCACTTCGCAATGATGACACAGCACTTTAGAGAT 1800  
Db 1741 GCAAGAGTGTGGGATCTGAGAAAGCACTTCGCAATGATGACACAGCACTTTAGAGAT 1800  
Qy 1801 AACGAGGCGGTAGAGATTCCTTTGTTGGCCGACGACAGAGAGAGAGCAACAGC 1860  
Db 1801 AACGAGGCGGTAGAGATTCCTTTGTTGGCCGACGACAGAGAGAGAGCAACAGC 1860  
Qy 1861 AACGTGAGTCAGACAGTATGATCCCGGATGCTGGCAGTGTTCACAGCAATGGAGAG 1920  
Db 1861 AACGTGAGTCAGACAGTATGATCCCGGATGCTGGCAGTGTTCACAGCAATGGAGAG 1920  
Qy 1921 ATGCAACAGCACTGTGATTTGCAATGTGTGTTCTCTGTTGTGTGAGCTTCACTTCT 1980  
Db 1921 ATGCAACAGCACTGTGATTTGCAATGTGTGTTCTCTGTTGTGTGAGCTTCACTTCT 1980  
Qy 1981 ACATGCGCTGTGGACAGCTTCTGACAGAGGATATATGATTAAGCAAGCTATGATAC 2040  
Db 1981 ACATGCGCTGTGGACAGCTTCTGACAGAGGATATATGATTAAGCAAGCTATGATAC 2040  
Qy 2041 AATGGAACCAACCTGTAACCTGAAATGAGAAAGAGAGGTCAGTTCTTCCAGCTTTCC 2100  
Db 2041 AATGGAACCAACCTGTAACCTGAAATGAGAAAGAGAGGTCAGTTCTTCCAGCTTTCC 2100  
Qy 2101 ATGCACTTCTGAGAGATCTTCCCAAGGCAAGCAAGATGATATGACGACTTCTA 2160  
Db 2101 ATGCACTTCTGAGAGATCTTCCCAAGGCAAGCAAGATGATATGACGACTTCTA 2160  
Qy 2161 ACAATATAGTAGAGAACTGTAAGATTCAGAGGAGAAATGCGCCCTGTTGATATAA 2220  
Db 2161 ACAATATAGTAGAGAACTGTAAGATTCAGAGGAGAAATGCGCCCTGTTGATATAA 2220  
Qy 2221 TTTTCAACATATTTCTATATCTGAGACTGTTCTCCATATTTGTTAAAAAGTAAACATGTT 2280  
Db 2221 TTTTCAACATATTTCTATATCTGAGACTGTTCTCCATATTTGTTAAAAAGTAAACATGTT 2280  
Qy 2281 GTCAACCTGTGTGATGAGCACTTGTGACTGAGCTGAGCACTGATATGCTTGA 2340  
Db 2281 GTCAACCTGTGTGATGAGCACTTGTGACTGAGCTGAGCACTGATATGCTTGA 2340  
Qy 2341 AATACCTTTTCAATGAGGATGAGCACTATCCAAATGAGGAGCACTTAAATATGCTT 2400  
Db 2341 AATACCTTTTCAATGAGGATGAGCACTATCCAAATGAGGAGCACTTAAATATGCTT 2400  
Qy 2401 ACAGTAGAAACTTGTATATCACTGAGATCTTTACAGCAAGAAATGTTCTGAAATATTT 2460  
Db 2401 ACAGTAGAAACTTGTATATCACTGAGATCTTTACAGCAAGAAATGTTCTGAAATATTT 2460  
Qy 2461 GCAATGATCTCTATATATTTTCCAAAGAGCTGGAATATCTTTGACGAGTTTATTTG 2520  
Db 2461 GCAATGATCTCTATATATTTTCCAAAGAGCTGGAATATCTTTGACGAGTTTATTTG 2520  
Qy 2521 ACAGTACCTGTGTGAGTATGAGCTGCAATGAGGAGATTAATGTTCTGCTGCTCA 2580  
Db 2521 ACAGTACCTGTGTGAGTATGAGCTGCAATGAGGAGATTAATGTTCTGCTGCTCA 2580



OY 2581 TTTCGATTCCTGCGAGTTTCAAGTTGGCAAAATCTTGGCCAACTTAAATATGCTAATA 2640  
DB 2581 TTTCGATTCCTGCGAGTTTCAAGTTGGCAAAATCTTGGCCAACTTAAATATGCTAATA 2640  
OY 2641 MAGATCATGCGAATTCCTGGGGGCTCTGGAAATTTAAACCTCTCTTGGCCATCATC 2700  
DB 2641 MAGATCATGCGAATTCCTGGGGGCTCTGGAAATTTAAACCTCTCTTGGCCATCATC 2700  
OY 2701 GTCCTCATTTTCCGCTGGTGGGCGATGCGACTCTTGGTAAAGCTTAAAGATTGTGTC 2760  
DB 2701 GTCCTCATTTTCCGCTGGTGGGCGATGCGACTCTTGGTAAAGCTTAAAGATTGTGTC 2760  
OY 2761 TCCAAAGTCCGAGTATGTCACCTCCAGCTGGCAGATGAAATGACTTCTCCACTCC 2820  
DB 2761 TCCAAAGTCCGAGTATGTCACCTCCAGCTGGCAGATGAAATGACTTCTCCACTCC 2820  
OY 2821 TTTCGATTTGTCTCCGCTGCTGTGTGGGAGTGGATAGAGACATGTGGGACTGTATG 2880  
DB 2821 TTTCGATTTGTCTCCGCTGCTGTGTGGGAGTGGATAGAGACATGTGGGACTGTATG 2880  
OY 2881 GAGGTTCGCTGCAAGCCATGTCCTTACTGCTTCAATGATGCTATGCTGATGGAAC 2940  
DB 2881 GAGGTTCGCTGCAAGCCATGTCCTTACTGCTTCAATGATGCTATGCTGATGGAAC 2940  
OY 2941 CTAGTGTCTGAAATCTCTTCTGGCCTGCTTMTGAGCTCATTTAGTGCAGAACCTT 3000  
DB 2941 CTAGTGTCTGAAATCTCTTCTGGCCTGCTTMTGAGCTCATTTAGTGCAGAACCTT 3000  
OY 3001 GCAGCCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3060  
DB 3001 GCAGCCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3060  
OY 3061 AAAGAGTATGCTATGCTGAAAGAAATATATGATGATGATGATGATGATGATGATG 3120  
DB 3061 AAAGAGTATGCTATGCTGAAAGAAATATATGATGATGATGATGATGATGATGATG 3120  
OY 3121 AAACAAAAGATTTTATGATGATGATGATGATGATGATGATGATGATGATGATG 3180  
DB 3121 AAACAAAAGATTTTATGATGATGATGATGATGATGATGATGATGATGATGATG 3180  
OY 3181 TGTATGCTCAATCAACAGCAAGAAATTTGGGAAAGATCTTGAATCTTAAATGTAAT 3240  
DB 3181 TGTATGCTCAATCAACAGCAAGAAATTTGGGAAAGATCTTGAATCTTAAATGTAAT 3240  
OY 3241 GGAATCAAGTGTATGGAAGTGGCAAGTGTGAAATTAATTAATTAATTAATTAAT 3300  
DB 3241 GGAATCAAGTGTATGGAAGTGGCAAGTGTGAAATTAATTAATTAATTAATTAAT 3300  
OY 3301 GATTTATGCTATTAATTAACACCCAGTCTTACTGTGACTGTACCAATGCTGTAGGA 3360  
DB 3301 GATTTATGCTATTAATTAACACCCAGTCTTACTGTGACTGTACCAATGCTGTAGGA 3360  
OY 3361 GAAATCTGACTTTGAAATTTTAAACACGGAAGACTTTAGTAGGAATCGGATCTGGAGAA 3420  
DB 3361 GAAATCTGACTTTGAAATTTTAAACACGGAAGACTTTAGTAGGAATCGGATCTGGAGAA 3420  
OY 3421 AGCAAAAGAAAGTGAATGAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 3480  
DB 3421 AGCAAAAGAAAGTGAATGAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 3480  
OY 3481 GCACCTGTAGAGAAAGACCCGCTAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 3540  
DB 3481 GCACCTGTAGAGAAAGACCCGCTAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 3540  
OY 3541 TTCACTGAAGCTGTGTCAAAAGATTTCAAGTGTGTCAAAATCAAGTGTGAAGAGGAGAA 3600  
DB 3541 TTCACTGAAGCTGTGTGTCAAAAGATTTCAAGTGTGTCAAAATCAAGTGTGAAGAGGAGAA 3600  
OY 3601 GGAAGAAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGA 3660  
DB 3601 GGAAGAAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGA 3660

OY 3661 GAGACCTTCATTTGTTTCATGATTCCTTATGATGAGTGTGCTGGGATTTGAAGATATA 3720  
DB 3661 GAGACCTTCATTTGTTTCATGATTCCTTATGATGAGTGTGCTGGGATTTGAAGATATA 3720  
OY 3721 TATATGATCAGCGAAGAGAGATTAAGAGATGTTGGAATATGCTGCAAGGTTTTCAT 3780  
DB 3721 TATATGATCAGCGAAGAGAGATTAAGAGATGTTGGAATATGCTGCAAGGTTTTCAT 3780  
OY 3781 TACATTTTCATTTGGAAGATTCCTTAAATGGGTGCAATGAGCTATCAAAATATTC 3840  
DB 3781 TACATTTTCATTTGGAAGATTCCTTAAATGGGTGCAATGAGCTATCAAAATATTC 3840  
OY 3841 ACCAATGCTGTGTGGTGGGAGCTTCTTAAATGTTGATGTTTCATTTGTCAGTTTACA 3900  
DB 3841 ACCAATGCTGTGTGGTGGGAGCTTCTTAAATGTTGATGTTTCATTTGTCAGTTTACA 3900  
OY 3901 GCAAAATGCTTGGGTACTGCAAGATTTGAGCCATCAATCTCTCAGGACCTAAGACT 3960  
DB 3901 GCAAAATGCTTGGGTACTGCAAGATTTGAGCCATCAATCTCTCAGGACCTAAGACT 3960  
OY 3961 CTGAGACCTCTAAGACCTTATCTGATTTGAAGGATGAGGCTGTGATGCTT 4020  
DB 3961 CTGAGACCTCTAAGACCTTATCTGATTTGAAGGATGAGGCTGTGATGCTT 4020  
OY 4021 TTAGAGCAATTTCCATCATCATGATGATGATGATGATGATGATGATGATGATGAT 4080  
DB 4021 TTAGAGCAATTTCCATCATCATGATGATGATGATGATGATGATGATGATGATGAT 4080  
OY 4081 TTGAGCATCATGAGGCTTAAATTTGTTGCTGGCAATTTACACATGATTTAACACACA 4140  
DB 4081 TTGAGCATCATGAGGCTTAAATTTGTTGCTGGCAATTTACACATGATTTAACACACA 4140  
OY 4141 ACTGTGACAGGTTTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 4200  
DB 4141 ACTGTGACAGGTTTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 4200  
OY 4201 GAAAGAAATGAGACCTCTGATGGAAGAAATGTAAGTAACTTGAATATGAGATTT 4260  
DB 4201 GAAAGAAATGAGACCTCTGATGGAAGAAATGTAAGTAACTTGAATATGAGATTT 4260  
OY 4261 GGGTATCTCTCTTGGCTTCAAGTGTGCAATTTCCAAAGTATGATGATGATGATG 4320  
DB 4261 GGGTATCTCTCTTGGCTTCAAGTGTGCAATTTCCAAAGTATGATGATGATGATGATG 4320  
OY 4321 GCAGTGTATTCAGAAATGATGAACTGCAAGCTTAAATGATGAAAGTGTGATCATGTAT 4380  
DB 4321 GCAGTGTATTCAGAAATGATGAACTGCAAGCTTAAATGATGAAAGTGTGATCATGTAT 4380  
OY 4381 CTTTACTTGTATTTTCAATCATCTTGGGCTCTTCACTTGAACCTGTTATTTGG 4440  
DB 4381 CTTTACTTGTATTTTCAATCATCTTGGGCTCTTCACTTGAACCTGTTATTTGG 4440  
OY 4441 GTTCATATGATTAATTTCAACAGCAAGAAAGAAAGTGTGGAGTCAAAACATCTTANG 4500  
DB 4441 GTTCATATGATTAATTTCAACAGCAAGAAAGAAAGTGTGGAGTCAAAACATCTTANG 4500  
OY 4501 ACAGAGAAAGAGAAAGAAATCTATATGCAATGAAAGAAATTTGGAATGCAAAACCGCAA 4560  
DB 4501 ACAGAGAAAGAGAAAGAAATCTATATGCAATGAAAGAAATTTGGAATGCAAAACCGCAA 4560  
OY 4561 AAGCCTATACCTGACACAGAAACAATTTCAAGAAATGCTCTTGAATCTGTAACCAAA 4620  
DB 4561 AAGCCTATACCTGACACAGAAACAATTTCAAGAAATGCTCTTGAATCTGTAACCAAA 4620  
OY 4621 CAAGTTTGAATTAAGCATGATGATGATGATGATGATGATGATGATGATGATGATG 4680  
DB 4621 CAAGTTTGAATTAAGCATGATGATGATGATGATGATGATGATGATGATGATGATG 4680  
OY 4681 GAAAGATGACCAAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATG 4740  
DB 4681 GAAAGATGACCAAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATG 4740  
OY 4741 ATTGTGCTATTTACTGAGAGTGTACTGAATCATCTCTACGCAATATATATTT 4800



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DB 4741 ATGTCATTTACTGAGAGGTGTACTGAAACATCTCTCTACGCATATATATTT 4800
OY 4801 ACCATGAGAGAAATATTTTGTATTTGTGTGTCATCTCTCATTTAGTATGTT 4860
DB 4801 ACCATGAGAGAAATATTTTGTATTTGTGTGTCATCTCTCATTTAGTATGTT 4860
OY 4861 CTGCGGAGCTGTATGAAAGATTTTCTGTCCTTACCTCTTCCGANTATCCGCTT 4920
DB 4861 CTGCGGAGCTGTATGAAAGATTTTCTGTCCTTACCTCTTCCGANTATCCGCTT 4920
OY 4921 GCTAGATTTGGCCGAATCTGATGATCAAGAGAGAGAGAGAGAGAGAGAGAGAG 4980
DB 4921 GCTAGATTTGGCCGAATCTGATGATCAAGAGAGAGAGAGAGAGAGAGAGAGAG 4980
OY 4981 TTTGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5040
DB 4981 TTTGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5040
OY 5041 ATGTCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5100
DB 5041 ATGTCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5100
OY 5101 ATGTCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5160
DB 5101 ATGTCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5160
OY 5161 ACACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5220
DB 5161 ACACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5220
OY 5221 TGTGACCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 5280
DB 5221 TGTGACCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 5280
OY 5281 GTTGAATTTTCTTTTGTGATGATGATGATGATGATGATGATGATGATGATGATG 5340
DB 5281 GTTGAATTTTCTTTTGTGATGATGATGATGATGATGATGATGATGATGATGATG 5340
OY 5341 TACATCGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5400
DB 5341 TACATCGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5400
OY 5401 AGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5460
DB 5401 AGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5460
OY 5461 CAGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5520
DB 5461 CAGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5520
OY 5521 CTGCGACACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 5580
DB 5521 CTGCGACACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 5580
OY 5581 CGGATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5640
DB 5581 CGGATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5640
OY 5641 GAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5700
DB 5641 GAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5700
OY 5701 GTCTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5760
DB 5701 GTCTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5760
OY 5761 ATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5820
DB 5761 ATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5820
OY 5821 ACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5880
DB 5821 ACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5880

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DB 5821 ACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5880
OY 5881 ATTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5940
DB 5881 ATTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5940
OY 5941 GCTTGTCCACTCTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6000
DB 5941 GCTTGTCCACTCTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6000
OY 6001 GCGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6027
DB 6001 GCGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6027
OY 6027 GCGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6027
DB 6027 GCGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6027

RESULT 4
AAH55764
ID AAH55764 standard; cDNA; 8378 BP.
XX
AC AAH55764;
XX
DT 04-SEP-2001 (first entry)
XX
DE Human neonatal form of SCN1A nucleotide sequence SEQ ID NO:2.
XX
KW Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;
XX diagnosis; mutation; chromosome 2q23-q31; neurological disorder;
XX anticonvulsant; neuroprotective; ss.
XX Homo sapiens.
XX
PN WO200138564-A2.
XX
PD 31-MAY-2001.
XX
PF 24-NOV-2000; 2000WO-CA01404.
XX
PR 26-NOV-1999; 99US-0167623.
XX
PA (UYN-) UNIV MCGILL.
XX
PI Rouleau GA, Lafreniere RG, Rochefort D, Cossette P, Ragsdale D;
XX
DR WPI: 2001-355945/37.
XX
DR P-PSDB: AAB99675.
XX
PT Determining a predisposition to epilepsy and/or development of epilepsy
PT comprises determining the genotype of at least one gene selected
PT DNA variant, equivalent, or mutation which shows a linkage
PT disequilibrium.
XX
PS Disclosure; Page 93-96; 268pp; English.
XX
PX The present invention describes a method (M1) of determining an
XX individual's predisposition to epilepsy and/or development of epilepsy,
XX as well as predicting the individual's response to medication. The
XX method comprises determining the genotype of at least one gene selected
XX from SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation
XX which shows a linkage disequilibrium. SCN1A, SCN2A and SCN3A are all
XX sodium channel genes located on chromosome 2. The idiopathic generalised
XX epilepsy (IGE) gene is more specifically localised on chromosome
XX 2q23-q31. Compounds identified as modulators of the biological activity
XX of SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating
XX epilepsy or other neurological disorders. They have anticonvulsant and
XX neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to
XX AAB99679 represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR
XX primers, oligonucleotides and proteins given in the exemplification of
XX the present invention.
XX
SQ Sequence 8378 BP; 2498 A; 1571 C; 1775 G; 2534 T; 0 other;
XX
Query Match 98.9%; Score 5963.2; DB 22; Length 8378;
Best Local Similarity 99.5%; Pred. No. 0;

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Matches 5999; Conservative 3; Mismatches 26; Indels. 2; Gaps 2;

|    |      |  |      |
|----|------|--|------|
| OY | 1    | ATGAGCAAAAGAGCTCTGTATCCACACAGAGACTGACAGCTTCAACTTCTTCCACAGAGA       | 60   |
| Db | 266  | ATGGAGCAAAAGAGCTCTGTATCCACACAGAGACTGACAGCTTCAACTTCTTCCACAGAGA      | 325  |
| OY | 61   | TCTCTGGGCGTATTTGAAAGAGCAGATTGCAAGAAAGAAAGCAAGAAATCCCAACAGAC        | 120  |
| Db | 326  | TCTCTGGGCGTATTTGAAAGAGCAGATTGCAAGAAAGAAAGCAAGAAATCCCAACAGAC        | 385  |
| OY | 121  | AAAAAGATGACAGAGAAATGSCCCAAAGCCAAATAGTACTTTGGAACTGGAAAGAC           | 180  |
| Db | 386  | AAAAAGATGACAGAGAAATGSCCCAAAGCCAAATAGTACTTTGGAACTGGAAAGAC           | 445  |
| OY | 181  | CTTCCATTATTTATTTGAGAGACATTCCTCCAGAGATGGTGTCCAGAGCCCTGGAGAGACTG     | 240  |
| Db | 446  | CTTCCATTATTTATTTGAGAGACATTCCTCCAGAGATGGTGTCCAGAGCCCTGGAGAGACTG     | 505  |
| OY | 241  | GACCCCTACTATTCATTAAGAAACCTTTATATGATTTGAATTAAGAGAGAGCCATCTTC        | 300  |
| Db | 506  | GACCCCTACTATTCATTAAGAAACCTTTATATGATTTGAATTAAGAGAGAGCCATCTTC        | 565  |
| OY | 301  | CGGTCACTGGCCACTCTGCCCTGTAAATTTTAATCTCCCTCAATCTCTTATGGAAATA         | 360  |
| Db | 566  | CGGTCACTGGCCACTCTGCCCTGTAAATTTTAATCTCCCTCAATCTCTTATGGAAATA         | 625  |
| OY | 361  | GCATTTAAGATTTTGGTATCATCTATTTATTCAGAGATGCTAATTTATGGCACTTATTTGACA    | 420  |
| Db | 626  | GCTATTTAAGATTTTGGTATCATCTATTTATTCAGAGATGCTAATTTATGGCACTTATTTGACA   | 685  |
| OY | 421  | AACGTGTGTTTATGACATGATGATACCCCTCGATTTGGACAAAGATGTAGAAATCACCC        | 480  |
| Db | 686  | AACGTGTGTTTATGACATGATGATACCCCTCGATTTGGACAAAGATGTAGAAATCACACC       | 745  |
| OY | 481  | TTCCAGAGAAATATATCTTTTGAATTCCTATTAATAAATTTATGCAAGGGATCTCGTTTA       | 540  |
| Db | 746  | TTCCAGAGAAATATATCTTTTGAATTCCTATTAATAAATTTATGCAAGGGATCTCGTTTA       | 805  |
| OY | 541  | GAAGATTTTACTTTTCCTTGGGATTCATGMACTGGCTCGATTTCACTCTCATTTACATTT       | 600  |
| Db | 806  | GAAGATTTTACTTTTCCTTGGGATTCATGMACTGGCTCGATTTCACTCTCATTTACATTT       | 865  |
| OY | 601  | GGGTACGTCACAGGTTTGTGGACCTGGGCAATCTCTGGCACTATGGAACATTCAGAGTT        | 660  |
| Db | 866  | GGGTTTTGAACAGATTTTGTGAACCTTAGGCAATTTTTCAGCTCTTCGCACTTTCAGAGTTC     | 925  |
| OY | 661  | CTCCGAGCATTTGAAGAGATTTTCAGTCACTTCCAGGCTCCAAAACATTTTGGGACCCCTG      | 720  |
| Db | 926  | TTGAGAGCTTTGAAAACCTATTTTGGTATTTCCAGGCTTAATAACCATTTGTGGAGCCCTG      | 985  |
| OY | 721  | ATCCAGTCTGTGAAGAAAGCTTCCAGATGTATATGATCCTGACTGTGTCTGTAGGCGTA        | 780  |
| Db | 986  | ATCCAGTCTGTGAAGAAAGCTTCCAGATGTATATGATCCTGACTGTGTCTGTAGGCGTA        | 1045 |
| OY | 781  | TTTCTCTTAATTTGGGCGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG       | 840  |
| Db | 1046 | TTTCTCTTAATTTGGGCGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG       | 1105 |
| OY | 841  | CTCTCCACCAATGCTCTCTTGGAGAGAACATGTATGAAGAAAGATATAACTGTGAATTT        | 900  |
| Db | 1106 | CTCTCCACCAATGCTCTCTTGGAGAGAACATGTATGAAGAAAGATATAACTGTGAATTT        | 1165 |
| OY | 901  | AATGCTACACTTATTAATTAAGAAACCTGTGTTGATGTGGAAGTCACTATATTTCAAGAT       | 960  |
| Db | 1166 | AATGCTACACTTATTAATTAAGAAACCTGTGTTGATGTGGAAGTCACTATATTTCAAGAT       | 1225 |
| OY | 961  | TCAAGATATCATTTTCTCTGAGAGGTTTTTTAGATGCACTACTATGTGGAAGATAGCTCT       | 1020 |
| Db | 1226 | TCAAGATATCATTTTCTCTGAGAGGTTTTTTAGATGCACTACTATGTGGAAGATAGCTCT       | 1285 |
| OY | 1021 | GATCAGAGCCAAATGCTCCAGAGGATATATGTGTGTGAAGAGCTGTGTGAAGAAATCCCAATTTAT | 1080 |
| Db | 1286 | GATCAGAGCCAAATGCTCCAGAGGATATATGTGTGTGAAGAGCTGTGTGAAGAAATCCCAATTTAT | 1345 |

|    |      |   |      |
|----|------|---|------|
| OY | 1081 | GGCTACACAACTTGTGATACCTTAGTGGGCTTTTGGCTGGTCTGGTACATAAGCT         | 1140 |
| Db | 1346 | GGCTACACAACTTGTGATACCTTAGTGGGCTTTTGGCTGGTCTGGTACATAAGCT         | 1405 |
| OY | 1141 | CAGGACTCTGGGAAAATCTTTATCACTACATTAAGTGCTGCTGGGAAAACGTACATG       | 1200 |
| Db | 1406 | CAGGACTCTGGGAAAATCTTTATCACTACATTAAGTGCTGCTGGGAAAACGTACATG       | 1465 |
| OY | 1201 | ATATTTTTTGTTGGTGTGCTATTTTCTTGGGCTCATTTCTACTAATTAATTGATCTGGCT    | 1260 |
| Db | 1466 | ATATTTTTTGATTGGTGTGCTATTTCTTGGGCTCATTTCTACTAATTAATTGATCTGGCT    | 1525 |
| OY | 1261 | GTGGTGCCATGAGCCTACAGAGAAACAGAAATCAGGCCACCTTGGAGAAACACAAACGAA    | 1320 |
| Db | 1526 | GTGGTGCCATGAGCCTACAGAGAAACAGAAATCAGGCCACCTTGGAGAAACACAAACGAA    | 1585 |
| OY | 1321 | GAGGCCGATTTTCAGCAGATGATTGAACAGCTTAAAGCAACAGGAGGACAGCTCAGAG      | 1380 |
| Db | 1586 | GAGGCCGAAATTTTCAGCAGATGATTGAACAGCTTAAAGCAACAGGAGGACAGCTCAGAG    | 1645 |
| OY | 1381 | GCAGCAACGGCACTGGCTCTGAGAAACATTCAGAGAGACCCAGTGCAGCAGGACGCTCTCA   | 1440 |
| Db | 1646 | GCAGCAACGGCACTGGCTCTGAGAAACATTCAGAGAGACCCAGTGCAGCAGGACGCTCTCA   | 1705 |
| OY | 1441 | GACAGCTCATCTGAAAGCCTTAAGTTGAGTTCCAGAGTGTCTAAGGAAAGAAATATCG      | 1500 |
| Db | 1706 | GACAGCTCATCTGAAAGCCTTAAGTTGAGTTCCAGAGTGTCTAAGGAAAGAAATATCG      | 1765 |
| OY | 1501 | AGGAAAGAAAAGAAAACGAAAAGACAGCTCTGGTGGGAAAAGAAAAGATGAGATGATTC     | 1560 |
| Db | 1766 | AGGAAAGAAAAGAAAACGAAAAGACAGCTCTGGTGGGAAAAGAAAAGATGAGATGATTC     | 1825 |
| OY | 1561 | CAAAATCTGATCTGATCTGAGGACAGCATTCAGAGGAAAGTTTTGCGTCCCTTCAAGG      | 1620 |
| Db | 1826 | CAAAATCTGATCTGATCTGAGGACAGCATTCAGAGGAAAGTTTTGCGTCCCTTCAAGG      | 1885 |
| OY | 1621 | AACCGATTGACATGTGAAAAGAGGTACTCCTCCCAACACAGCTTTTGTGGACATCCGT      | 1680 |
| Db | 1886 | AACCGATTGACATGTGAAAAGAGGTACTCCTCCCAACACAGCTTTTGTGGACATCCGT      | 1945 |
| OY | 1681 | GGCTCCCTATTTTCAACCAAGGCGAAAATGAGAGAAACAAGCTTTTCAAGCTTATAGAGGGGA | 1740 |
| Db | 1946 | GGCTCCCTATTTTCAACCAAGGCGAAAATGAGAGAAACAAGCTTTTCAAGCTTATAGAGGGGA | 2005 |
| OY | 1741 | GCAAGAGATGTGGATCTGAGAACGCACTTCGCGAGATGATGAGACAGCAGCTTTGAGAT     | 1800 |
| Db | 2006 | GCAAGAGATGTGGATCTGAGAACGCACTTCGCGAGATGATGAGACAGCAGCTTTGAGAT     | 2064 |
| OY | 1801 | AACGAGAGCCGTAGAGATTCTCTGTTGTGTGCCCCGACGACGAGAGAGACGCAACGC       | 1860 |
| Db | 2065 | AACGAGAGCCGTAGAGATTCTCTGTTGTGTGCCCCGACGACGAGAGAGAGACGCAACGC     | 2124 |
| OY | 1861 | AACCTGAGTCAGACAGATAGTATCCCGATGTCGGCAGTGTTCACAGCAATGGGAG         | 1920 |
| Db | 2125 | AACCTGAGTCAGACAGATAGTATCCCGATGTCGGCAGTGTTCACAGCAATGGGAG         | 2184 |
| OY | 1921 | ATGCAACGCACTGTGATTCGAATGAGTGTGTGTTCTCTGTTGTGTGACCTTCAGTTCTCT    | 1980 |
| Db | 2185 | ATGCAACGCACTGTGATTCGAATGAGTGTGTGTTCTCTGTTGTGTGACCTTCAGTTCTCT    | 2244 |
| OY | 1981 | ACATGCGCTTTGAGACAGCTTCCGACAGAGGGATTAATAGATAACCGCAAGCTACAGATGAC  | 2040 |
| Db | 2245 | ACATGCGCTTTGAGACAGCTTCCGACAGAGGGATTAATAGATAACCGCAAGCTACAGATGAC  | 2304 |
| OY | 2041 | AATGGAACAACAAGCTGAAATGAGAAAGAGAGAGGTCAAGTTCTTTCACAGTTTCC        | 2100 |
| Db | 2305 | AATGGAACAACAAGCTGAAATGAGAAAGAGAGAGGTCAAGTTCTTTCACAGTTTCC        | 2364 |
| OY | 2101 | ATGAGACTTTTAAAGATCTCTTCCAAAGGCAACGACGAATGAGATATGCGCAGATTTCTA    | 2160 |
| Db | 2365 | ATGAGACTTTTAAAGATCTCTTCCAAAGGCAACGACGAATGAGATATGCGCAGATTTCTA    | 2424 |

|    |      |  |      |
|----|------|--|------|
| QY | 2161 | ACAAATACATAGAAAGACTTGANAGAAATCCAGGAGAAATGCCACCTGTGGTATPAA      | 2220 |
| Db | 2425 | ACAAATACATAGAAAGACTTGAGAAATCCAGGAGAAATGCCACCTGTGGTATPAA        | 2484 |
| QY | 2221 | TTTTCACAAATATCTTAATCTGGAGCTTCTCCATATATGGTTAAAGTGAACATGTT       | 2280 |
| Db | 2485 | TTTTCCAAATATCTTAAATCTGGAGCTTCTCCATATATGGTTAAAGTGAACATGTT       | 2544 |
| QY | 2281 | GTCAACCTGGTGTGATGAGACCCATTTGTTGACCTGGCCATCCACATCTGATTTGCTTA    | 2340 |
| Db | 2545 | GTCAACCTGGTGTGATGAGACCCATTTGTTGACCTGGCCATCCACATCTGATTTGCTTA    | 2604 |
| QY | 2341 | AATACCTTTTTCATGCGCATGAGAGACATATCCAAATGAGGAGACATTTTAAATATGTCCT  | 2400 |
| Db | 2605 | AATACCTTTTTCATGCGCATGAGAGACATATCCAAATGAGGAGACATTTTAAATATGTCCT  | 2664 |
| QY | 2401 | ACATATAGAAACATGTTGTTTCACTGGGACTTTTACAGAGAAATGTTTCTGAAATATTT    | 2460 |
| Db | 2665 | ACATATAGAAACATGTTGTTTCACTGGGACTTTTACAGAGAAATGTTTCTGAAATATTT    | 2724 |
| QY | 2461 | GCCATGATCCTTACTATTTATTTTCCAAAGAGCTGGAAATATCTTTGACGCTTTATTTG    | 2520 |
| Db | 2725 | GCCATGATCCTTACTATTTATTTTCCAAAGAGCTGGAAATATCTTTGACGCTTTATTTG    | 2784 |
| QY | 2521 | ACGCTTACGCTGGTAGACTTGAGACTGCGCAATGTGGAAGATTATCTGTTCTCCGTTCA    | 2580 |
| Db | 2785 | ACGCTTACGCTGGTAGACTTGAGACTGCGCAATGTGGAAGATTATCTGTTCTCCGTTCA    | 2844 |
| QY | 2581 | TTTCGATTTGCTGGAGATTTTCAAGTTGGGCAAAATCTGGGCCAAGCTTAAATATGCTATA  | 2640 |
| Db | 2845 | TTTCGATTTGCTGGAGATTTTCAAGTTGGGCAAAATCTGGGCCAAGCTTAAATATGCTATA  | 2904 |
| QY | 2641 | AAAGATCATCGGCAATTTCCGTGGGGGCTCTGGGAAATTTTAAACCTGTCTTGGCCATATC  | 2700 |
| Db | 2905 | AAAGATCATCGGCAATTTCCGTGGGGGCTCTGGGAAATTTTAAACCTGTCTTGGCCATATC  | 2964 |
| QY | 2701 | GCTCTCAATTTTGGCGGTGGTGGCATGACACTTTTGGTAAAGCTACAAAGATTGTGTC     | 2760 |
| Db | 2965 | GCTCTCAATTTTGGCGGTGGTGGCATGACACTTTTGGTAAAGCTACAAAGATTGTGTC     | 3024 |
| QY | 2761 | TGCAAGATCGGCAAGTATTTTCAAATCCCAAGCTGGGCACATGAAATGACTCTTCCACATCC | 2820 |
| Db | 3025 | TGCAAGATCGGCAAGTATTTTCAAATCCCAAGCTGGGCACATGAAATGACTCTTCCACATCC | 3084 |
| QY | 2821 | TTCCGTGATTTGTTCCCGCTGCTGTGTGGGAGATGGATAGAACCATGTGGGACTGTATG    | 2880 |
| Db | 3085 | TTCCGTGATTTGTTCCCGCTGCTGTGTGGGAGATGGATAGAACCATGTGGGACTGTATG    | 3144 |
| QY | 2881 | GAGGTGCTGTGCAAGCCATGTGCTTACTGTCTTCATGATGTCGTATGTGATTTGGAAC     | 2940 |
| Db | 3145 | GAGGTGCTGTGCAAGCCATGTGCTTACTGTCTTCATGATGTCGTATGTGATTTGGAAC     | 3204 |
| QY | 2941 | CTATGTGCTGGAATCTCTTCTGAGCTTGCTTMMGAGTCAATTAAGTGCAGACAACCTT     | 3000 |
| Db | 3205 | CTATGTGCTGGAATCTCTTCTGAGCTTGCTTMMGAGTCAATTAAGTGCAGACAACCTT     | 3264 |
| QY | 3001 | GCAGCCACTGATGATGATTAATGAAGAAATTAATCTCCAAATTCGTGATAGATGCAC      | 3060 |
| Db | 3265 | GCAGCCACTGATGATGATTAATGAAGAAATTAATCTCCAAATTCGTGATAGATGCAC      | 3324 |
| QY | 3061 | AAAGAGTAGCTTATGTGAAAGAAATATATATGAATTTATTCACACACTCTCTTATTAAG    | 3120 |
| Db | 3325 | AAAGAGTAGCTTATGTGAAAGAAATATATATGAATTTATTCACACACTCTCTTATTAAG    | 3384 |
| QY | 3121 | AAACAAAGATTTAGTATGAATTAACCAACTGATGATCTAAACAACAAGAAAGACGT       | 3180 |
| Db | 3385 | AAACAAAGATTTAGTATGAATTAACCAACTGATGATCTAAACAACAAGAAAGACGT       | 3444 |
| QY | 3181 | TGATATGTCATCATACACAGAAATTTGGAAAGATCTGATATCTTAAAGATGTAAAT       | 3240 |
| Db | 3445 | TGATATGTCATCATACACAGAAATTTGGAAAGATCTGATATCTTAAAGATGTAAAT       | 3504 |
| QY | 3241 | GGAATCAACAGTGTATAGGAACCTGCGACGACTGTTGAAAAATATATTATGTGAAAGT     | 3300 |

|    |      |   |      |
|----|------|---|------|
| Db | 3505 | GGAACTCAAGTGGTATAGGAATCGGCACAGCTTTGAAAAATACATTATTGATGAAAGT    | 3554 |
| Oy | 3301 | GATTACATGTCATTCAATAAACAACCCAGCTTACTGTGACTGTACCAATTGCTGTAGA    | 3360 |
| Db | 3565 | GATTACATGTCATTCAATAAACAACCCAGCTTACTGTGACTGTACCAATTGCTGTAGA    | 3624 |
| Oy | 3361 | GAATCTGACTTTGAAAATTTAAACACGGAGACTTATAGTAGGAATCGGATCTGGAGAA    | 3420 |
| Db | 3625 | GAATCTGACTTTGAAAATTTAAACACGGAGACTTATAGTAGGAATCGGATCTGGAGAA    | 3684 |
| Oy | 3421 | AGCAAGAAGAAACGAATGAAACACGTACGTACATCGAAGTAGAGACGTGTGACATGTGGC  | 3480 |
| Db | 3685 | AGCAAGAAGAAACGAATGAAACACGTACGTACATCGAAGTAGAGACGTGTGACATGTGGC  | 3744 |
| Oy | 3481 | GCACCTGTAGAAAGAACAGCCCGTAGTGGAACTGGAAGAACTCTTGAACACGAAGCTTGT  | 3540 |
| Db | 3745 | GCACCTGTAGAAAGAACAGCCCGTAGTGGAACTGGAAGAAACCTTGAACACGAAGCTTGT  | 3804 |
| Oy | 3541 | TTCACTGAGAGCGCTGTGTACAAAGATTCAGATGTGTCAATCAATGTGGAAGAGGAGA    | 3600 |
| Db | 3805 | TTCACTGAGAGCGCTGTGTACAAAGATTCAGATGTGTCAATCAATGTGGAAGAGGAGA    | 3864 |
| Oy | 3601 | GGAAAAAAGTGTGGAAACCGGAGAAGAGCTGTTCCGAATAGTGAACATPAACCTGGTT    | 3666 |
| Db | 3865 | GGAAAAAAGTGTGGAAACCGGAGAAGAGCTGTTCCGAATAGTGAACATPAACCTGGTT    | 3924 |
| Oy | 3661 | GAGACCTTCATGTTGTTTCATGATTCCTGTAGTAGTGGGTCTGTGGCAATTTGAAATATA  | 3720 |
| Db | 3925 | GAGACCTTCATGTTGTTTCATGATTCCTGTAGTAGTGGGTCTGTGGCAATTTGAAATATA  | 3984 |
| Oy | 3721 | TATATTGATCAGCGAAGAGGATTTAAGACATGTGTGGAAATATGTGTACAGAGGTTTTCCT | 3780 |
| Db | 3985 | TATATTGATCAGCGAAGAGGATTTAAGACATGTGTGGAAATATGTGTACAGAGGTTTTCCT | 4044 |
| Oy | 3781 | TGACATTTTCATCTCGGAAAAGCTTCTTAAAAATGGGTGGCATAGGCTATCAACAATATTC | 3840 |
| Db | 4045 | TGACATTTTCATCTCGGAAAAGCTTCTTAAAAATGGGTGGCATAGGCTATCAACAATATTC | 4103 |
| Oy | 3841 | ACCAATGCCGTGGTTGGCTGGAGACTTCTTAATGTGTGAATGTTCAATGGCTAGTTTAA   | 3900 |
| Db | 4104 | ACCAATGCCGTGGTTGGCTGGAGACTTCTTAATGTGTGAATGTTCAATGGCTAGTTTAA   | 4163 |
| Oy | 3901 | GCAAAATGCCCTGGTGTACTCAGAACTTGAAGCCATCAAAATCTCAGACACTAAGAGCT   | 3966 |
| Db | 4164 | GCAAAATGCCCTGGTGTACTCAGAACTTGAAGCCATCAAAATCTCAGACACTAAGAGCT   | 4223 |
| Oy | 3961 | CTGAGACCTCTAAGAGCCTTATCTCCATTTGAAGGATATAGGGTGGTGTGAATGCCCTT   | 4020 |
| Db | 4224 | CTGAGACCTCTAAGAGCCTTATCTCCATTTGAAGGATATAGGGTGGTGTGAATGCCCTT   | 4283 |
| Oy | 4021 | TTAGAGCAAAATTCATCATCATCATGAAATGTGCTCTGGTTGTCTTATATTTGGGCTAAT  | 4088 |
| Db | 4284 | TTAGAGCAAAATTCATCATCATCATGAAATGTGCTCTGGTTGTCTTATATTTGGGCTAAT  | 4343 |
| Oy | 4081 | TTTCAGCATCATGGCGCTAAATTTTGTGTGTGGCAATTTCTACACTGTATTTAACACACA  | 4140 |
| Db | 4344 | TTTCAGCATCATGGCGCTAAATTTTGTGTGTGGCAATTTCTACACTGTATTTAACACACA  | 4403 |
| Oy | 4141 | ACTGTGTACAGGTTTGACATCGAAGACGTGAATATCATATCTGATTTGCTTAAACTAATA  | 4200 |
| Db | 4404 | ACTGTGTACAGGTTTGACATCGAAGACGTGAATATCATATCTGATTTGCTTAAACTAATA  | 4463 |
| Oy | 4201 | GAAGAAGATGAGACTGTGTGATGAGAAAATGTGAAGTAAACTTTGGATPAATGTAGATTT  | 4266 |
| Db | 4464 | GAAGAAGATGAGACTGTGTGATGAGAAAATGTGAAGTAAACTTTGGATPAATGTAGATTT  | 4523 |
| Oy | 4261 | GGGATATCTCTTCTTCAAGTTGGCACATTCGAAGATGAGATGGATATATATGTATCA     | 4320 |
| Db | 4524 | GGGATATCTCTTCTTCAAGTTGGCACATTCGAAGATGAGATGGATATATATGTATCA     | 4583 |
| Oy | 4321 | GCAATGATTTCCAGAAATGTGGAACTTCAGCTTAAGTATGAAGAAAGTCTGTACATGTAT  | 4380 |

Db 4584 GCAGTGGATTCAGAAATGTGGAACTCCAGCCTTAAGTATGAAGAAAGTCTGTACATGTAT 4643  
 Qy 4381 CTTTACCTTTGTTATTTTCATCATCTTTGGGTCCTCTTCACTGTAACCTGTTATTTGT 4440  
 Db 4644 CTTTACCTTTGTTATTTTCATCATCTTTGGGTCCTCTTCACTGTAACCTGTTATTTGT 4703  
 Qy 4441 GTTCATCATAGATTAATTTCAACGACAGAAAAAGATTGGAGTCAAGACATCTTTATG 4500  
 Db 4704 GTTCATCATAGATTAATTTCAACGACAGAAAAAGATTGGAGTCAAGACATCTTTATG 4763  
 Qy 4501 ACAGAGAGACAGAGAAATTAATTAATGCAATGAAAAAATTGATGCAAAAAACCCGA 4560  
 Db 4764 ACAGAGAGACAGAGAAATTAATTAATGCAATGAAAAAATTGATGCAAAAAACCCGA 4823  
 Qy 4561 AAGCCTATACCTCGACGAGAAACAAATTTCAAGGAATGGCTTGTAGTCAACCGA 4620  
 Db 4824 AAGCCTATACCTCGACGAGAAACAAATTTCAAGGAATGGCTTGTAGTCAACCGA 4883  
 Qy 4621 CAACTTTTGAATTAAGATCATGATCTGATCTGTTAAACATGATGATGATG 4680  
 Db 4884 CAACTTTTGAATTAAGATCATGATCTGATCTGTTAAACATGATGATGATG 4943  
 Qy 4681 GAAACAGATGACAGAGATTAATTAATGCAATGAAAAAATTGATGCAAAAAACCCGA 4740  
 Db 4944 GAAACAGATGACAGAGATTAATTAATGCAATGAAAAAATTGATGCAAAAAACCCGA 5003  
 Qy 4741 ATTGCTATTTAGTGGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 4800  
 Db 5004 ATTGCTATTTAGTGGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 5063  
 Qy 4801 ACCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4860  
 Db 5064 ACCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5123  
 Qy 4861 CTGCGCGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4920  
 Db 5124 CTGCGCGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5183  
 Qy 4921 GCTAGGATTTGGCGGAACTCTGATGATGATGATGATGATGATGATGATGATGATG 4980  
 Db 5184 GCTAGGATTTGGCGGAACTCTGATGATGATGATGATGATGATGATGATGATGATG 5243  
 Qy 4981 TTTGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5040  
 Db 5244 TTTGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5303  
 Qy 5041 ATGTTTATCTTACGCGCATCTTTGGATGATGATGATGATGATGATGATGATGATG 5100  
 Db 5304 ATGTTTATCTTACGCGCATCTTTGGATGATGATGATGATGATGATGATGATGATG 5363  
 Qy 5101 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5160  
 Db 5364 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5423  
 Qy 5161 ACAACCTGCTGCTGGATGATGATGATGATGATGATGATGATGATGATGATGATG 5220  
 Db 5424 ACAACCTGCTGCTGGATGATGATGATGATGATGATGATGATGATGATGATGATG 5483  
 Qy 5221 TGTGACCTTATTAAGTAAACCTGGAAGCTCAATTAAGGAGAGCTGGAGAACCACT 5280  
 Db 5484 TGTGACCTTATTAAGTAAACCTGGAAGCTCAATTAAGGAGAGCTGGAGAACCACT 5543  
 Qy 5281 GTTGAATTTCTTTTGTGATGATGATGATGATGATGATGATGATGATGATGATG 5340  
 Db 5544 GTTGAATTTCTTTTGTGATGATGATGATGATGATGATGATGATGATGATGATG 5603  
 Qy 5341 TACATCGGCTGATCTGAGAGACTTCACTGATGATGATGATGATGATGATGATG 5400  
 Db 5604 TACATCGGCTGATCTGAGAGACTTCACTGATGATGATGATGATGATGATGATG 5663  
 Qy 5401 AGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5460  
 Db 5664 AGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5723

Qy 5461 CAGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5520  
 Db 5724 CAGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5783  
 Qy 5521 CTGCGCACCAACCAACCACTGATGATGATGATGATGATGATGATGATGATGATG 5580  
 Db 5784 CTGCGCACCAACCAACCACTGATGATGATGATGATGATGATGATGATGATGATG 5843  
 Qy 5581 CGATTCACCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 5640  
 Db 5844 CGATTCACCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 5903  
 Qy 5641 GAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5700  
 Db 5904 GAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5963  
 Qy 5701 GTCTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5760  
 Db 5964 GTCTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6023  
 Qy 5761 ATTATTCAGCTGCTTACAGACGCCACCTTTTAAAGCGAAGTGTAAACAAAGCTT 5820  
 Db 6024 ATTATTCAGCTGCTTACAGACGCCACCTTTTAAAGCGAAGTGTAAACAAAGCTT 6083  
 Qy 5821 ACATACATTAACCAACCAATGATGATGATGATGATGATGATGATGATGATG 5880  
 Db 6084 ACATACATTAACCAACCAATGATGATGATGATGATGATGATGATGATGATG 6143  
 Qy 5881 ATTACAGAAATTAACCAACCAATGATGATGATGATGATGATGATGATGATG 5940  
 Db 6144 ATTACAGAAATTAACCAACCAATGATGATGATGATGATGATGATGATGATG 6203  
 Qy 5941 GCTTGTCCACCTTCTTATGATGATGATGATGATGATGATGATGATGATGATG 6000  
 Db 6204 GCTTGTCCACCTTCTTATGATGATGATGATGATGATGATGATGATGATGATG 6263  
 Qy 6001 GGCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6060  
 Db 6264 GGCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6323

RESULT 5  
 AAD32839  
 ID AAD32839 standard; cDNA; 5997 BP.  
 XX  
 AC AAD32839;  
 DT 01-JUL-2002 (first entry)  
 DE Human ion channel cDNA #1.  
 XX  
 KW Human; novel human protein; NHP; voltage-gated sodium channel;  
 KW gene therapy; bioelectronic; mental disorder; biological disorder;  
 KW gene; medical disorder; ss.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT 1..5997  
 FT CDS  
 FT /\*tag= a  
 FT /product= "Human ion channel protein #1"  
 FT /transl\_except= (pos:2941..2943, aa:taa)  
 FT /transl\_except= (pos:3166..3168, aa:taa)  
 FT /note= "Xaa = any amino acid"  
 XX  
 PN WO200214498-A2.  
 PD 21-FEB-2002.  
 XX  
 PE 15-AUG-2001; 2001WO-US25650.  
 XX  
 PR 16-AUG-2000; 2000US-225989P.

|    |      |   |      |
|----|------|---|------|
| Oy | 421  | AACGTGCTTAAAGACAATGAGAAACCCGCGATGTGGACCAAAAGATGCAATACAC         | 480  |
| Db | 421  | AACGTGCTTAAAGACAATGAGAAACCCGCGATGTGGACCAAAAGATGCAATACAC         | 480  |
| Oy | 481  | TTACAGGAATATATACCTTTTGATCAGTATATAAAATTAATGCAAGGGATTCGT          | 540  |
| Db | 481  | TTACAGGAATATATACCTTTTGATCAGTATATAAAATTAATGCAAGGGATTCGT          | 540  |
| Oy | 541  | GAAGATTTTACTTTCCCTTCGGGATCCATGGAACCTGGCTGCATTTCACTGCAATTT       | 600  |
| Db | 541  | GAAGATTTTACTTTCCCTTCGGGATCCATGGAACCTGGCTGCATTTCACTGCAATTT       | 600  |
| Oy | 601  | GCATACGTCACAGAGTTGTGAGACCTGGGCAATGCTCCGGCATTTGGAATTCAGAGTT      | 660  |
| Db | 601  | GCATACGTCACAGAGTTGTGAGACCTGGGCAATGCTCCGGCATTTGGAATTCAGAGTT      | 660  |
| Oy | 661  | CTCCGAGCATTTGAAGACGATTTTCAGTCATTCAGGCGCTGAAAAACCATTTGTGGAGCCCTG | 720  |
| Db | 661  | CTCCGAGCATTTGAAGACGATTTTCAGTCATTCAGGCGCTGAAAAACCATTTGTGGAGCCCTG | 720  |
| Oy | 721  | ATCCAGTCTGGAAGAGCTCCAGATGTATATATCCATGCTGTCTGCTGTGAGCGTA         | 780  |
| Db | 721  | ATCCAGTCTGGAAGAGCTCCAGATGTATATATCCATGCTGTCTGCTGTGAGCGTA         | 780  |
| Oy | 781  | TTTGCTCTAATTTGGGCGTCAGCTGTTCATGCGGCAACCTGAGGAATAATGTATACAAATGG  | 840  |
| Db | 781  | TTTGCTCTAATTTGGGCGTCAGCTGTTCATGCGGCAACCTGAGGAATAATGTATACAAATGG  | 840  |
| Oy | 841  | CCCTCCCAACCAATGCTTCTCTTGAGAGCAATAGTATGAAAAGAAATATACTGTGAATAT    | 900  |
| Db | 841  | CCCTCCCAACCAATGCTTCTCTTGAGAGCAATAGTATGAAAAGAAATATACTGTGAATAT    | 900  |
| Oy | 901  | AATGATACACTTATTAATTAATGAAACCTGCTTGTGATTTGATCGGGAAGCATATTTCAAT   | 960  |
| Db | 901  | AATGATACACTTATTAATTAATGAAACCTGCTTGTGATTTGATCGGGAAGCATATTTCAAT   | 960  |
| Oy | 961  | TCAGATATATCATTTATTTCTGAGAGGCTTTTGTAGATGACACTATGTTGGAATAGCTCT    | 1020 |
| Db | 961  | TCAGATATATCATTTATTTCTGAGAGGCTTTTGTAGATGACACTATGTTGGAATAGCTCT    | 1020 |
| Oy | 1021 | GATCAGAGCCAAATGCCAGAGGGGATATATGTGTGTAAGAGCGATGTAAGAAATCCCAATAT  | 1080 |
| Db | 1021 | GATCAGAGCCAAATGCCAGAGGGGATATATGTGTGTAAGAGCGATGTAAGAAATCCCAATAT  | 1080 |
| Oy | 1081 | GGCTACACAAAGCTTTGATACCTTCAGTTGGGCTTTTGTGCTTGTTGCACTAATGACT      | 1140 |
| Db | 1081 | GGCTACACAAAGCTTTGATACCTTCAGTTGGGCTTTTGTGCTTGTTGCACTAATGACT      | 1140 |
| Oy | 1141 | CAGACATTCCTGGGAAATCTTTATCAACTATACATTAACGTGCTGTGGAAAAACGTACATG   | 1200 |
| Db | 1141 | CAGACATTCCTGGGAAATCTTTATCAACTATACATTAACGTGCTGTGGAAAAACGTACATG   | 1200 |
| Oy | 1201 | ATATTTTGTGTGTGTCATTTCTTGGGCTCATTTACTACTATATAATTTGATCCTGGCT      | 1260 |
| Db | 1201 | ATATTTTGTGTGTGTCATTTCTTGGGCTCATTTACTACTATATAATTTGATCCTGGCT      | 1260 |
| Oy | 1261 | GTGTGGCCATGTGGCTTCAGAGAAACAGAAATCAGGCCACCTTGGAAGAGCAGAAACAGAA   | 1320 |
| Db | 1261 | GTGTGGCCATGTGGCTTCAGAGAAACAGAAATCAGGCCACCTTGGAAGAGCAGAAACAGAA   | 1320 |
| Oy | 1321 | GAGGCGCAATTTACAGAGATGATTTGAACAGCTTAAAAACCAACAGAGGCACTCAGAG      | 1380 |
| Db | 1321 | GAGGCGCAATTTACAGAGATGATTTGAACAGCTTAAAAACCAACAGAGGCACTCAGAG      | 1380 |
| Oy | 1381 | GCAGCAACGGCAACTGCTCAGAACATTTCCAGAGAGCCCAAGTCAGACAGGCGCTCA       | 1440 |
| Db | 1381 | GCAGCAACGGCAACTGCTCAGAACATTTCCAGAGAGCCCAAGTCAGACAGGCGCTCA       | 1440 |
| Oy | 1441 | GACAGCTATCTGAAGCTCTTAAGTGAATGATCCAAAGTGTCAAGAGAAAGAAATTCGG      | 1500 |
| Db | 1441 | GACAGCTATCTGAAGCTCTTAAGTGAATGATCCAAAGTGTCAAGAGAAAGAAATTCGG      | 1500 |



[illegible]



|   |      |  |      |
|---|------|--|------|
| D | 3628 | GAGACCTCAATTCGTTTTCATGATTCCTCCTTAATAGTGGCTCTGCGATTGGAAGATATA | 3667 |
| Q | 3721 | TATATTGATCAGGAAGAAGCATTTAAGACGATGTTGGAATATGCTGACAAAGTTTTCACT | 3780 |
| D | 3688 | TATATTGATCAGGAAGAAGCATTTAAGACGATGTTGGAATATGCTGACAAAGTTTTCACT | 3747 |
| Q | 3781 | TACATTTTCATTCGGAATGCTTCGAAATGGGTGGCATATAGGTATCAACATATATTC    | 3840 |
| D | 3748 | TACATTTTCATTCGGAATGCTTCGAAATGGGTGGCATATAGGTATCAACATATATTC    | 3807 |
| Q | 3841 | ACCAATGCCGTGGTGGCTGGACCTTAAATGTTGATGTTTCATTGTCAGATTAA        | 3900 |
| D | 3808 | ACCAATGCCGTGGTGGCTGGACCTTAAATGTTGATGTTTCATTGTCAGATTAA        | 3867 |
| Q | 3901 | GCAAAATCCCTGGGTTACTCGAAGACTTGAGGACATCAATCTCTCAGACACTAAGACT   | 3960 |
| D | 3868 | GCAAAATCCCTGGGTTACTCGAAGACTTGAGGACATCAATCTCTCAGACACTAAGACT   | 3927 |
| Q | 3961 | CTGAGACCTCTAAGACCTTATTCGATTTGAAGGATGAGGGTGGTGTGAAGCCCT       | 4020 |
| D | 3928 | CTGAGACCTCTAAGACCTTATTCGATTTGAAGGATGAGGGTGGTGTGAAGCCCT       | 3987 |
| Q | 4021 | TTAGAGCAATTCATCCATCCATGATGATGCTCGGTTGGTCTAATATTCGGCTAAT      | 4080 |
| D | 3988 | TTAGAGCAATTCATCCATCCATGATGATGCTCGGTTGGTCTAATATTCGGCTAAT      | 4047 |
| Q | 4081 | TTGAGCATCATGGGCGTAATTTGTTGGCTGGCAAAATCTACACCTGATTTAACACCA    | 4140 |
| D | 4048 | TTGAGCATCATGGGCGTAATTTGTTGGCTGGCAAAATCTACACCTGATTTAACACCA    | 4107 |
| Q | 4141 | ACTGGTGACAGGTTTGACATCGAAGCGTAATCATCTGATGCTTAAACTAATA         | 4200 |
| D | 4108 | ACTGGTGACAGGTTTGACATCGAAGCGTAATCATCTGATGCTTAAACTAATA         | 4167 |
| Q | 4201 | GAAGAATATGAGACTGCTGCATGTAAGAAATATGAAAGTAATCTTGATTAATGTGANT   | 4260 |
| D | 4168 | GAAGAATATGAGACTGCTGCATGTAAGAAATATGAAAGTAATCTTGATTAATGTGANT   | 4227 |
| Q | 4261 | GGGATCTCTCTTGGCTCAAGTTGGCACATTCAAAGATGAGTATATATATGCA         | 4320 |
| D | 4228 | GGGATCTCTCTTGGCTCAAGTTGGCACATTCAAAGATGAGTATATATATGCA         | 4287 |
| Q | 4321 | GCAATGATTCACAGAAATGTGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGAT   | 4380 |
| D | 4288 | GCAATGATTCACAGAAATGTGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGAT   | 4347 |
| Q | 4381 | CTTTACTTGTGTATTTTCATCATCTTTGGTGCTCTTCACCTTAACCTGTATATGGT     | 4440 |
| D | 4348 | CTTTACTTGTGTATTTTCATCATCTTTGGTGCTCTTCACCTTAACCTGTATATGGT     | 4407 |
| Q | 4441 | GTCATCATAGATATTTCAACACGACGAAAAAAGATTGGAGTCAAGACATCTTATG      | 4500 |
| D | 4408 | GTCATCATAGATATTTCAACACGACGAAAAAAGATTGGAGTCAAGACATCTTATG      | 4467 |
| Q | 4501 | ACAGAGAACAGAAAGAAATCTATTAATGCAATGAAAAAATTAGATCGAAAAACCGCA    | 4560 |
| D | 4468 | ACAGAGAACAGAAAGAAATCTATTAATGCAATGAAAAAATTAGATCGAAAAACCGCA    | 4527 |
| Q | 4561 | AAGCCTATACCTGCACAGAAACAAATTTCAAGAAATGCTGTTGACTGTGAACCGA      | 4620 |
| D | 4528 | AAGCCTATACCTGCACAGAAACAAATTTCAAGAAATGCTGTTGACTGTGAACCGA      | 4587 |
| Q | 4621 | CAAGTTTTTGACATTAACATCATGATTCATCTGCTTAACATGGTCACATGATGGTG     | 4680 |
| D | 4588 | CAAGTTTTTGACATTAACATCATGATTCATCTGCTTAACATGGTCACATGATGGTG     | 4647 |
| Q | 4681 | GAACAGATGACAGAGTGAATATGTGACTACCAATTTTGACAGCATCAATCTGGTGT     | 4740 |
| D | 4648 | GAACAGATGACAGAGTGAATATGTGACTACCAATTTTGACAGCATCAATCTGGTGT     | 4707 |
| Q | 4741 | ATTGCTGCTATTACTGGAAGAGTGTGTAAGTAACCTATCTCTACGCAATATATATTT    | 4800 |
| D | 4708 | ATTGCTGCTATTACTGGAAGAGTGTGTAAGTAACCTATCTCTACGCAATATATATTT    | 4767 |

|    |      |  |      |
|----|------|--|------|
| QY | 4801 | ACCAATTGGATGGAAATATTTTGAATTTTGCGTTGATCTCTCCATCTTGATGGATATGTTT    | 4860 |
| Db | 4768 | ACCAATTGGATGGAAATATTTTGAATTTTGCGTTGATCTCTCCATCTTGATGGATATGTTT    | 4827 |
| QY | 4861 | CTTCCGAGCGTAAATAGAAAAAGTATTTTCGTTCCGTTCCCGTACCCGTTCCAGTATCCGCTCT | 4920 |
| Db | 4828 | CTTCCGAGCGTAAATAGAAAAAGTATTTTCGTTCCGTTCCCGTACCCGTTCCAGTATCCGCTCT | 4887 |
| QY | 4921 | GCTAGATTGGCCGAATCTACGCTGATCAAGAGACAAAGGAGATCCGACGCTGCTC          | 4980 |
| Db | 4888 | GCTAGATTGGCCGAATCTACGCTGATCAAGAGAGCAAAAGGAGATCCGACGCTGCTC        | 4947 |
| QY | 4981 | TTTGCTTTGATGATGTCCTCTCTCGCTGTGTTTAACATCAGGCTCTCTACTCTTCTCTAGTC   | 5040 |
| Db | 4948 | TTTGCTTTGATGATGTCCTCTCTCGCTGTGTTTAACATCAGGCTCTCTACTCTTCTCTAGTC   | 5007 |
| QY | 5041 | ATGTTCACTAACGCCATCTTTGGAGATGCCAATTGGCTATGTTAAGAGGAAGTTGGG        | 5100 |
| Db | 5008 | ATGTTCACTAACGCCATCTTTGGAGATGCCAATTGGCTATGTTAAGAGGAAGTTGGG        | 5067 |
| QY | 5101 | ATCCATGACATGTTCAACTTTGAGACCTTTGGCAACAGATGATCTGCCTATTCGAAAT       | 5160 |
| Db | 5068 | ATCCATGACATGTTCAACTTTGAGACCTTTGGCAACAGATGATCTGCCTATTCGAAAT       | 5127 |
| QY | 5161 | ACAACCTCTGCTGCGCTGGAGTGGATGTTGTAAGCACCCATTTCTACAGTAAGCACCCGAC    | 5220 |
| Db | 5128 | ACAACCTCTGCTGCGCTGGAGTGGATGTTGTAAGCACCCATTTCTACAGTAAGCACCCGAC    | 5187 |
| QY | 5221 | TGTACCCCTAATAAGTTAACTCGGAACCTCAGTTAAGGGAGACTGTGGGAACCCATCT       | 5280 |
| Db | 5188 | TGTACCCCTAATAAGTTAACTCGGAACCTCAGTTAAGGGAGACTGTGGGAACCCATCT       | 5247 |
| QY | 5281 | GTGGAAATTTCTTTTGTGCACTGATCAATCAATATCTTCTGTTGGTGGTAACATG          | 5340 |
| Db | 5248 | GTGGAAATTTCTTTTGTGCACTGATCAATCAATATCTTCTGTTGGTGGTAACATG          | 5307 |
| QY | 5341 | TACATTCGCGGTCACTCGTGAGAACTTCAGTGTGCTACTGAGAAAGTGACAGAGCTCTG      | 5400 |
| Db | 5308 | TACATTCGCGGTCACTCGTGAGAACTTCAGTGTGCTACTGAGAAAGTGACAGAGCTCTG      | 5367 |
| QY | 5401 | AGTAGAGATGACTTTGATGATGTTCTATAGAGTTTGGGAGATTTGATCCGATGCAACT       | 5460 |
| Db | 5368 | AGTAGAGATGACTTTGATGATGTTCTATAGAGTTTGGGAGATTTGATCCGATGCAACT       | 5427 |
| QY | 5461 | CAGTTCATGGAAATTTGAAAAATATATCCAGTTTGCAGCTGGCCTTGAACCGGCTCTCAT     | 5520 |
| Db | 5428 | CAGTTCATGGAAATTTGAAAAATATATCCAGTTTGCAGCTGGCCTTGAACCGGCTCTCAT     | 5487 |
| QY | 5521 | CTGCACACCAACCAAACTCCAGCTCATTTGCCATGATTTGCCATGGTAGTGGTAC          | 5580 |
| Db | 5488 | CTGCACACCAACCAAACTCCAGCTCATTTGCCATGATTTGCCATGGTAGTGGTAC          | 5547 |
| QY | 5581 | CGGATCCACTGTCTTGATATCTTATTTGCTTTACAAAGCGGGTCTTAGAGAGATGTGA       | 5640 |
| Db | 5548 | CGGATCCACTGTCTTGATATCTTATTTGCTTTACAAAGCGGGTCTTAGAGAGATGTGA       | 5607 |
| QY | 5641 | GAGATGATGTCTAGCAATACAGATGGAAGAGACGATTCATGGCTCCAAATCCTCCAG        | 5700 |
| Db | 5608 | GAGATGATGTCTAGCAATACAGATGGAAGAGACGATTCATGGCTCCAAATCCTCCAG        | 5667 |
| QY | 5701 | GTCCTCATACGCCAATCACTACTACTTTAAAAAGCAAGAGAGAAATATCTGCTGC          | 5760 |
| Db | 5668 | GTCCTCATACGCCAATCACTACTACTTTAAAAAGCAAGAGAGAAATATCTGCTGC          | 5727 |
| QY | 5761 | ATTATTCAGCGTGTACAGACGCCACTTTTAAACGGAACGTATAAACAGCTTCCCTT         | 5820 |
| Db | 5728 | ATTATTCAGCGTGTACAGACGCCACTTTTAAACGGAACGTATAAACAGCTTCCCTT         | 5787 |
| QY | 5821 | ACGTACATATAAAACAAATCAAAAGTGGGGCTAATCTCTTATAAAAGAACATATGATA       | 5880 |
| Db | 5788 | ACGTACATATAAAACAAATCAAAAGTGGGGCTAATCTCTTATAAAAGAACATATGATA       | 5847 |

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 ABL39689  
 ID ABL39689 standard; cDNA; 8131 BP.  
 AC ABL39689;  
 XX 10-MAY-2002 (first entry)  
 DT  
 XX Human sodium channel SCN1A encoding cDNA SEQ ID NO:1.  
 DE  
 XX Human: sodium channel; SCN1A: chromosome 2q24; gene; ss;  
 KM familial hypercalcaemic periodic paralysis; motor endplate disease.  
 XX Homo sapiens.  
 OS  
 FH Key Location/Qualifiers  
 FT CDS 15..6018  
 FT /tag= a  
 FT /product= "sodium channel SCN1A"  
 FT  
 FT  
 PN WO200196552-A1.  
 XX 20-DEC-2001.  
 PD  
 XX 12-JUN-2001; 2001WO-IP04956.  
 PF  
 XX 13-JUN-2000; 2000JP-0177540.  
 PR 13-JUN-2000; 2000JP-0177544.  
 XX  
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
 XX Kanazawa I, Goto J, Jeong S;  
 PI WPI; 2002-098066/13.  
 DR P-PDB; ABB06026.  
 DR  
 XX  
 PT Human sodium channels SCN1A and SCN3A and encoded genes, useful in  
 PT studying physiological mechanism in which excitant cells participate  
 PT and causes of diseases and developing drugs for motor endplate disease  
 PT  
 PT  
 XX  
 PS Claim 5; Page 20-40; 88pp; Japanese.  
 CC The present invention describes human sodium channels SCN1A and SCN3A.  
 CC The present sequence encodes the human sodium channel SCN1A. SCN1A and  
 CC SCN3A have been located to the human chromosome 2 long arm, positions  
 CC 2q24 and 2q24-31 respectively. The sodium channel proteins are useful  
 CC in studying the physiological mechanism in which excitant cells  
 CC participate and cause human diseases, and in developing remedies for  
 CC e.g. familial hypercalcaemic periodic paralysis of extremities and  
 CC motor endplate disease.  
 CC  
 SO Sequence 8131 BP; 2453 A; 1530 C; 1719 G; 2422 T; 7 other:  
 Query Match 98.1%; Score 5917.4; DB 24; Length 8131;  
 Best Local Similarity 99.1%; Pred. No. 0;  
 Matches 5960; Conservative 3; Mismatches 14; Indels 36; Gaps 2;  
 OY 1 ATGAGCAAAACAGTGTGATACACAGGACGTGACAGCTTCAACTTCTTACACAGAGAA 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

DB 19 ATGAGCAAAACAGTGTGATACACAGGACGTGACAGCTTCAACTTCTTACACAGAGAA 78  
 OY 61 TCTCTTCGGCGTATTGTAAGAACCGCATTCAGAAAGAAAGCAAGATCCCAACAGAC 120  
 DB 79 TCTCTTCGGCGTATTGTAAGAACCGCATTCAGAAAGAAAGCAAGATCCCAACAGAC 138  
 OY 121 AAAAAAGATGACAGCAAGAAATGGCCCAAGCCAAATATGACTTGGAAAGCTGAAAGAAC 180  
 DB 139 AAAAAAGATGACAGCAAGAAATGGCCCAAGCCAAATATGACTTGGAAAGCTGAAAGAAC 198  
 OY 181 CTTCATTTTATATGAGACATTCCTCCAGAGATGCTGACAGAGCCCTGGAGAGACCTG 240  
 DB 199 CTTCATTTTATATGAGACATTCCTCCAGAGATGCTGACAGAGCCCTGGAGAGACCTG 258  
 OY 241 GACCCCTACTATATCAATTAAGAAACTTTATATGATTTGAATTAAGGAGGACCATCTG 300  
 DB 259 GACCCCTACTATATCAATTAAGAAACTTTATATGATTTGAATTAAGGAGGACCATCTG 318  
 OY 301 CGGTTGAGTCCACCTCTGCGCTGTACATTTTAACCTCCCTTAATCCCTTAGGAAATA 360  
 DB 319 CGGTTGAGTCCACCTCTGCGCTGTACATTTTAACCTCCCTTAATCCCTTAGGAAATA 378  
 OY 361 GCTATTAAAGATTTGGTACATTCATTTATGACATGCTAATTTTGTGCACTATTTTGACA 420  
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 OY 481 TTCACAGAAATATATACCTTTGTAATCACTATTAATAATATTCAGAGGGATTCGTGTA 540  
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 OY 541 GAAGATTTTACTTTCCTTGGGATTCAGATGGAATCGCTGATTTTCATCTGATTAACATT 600  
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 OY 601 GCGTACGTCACAGATTTGAGACCTGGGCAATGTCGCGCATTTGAGAAACATTCAGAGTT 660  
 DB 619 GCGTACGTCACAGATTTGAGACCTGGGCAATGTCGCGCATTTGAGAAACATTCAGAGTT 678  
 OY 661 CTCGAGCATTTGAAGACGATTTCAATCCAGGCTGAGAAACATTTGTGGAGCCCTG 720  
 DB 679 CTCGAGCATTTGAAGACGATTTCAATCCAGGCTGAGAAACATTTGTGGAGCCCTG 738  
 OY 721 ATCCAGTCTGTGAAGAGCTCTAGATGTAATATCTGACTGTGCTGTGAGCGTA 780  
 DB 739 ATCCAGTCTGTGAAGAGCTCTAGATGTAATATCTGACTGTGCTGTGAGCGTA 798  
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 OY 1021 GATGACGGCCAAATGTCACAGAGGATATATGTGTGAAGAGCTGTAAGAAATCCCAATTA 1080  
 DB 1039 GATGACGGCCAAATGTCACAGAGGATATATGTGTGAAGAGCTGTAAGAAATCCCAATTA 1098  
 OY 1081 GGTATACAAAGCTTTGATACCTTCAAGTGGGCTTTTCTCTGTTTGACATTAATGACT 1140  
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Db 2641 AAGATCAATCGCAATTCGCGGGGCTCTGGGAATTTAACCCCTGCTTGGCCATATC 2700
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Db 3841 ACCAATGCTGTGTGTGCTGAGACTTCTTAATTTGATGATGATGATGATGATGATGATG 3900
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Db 4201 GAAAGAAATGAGACTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 4260
Qy 4261 GGGTATCTCTCTTCTTCAAGTGTGCAATTTCAAGATGATGATGATGATGATGATGATG 4320
Db 4261 GGGTATCTCTCTTCTTCAAGTGTGCAATTTCAAGATGATGATGATGATGATGATGATG 4320
Qy 4321 GCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4380
Db 4321 GCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4380
Qy 4381 CTTTACTTGTATTTTCTATCATCTTTGGGCTCTTCTTCACTGATGATGATGATGATG 4440
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Qy 4501 ACAGAAAGAAAGAAATATATATATGATGATGATGATGATGATGATGATGATGATGATG 4560
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Qy 4561 AAGCTATATACCTCGACAGAGAAATTTCAAGGAATGTTGACTTGTACACAGA 4620
Db 4561 AAGCTATATACCTCGACAGAGAAATTTCAAGGAATGTTGACTTGTACACAGA 4620
Qy 4621 CAAGTTTGTGATTAAGCATGATGATGATGATGATGATGATGATGATGATGATGATG 4680
Db 4621 CAAGTTTGTGATTAAGCATGATGATGATGATGATGATGATGATGATGATGATGATG 4680
Qy 4681 GAAACAGATGACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4740
Db 4681 GAAACAGATGACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4740
Qy 4741 ATTGTCTATTTTACGAGAGTGTACTGAAATGATGATGATGATGATGATGATGATGATG 4800
Db 4741 ATTGTCTATTTTACGAGAGTGTACTGAAATGATGATGATGATGATGATGATGATGATG 4800
Qy 4801 ACCATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4860
Db 4801 ACCATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4860
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4861 CTGGCCGAGCTGATAGAAAAGTATTTGCTGTCCTCCCTACCTGTCCTGAGATGATCCGCTTT 4920  
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 5161 ACACCTCTGCTGCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5220  
 5161 ACACCTCTGCTGCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5220  
 5221 TGTGACCTCTAATTAAGTTAACTCGGAGAGCTCACTTAAGGAGAGCTGTGGGACCAATCT 5280  
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 5281 GTTGGAAATTTCTTTTGTGAGTATGATGATGATGATGATGATGATGATGATGATGATG 5340  
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 5521 CTGCCACAACCAAAACAACTCCAGCTCATGTCATGATGATGATGATGATGATGATGATG 5580  
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 5581 CGGATCCACTGCTGCTGATATCTTATTTGCTTTTCAAAAGGGGCTTCAAGAGAGAGTGA 5640  
 5641 GAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5700  
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 5701 GTCCTCTATCAGCAATCACTACTACTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5760  
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 5761 ATTATTCAGCGCTGCTTACAGAGCCACCTTTTAAAGGGAAGTGTAAACAAGCTTCTTT 5820  
 5821 AGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5880  
 5821 AGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5880  
 5881 ATTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5940  
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 5941 ATTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5941

RESULT 8  
 AAD32840  
 ID AAD32840 standard; cDNA; 5889 BP.  
 XX  
 AC AAD32840;  
 XX  
 DT 01-JUL-2002 (first entry)  
 XX  
 DE Human ion channel cDNA #2.  
 XX  
 KW Human; novel human protein; NHP; voltage-gated sodium channel;  
 KW gene therapy; bioreactor; mental disorder; biological disorder;  
 KW gene; medical disorder; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PH Location/Qualifiers  
 FT 1..5889  
 FT CDS  
 FT /tag- a  
 FT /product= "Human ion channel protein #2"  
 FT /transl\_except= (pos:2941..2943, aa:Xaa)  
 FT /transl\_except= (pos:3166..3168, aa:Xaa)  
 FT /note= "Xaa = any amino acid"  
 XX  
 PN WO200214498-A2.  
 PD 21-FEB-2002.  
 XX  
 PF 15-AUG-2001; 2001WO-US25650.  
 XX  
 PR 16-AUG-2000; 2000US-225989P.  
 XX  
 PA (LEXI-) LEXICON GENETICS INC.  
 XX  
 PI Turner CA, Mathur B, Mathur D;  
 XX  
 DR WPI; 2002-280757/32.  
 DR P-PSDB; AAE20511.  
 XX  
 PT Novel polynucleotides encoding human sodium channel proteins,  
 PT particularly voltage-gated sodium channel proteins useful for drug  
 PT screening, diagnosis and in gene therapy of biological disorders  
 PS  
 PS Claim 1; Page 35-36; 83pp; English.  
 XX  
 CC The present sequence is a cDNA encoding novel human protein (NHP), ion  
 CC channel protein. NHP share structural similarity with mammalian sodium  
 CC channel proteins particularly voltage-gated sodium channel proteins.  
 CC NHP oligonucleotides are useful as hybridisation probes for screening  
 CC libraries and assessing gene expression patterns. Sequences derived  
 CC from regions adjacent to the intron/exon boundaries of NHP gene can be  
 CC used to design primers for use in amplification assays to detect  
 CC mutations within the exons, splice sites, introns that can be used in  
 CC diagnostics and pharmacogenomics. NHP nucleotide sequences are useful  
 CC for drug screening effective in the treatment of symptomatic or  
 CC phenotypic manifestations of perturbing the normal function of NHP in  
 CC the body, and nucleotide constructs encoding NHP products are useful to  
 CC genetically engineer host cells to express NHP products in vivo. These  
 CC delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion  
 CC protein to the body. Nucleotide construct encoding NHP products are  
 CC also useful in gene therapy for modulating NHP expression and to  
 CC produce genetically engineered host cells to express NHP products in  
 CC vivo. NHP nucleotide sequences may also be used as part of ribozyme  
 CC and/or tripeptide sequences that are useful for NHP gene regulation.  
 CC The NHP polypeptides are useful for generating antibodies, as  
 CC reagents in diagnostic assays, for identifying other cellular gene  
 CC products related to NHP and as reagents in assays for screening for  
 CC compounds that are useful in the treatment of mental, biological or  
 CC medical disorders and diseases.  
 CC  
 CC Sequence 5889 BP; 1733 A; 1161 C; 1313 G; 1679 T; 3 other;

Query Match 96.8%; Score 5839.8; DB 24; Length 5889;  
 Best Local Similarity 99.4%; Pred. No. 0;  
 Matches 5884; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

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QY 1 ATGAGCAACAGCTGTTGACACAGGACCTGACAGCTTCAACTCTTCCACGAGAA 60
DB 1 ATGAGCAACAGCTGTTGACACAGGACCTGACAGCTTCAACTCTTCCACGAGAA 60
QY 61 TCTCTGGGCTATTGAAAGAGCATTGACAGAAAGGCAAGAAATCCCAACGAGAC 120
DB 61 TCTCTGGGCTATTGAAAGAGCATTGACAGAAAGGCAAGAAATCCCAACGAGAC 120
QY 121 AAAAAAGATGACGAGAAATGCGCCCAAGCCAAATAGTACTTGGAAGCTGGAAGAAC 180
DB 121 AAAAAAGATGACGAGAAATGCGCCCAAGCCAAATAGTACTTGGAAGCTGGAAGAAC 180
QY 181 CTTCATTTTATTTATGAGACATCTCCAGAGATGGTGTAGAGCCCTGGAGAGACTG 240
DB 181 CTTCATTTTATTTATGAGACATCTCCAGAGATGGTGTAGAGCCCTGGAGAGACTG 240
QY 241 GACCCCTACTTATATCAATTAAGAAACTTTTATAGTATGATTAAGGGAAGGCCATCTTC 300
DB 241 GACCCCTACTTATATCAATTAAGAAACTTTTATAGTATGATTAAGGGAAGGCCATCTTC 300
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DB 301 CGGTTGAGTGCACCTCTGCCCTGTACATTTAACTCCCTTCAATCTCTTGAAGAAATA 360
QY 361 GCATTAAAGATTGTGATCATCTATATTCAGCATGCTAAATATGTGACATTTTGAACA 420
DB 361 GCATTAAAGATTGTGATCATCTATATTCAGCATGCTAAATATGTGACATTTTGAACA 420
QY 421 AACTGTGTGTTATGACAAATGATTAACCTCTGATTTGACAAAGAAATGTGAATACAC 480
DB 421 AACTGTGTGTTATGACAAATGATTAACCTCTGATTTGACAAAGAAATGTGAATACAC 480
QY 481 TTCACAGGAATATATCTTTTGAATCACTTAAATAATTTATGCAAGGGGATCTGTTTA 540
DB 481 TTCACAGGAATATATCTTTTGAATCACTTAAATAATTTATGCAAGGGGATCTGTTTA 540
QY 541 GAAATTTTCTCTCCCTGGGATCCAGAGAACTGGCTGCAATTCACATCTATATACATTT 600
DB 541 GAAATTTTCTCTCCCTGGGATCCAGAGAACTGGCTGCAATTCACATCTATATACATTT 600
QY 601 GCGTACGTCACAGAGATTGTGACCTGGGCAATGCTCGGATTTGAGAAACATTCAGAGTT 660
DB 601 GCGTACGTCACAGAGATTGTGACCTGGGCAATGCTCGGATTTGAGAAACATTCAGAGTT 660
QY 661 CTCGAGCATTTGAAGAGATTTCAATTCAGAGCCCTGAAGAACCATTTGGGAGCCCTG 720
DB 661 CTCGAGCATTTGAAGAGATTTCAATTCAGAGCCCTGAAGAACCATTTGGGAGCCCTG 720
QY 721 ATCCAGTCTGTGAAGAGCTCTCAGATATATGATCCTGACATGTCTGTCTGAGCTTA 780
DB 721 ATCCAGTCTGTGAAGAGCTCTCAGATATATGATCCTGACATGTCTGTCTGAGCTTA 780
QY 781 TTTCTCTAATTTGGGCTGACAGCTGTCTCATGAGCAACCTGAGAAATTAATGTATACATGG 840
DB 781 TTTCTCTAATTTGGGCTGACAGCTGTCTCATGAGCAACCTGAGAAATTAATGTATACATGG 840
QY 841 CCTCCACCAATGCTCTCTTGGAGAACATAGTATAGAAAAGAAATATTAACGTGAAATAT 900
DB 841 CCTCCACCAATGCTCTCTTGGAGAACATAGTATAGAAAAGAAATATTAACGTGAAATAT 900
QY 901 AATGCTACACTTAAATGAAGAACTGCTTTGAGTTGACTGGAAGTCAATATACAAAT 960
DB 901 AATGCTACACTTAAATGAAGAACTGCTTTGAGTTGACTGGAAGTCAATATACAAAT 960
QY 961 TCAAGATATCATATTTCTGAGAGGTTTTTATAGTCACTACTATGTGGAATAGCTCT 1020
DB 961 TCAAGATATCATATTTCTGAGAGGTTTTTATAGTCACTACTATGTGGAATAGCTCT 1020

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QY 1021 GATGAGGCCAATGTCAGAGGAAATATGTTGTGAAGGCTGTGAAGAAATCCCAATTT 1080
DB 1021 GATGAGGCCAATGTCAGAGGAAATATGTTGTGAAGGCTGTGAAGAAATCCCAATTT 1080
QY 1081 GGTACACAAAGCTTTGATACCTCAGTTGGGCTTTTGTCTTGTTCGATTAATGACT 1140
DB 1081 GGTACACAAAGCTTTGATACCTCAGTTGGGCTTTTGTCTTGTTCGATTAATGACT 1140
QY 1141 CAGGACTTGTGGAAATCTTTATCACTGATTAAGCTGTGCTGGAAAAAGTACATG 1200
DB 1141 CAGGACTTGTGGAAATCTTTATCACTGATTAAGCTGTGCTGGAAAAAGTACATG 1200
QY 1201 ATATTTTGTGTGTGATTTTCTGGGCTATTTCTACATTAATTAATTTGATCTGGCT 1260
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QY 1441 GACAGCTCATGTAAGCTCTAAGTGTGTCGAAGTGTGCTTAAGAAAGAAATATGG 1500
DB 1441 GACAGCTCATGTAAGCTCTAAGTGTGTCGAAGTGTGCTTAAGAAAGAAATATGG 1500
QY 1501 AGAAGAAAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATGATTC 1560
DB 1501 AGAAGAAAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATGATTC 1560
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QY 1741 GCAAGGATGTGGATCTGAGAACGATTCGAGATGATGACACAGCACCTTTGAGAT 1800
DB 1741 GCAAGGATGTGGATCTGAGAACGATTCGAGATGATGACACAGCACCTTTGAGAT 1800
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DB 1801 AACGAGAGCGGTAGAGATCTCTGTTTGGCCCGACACACAGGAGAGAGAGAGAGAG 1860
QY 1861 AACCTGATCAGACAGATGATCCGAGATGCTGAGAGTTCACAGCAATGGGAAG 1920
DB 1861 AACCTGATCAGACAGATGATCCGAGATGCTGAGAGTTCACAGCAATGGGAAG 1920
QY 1921 ATGCAACAGCTGTGATGCAATGTGTGTTTCTGTGTTGATGAGACCTTCACTTCT 1980
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QY 1981 ACATGCTCTGTGAGACACTTCTGCAAGAGTGAATATGATTAAGCACTACTATGAC 2040
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QY 2011 ---GGAACACACACTGAACTGAATGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAG 2067
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OY 2461 GCCATGGATCCTTACTATATTTCCAAAGAGGCTGGAATATCTTTGACGGTTTATGTTG 2520  
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OY 2941 CTAGTGTGCTGCAATCTCTTCTGGCTTGTGAGCTCATTTAGTSCAACAACCTT 3000  
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Db 3568 GGAAGAACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3627  
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Db 3748 TACATTTTCTGGAAGATGCTTCAAAATGGGAGCTATGATGATGATGATGATGATGATG 3807  
OY 3841 ACCAATGCTGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3900  
Db 3808 ACCAATGCTGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3867  
OY 3901 GCAAAATGCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3960  
Db 3868 GCAAAATGCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3927  
OY 3961 CTGAGACCTCTAAGAGCTTATCTGATTTGAAGGATGAGGCTGTGATGATGATGATGATG 4020  
Db 3928 CTGAGACCTCTAAGAGCTTATCTGATTTGAAGGATGAGGCTGTGATGATGATGATGATG 3987  
OY 4021 TTAGAGCAATTCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4080  
Db 3988 TTAGAGCAATTCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4047  
OY 4081 TTCAGATCATGGGCTAATTTGTTGCTGGCAATTTTACCATGATTAACACCA 4140  
Db 4048 TTCAGATCATGGGCTAATTTGTTGCTGGCAATTTTACCATGATTAACACCA 4107  
OY 4141 ACTGTGACAGTTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4200  
Db 4108 ACTGTGACAGTTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4167  
OY 4201 GAAAGAAATGAGACTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4260  
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OY 4261 GGGTATCTCTCTTGTCTTAATTTGCAATTCAAAGAGATGATGATGATGATGATGATGATGATG 4320  
Db 4228 GGGTATCTCTCTTGTCTTAATTTGCAATTCAAAGAGATGATGATGATGATGATGATGATGATGATG 4287  
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QY 4321 GCAGTTGATCCAGAAATGTGGAACTCCAGCTAAGATGAGAAGATCTGTACATGTAT 4380  
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 Db 4288 GCAGTTGATCCAGAAATGTGGAACTCCAGCTAAGATGAGAAGATCTGTACATGTAT 4347  
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 QY 4381 CTTTACTTTGTTATTTTCAATCTTTGGGTCCTTCTTCACTTGAACCTGTATTATGGT 4440  
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 Db 4348 CTTTACTTTGTTATTTTCAATCTTTGGGTCCTTCTTCACTTGAACCTGTATTATGGT 4407  
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 QY 4441 GTCATCATAGATTAATTTCAACACAGAGAAAAGATTTGGAGTCAAGACATCTTTATG 4500  
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 Db 4408 GTCATCATAGATTAATTTCAACACAGAGAAAAGATTTGGAGTCAAGACATCTTTATG 4467  
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 QY 4501 ACAGAGAAGCAAGAAATACTATATATGCAATGAAAAATTTAGATGAAAAACCCGAA 4560  
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 Db 4468 ACAGAGAAGCAAGAAATACTATATATGCAATGAAAAATTTAGATGAAAAACCCGAA 4527  
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 QY 4561 AAGCTTATCTCGACCAAGAAAACAAATTTCAAGGAATGGTCTTTGACTTGTACCAAGA 4620  
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 Db 4528 AAGCTTATCTCGACCAAGAAAACAAATTTCAAGGAATGGTCTTTGACTTGTACCAAGA 4587  
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 QY 4621 CAAGTTTTTGACATAGATCATGATCTCTGCTCTTAACATGATGACACATGATGATG 4680  
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 QY 4681 GAACAGATGACAGAGTGAATATGTACTACATTTTGTACAGCATCAATCTGTGTTC 4740  
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 Db 4648 GAACAGATGACAGAGTGAATATGTACTACATTTTGTACAGCATCAATCTGTGTTC 4707  
 |||||  
 QY 4741 ATTGTGCTATTACTGAGAGTGTGTACTGAACATCTCTCTAGCCATTTATTTT 4800  
 |||||  
 Db 4708 ATTGTGCTATTACTGAGAGTGTGTACTGAACATCTCTCTAGCCATTTATTTT 4767  
 |||||  
 QY 4801 ACCATTTGATGGAATTTTGTATTTGTGTGTCATCTCTCATTTGATGATGATG 4860  
 |||||  
 Db 4768 ACCATTTGATGGAATTTTGTATTTGTGTGTCATCTCTCATTTGATGATGATG 4827  
 |||||  
 QY 4861 CTTGCCGAGCTGATAGAAAATTTTGTGTGTGCCCTACCTGTTCCGAGTATCCGCTT 4920  
 |||||  
 Db 4828 CTTGCCGAGCTGATAGAAAATTTTGTGTGTGCCCTACCTGTTCCGAGTATCCGCTT 4887  
 |||||  
 QY 4921 GCTAGGATTTGGCCCAATCTTACGTCTGTATCAAAAGAGCAAAAGGGATTCGACCTGTC 4980  
 |||||  
 Db 4888 GCTAGGATTTGGCCCAATCTTACGTCTGTATCAAAAGAGCAAAAGGGATTCGACCTGTC 4947  
 |||||  
 QY 4981 TTTGCTTTGATGATGTCCCTCTCTGCGTTTAAACATCGGCTCTCACTCTTCTAGTC 5040  
 |||||  
 Db 4948 TTTGCTTTGATGATGTCCCTCTCTGCGTTTAAACATCGGCTCTCACTCTTCTAGTC 5007  
 |||||  
 QY 5041 ATGTTCATCTACGCCATCTTTGGAGTGTCAAACTTTGGCTATTTAAGAGGAAGTTGGG 5100  
 |||||  
 Db 5008 ATGTTCATCTACGCCATCTTTGGAGTGTCAAACTTTGGCTATTTAAGAGGAAGTTGGG 5067  
 |||||  
 QY 5101 ATGCATGACATGTTCAACTTTGAACCTTTGGCAACAGCATGATGCTTATTCGAAT 5160  
 |||||  
 Db 5068 ATGCATGACATGTTCAACTTTGAACCTTTGGCAACAGCATGATGCTTATTCGAAT 5127  
 |||||  
 QY 5161 ACAACCTCTGCTGGGATGATGTGTATGACACCAATTCACACAGTCAAGCCACCGAC 5220  
 |||||  
 Db 5128 ACAACCTCTGCTGGGATGATGTGTATGACACCAATTCACACAGTCAAGCCACCGAC 5187  
 |||||  
 QY 5221 TGTGACCTTAATAAGTTAACTGTGAAGTCACTTAAGGAGAGTGTGGAAACCAATCT 5280  
 |||||  
 Db 5188 TGTGACCTTAATAAGTTAACTGTGAAGTCACTTAAGGAGAGTGTGGAAACCAATCT 5247  
 |||||  
 QY 5281 GTTGAATTTTCTTTTGTGATACATCAATATCTCTGCTGTGTGTGAGACATG 5340  
 |||||  
 Db 5248 GTTGAATTTTCTTTTGTGATACATCAATATCTCTGCTGTGTGTGAGACATG 5307  
 |||||  
 QY 5341 TACATCGGCTCATCTGAGAGAACTTCAGTGTCTACTGTAAGAAATGCGACGCTCTG 5400  
 |||||  
 Db 5308 TACATCGGCTCATCTGAGAGAACTTCAGTGTCTACTGTAAGAAATGCGACGCTCTG 5367  
 |||||

QY 5401 AGTGAAGATGACCTTTGAGATGTTCTATGAGGTTTGGAGAAAGTTGATCCGATCACT 5460  
 |||||  
 Db 5368 AGTGAAGATGACCTTTGAGATGTTCTATGAGGTTTGGAGAAAGTTGATCCGATCACT 5427  
 |||||  
 QY 5461 CAGTTCAATGAAATTTGAAAAATTTATCTACAGTTTGCAGCTGGCGCTTGAACCCGCTCAAT 5520  
 |||||  
 Db 5428 CAGTTCAATGAAATTTGAAAAATTTATCTACAGTTTGCAGCTGGCGCTTGAACCCGCTCAAT 5487  
 |||||  
 QY 5521 CTGCCACAACCAAAACCTCCAGCTCATTTGCAATGATTTGGCCAGTGTAGTGAGAC 5580  
 |||||  
 Db 5488 CTGCCACAACCAAAACCTCCAGCTCATTTGCAATGATTTGGCCAGTGTAGTGAGAC 5547  
 |||||  
 QY 5581 CGGATCACTGTCTTGAATCTTATTTTGTCTTTTCAAAAGCGGGTTCTAGAGAGATGGA 5640  
 |||||  
 Db 5548 CGGATCACTGTCTTGAATCTTATTTTGTCTTTTCAAAAGCGGGTTCTAGAGAGATGGA 5607  
 |||||  
 QY 5641 GAGATGATGCTGTACAGAAATCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5700  
 |||||  
 Db 5608 GAGATGATGCTGTACAGAAATCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5667  
 |||||  
 QY 5701 GTCCTATACAGCCAACTACTACTTAAACAGAAAGAGAGAGAGAGATCTGTCTGTC 5760  
 |||||  
 Db 5668 GTCCTATACAGCCAACTACTACTTAAACAGAAAGAGAGAGAGAGATCTGTCTGTC 5727  
 |||||  
 QY 5761 ATTATTCAGCGTCTTACAGAGCGCACCTTTTAAAGCGAAGTGAACAGCTTCTCTT 5820  
 |||||  
 Db 5728 ATTATTCAGCGTCTTACAGAGCGCACCTTTTAAAGCGAAGTGAACAGCTTCTCTT 5787  
 |||||  
 QY 5821 ACCTACATTAATAAACAATTAAGTGGGGCTATCTCTTATTAAGAGAGATGATA 5880  
 |||||  
 Db 5788 ACCTACATTAATAAACAATTAAGTGGGGCTATCTCTTATTAAGAGAGATGATA 5847  
 |||||  
 QY 5881 ATTGACAGAAATTAATGAAGAACTATTATACAGAAAAA 5917  
 |||||  
 Db 5848 ATTGACAGAAATTAATGAAGAACTATTATACAGAAAAA 5884  
 |||||

## RESULT 9

AAD32846  
 ID AAD32846 standard; cDNA; 4362 BP.

AC AAD32846;

DT 01-JUL-2002 (first entry)

DE Human ion channel cDNA #8.

KW Human; novel human protein; NHP; voltage-gated sodium channel;

KW gene therapy; bioreactor; mental disorder; biological disorder;

OS Homo sapiens.

FH Key Location/Qualifiers

FT CDS

FT 1..4362

FT /\*tag= a /product= "Human ion channel protein #8"

FT /transl\_except= (pos:2974..2976, aa:Xaa)

FT /transl\_except= (pos:3199..3201, aa:Xaa)

FT /note= "Xaa = any amino acid"

PA (LEXI-) LEXICON GENETICS INC.

PI Turner CA, Mathur B, Mathur D;

XX



DR WPI: 2002-280757/32.  
 DR P-PSDB: AAE20517.

Novel polynucleotides encoding human sodium channel proteins,  
 particularly voltage-gated sodium channel proteins useful for drug  
 screening, diagnosis and in gene therapy of biological disorders -

Claim 1: Page 69-70; 83pp; English.

The present sequence is a cDNA encoding novel human protein (NHP), ion  
 channel protein. NHP share structural similarity with mammalian sodium  
 channel proteins particularly voltage-gated sodium channel proteins.  
 NHP oligonucleotides are useful as hybridisation probes for screening  
 libraries and assessing gene expression patterns. Sequences derived  
 from regions adjacent to the intron/exon boundaries of NHP gene can be  
 used to design primers for the in amplification assays to detect  
 mutations within the exons, splice sites, introns that can be used in  
 diagnostics and pharmacogenomics. NHP nucleotide sequences are useful  
 for drug screening effective in the treatment of symptomatic or  
 phenotypic manifestations of perturbing the normal function of NHP in  
 the body, and nucleotide constructs encoding NHP products are useful to  
 genetically engineer host cells to express NHP products in vivo. These  
 genetically engineered cells function as bioreactors in the body  
 delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion  
 protein to the body. Nucleotide construct encoding NHP products are  
 also useful in gene therapy for modulating NHP expression and to  
 produce genetically engineered host cells to express NHP products in  
 vivo. NHP nucleotide sequences may also be used as part of ribozyme  
 and/or triple helix sequences that are useful for NHP gene regulation.  
 The NHP polypeptides are useful for generating antibodies, as  
 reagents in diagnostic assays, for identifying other cellular gene  
 products related to NHP and as reagents in assays for screening for  
 compounds that are useful in the treatment of mental, biological or  
 medical disorders and diseases.

Sequence 4362 BP; 1300 A; 845 C; 995 G; 1219 T; 3 other;

Query Match 71.9%; Score 4336.8; DB 24; Length 4362;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAGCAAAAGAGTGTGTACACAGAGAGCTGACAGCTTCACTTCTTACACAGAA 60  
 DB 1 ATGGAGCAAAAGAGTGTGTACACAGAGAGCTGACAGCTTCACTTCTTACACAGAA 60  
 QY 61 TCTCTGGCGCTATTGGAAGAGCATTGAGAAAGAAAGCAAGAAATCCCAACAGAC 120  
 DB 61 TCTCTGGCGCTATTGGAAGAGCATTGAGAAAGAAAGCAAGAAATCCCAACAGAC 120  
 QY 121 AAAAAAGATGAGAGCAAGAAATGGCCCAAAAGCAAAATAGTACTTGAAGCTGGAAAGAC 180  
 DB 121 AAAAAAGATGAGAGCAAGAAATGGCCCAAAAGCAAAATAGTACTTGAAGCTGGAAAGAC 180  
 QY 181 CTTCATTATTATGAGAGCAATCTCTCCAGAGATGGTGTGAGAGCCCTGAGAGACCTG 240  
 DB 181 CTTCATTATTATGAGAGCAATCTCTCCAGAGATGGTGTGAGAGCCCTGAGAGACCTG 240  
 QY 241 GACCCCTACTATATCAATTAAGAAACTTTATAGTATGAAATGAAGAGGCACTTCC 300  
 DB 241 GACCCCTACTATATCAATTAAGAAACTTTATAGTATGAAATGAAGAGGCACTTCC 300  
 QY 301 CGGTTAGTGACACCTCTCCCTGTACATTTAACTCCCTCAATCTCTTGAAGAAATA 360  
 DB 301 CGGTTAGTGACACCTCTCCCTGTACATTTAACTCCCTCAATCTCTTGAAGAAATA 360  
 QY 361 GCTATTAATTTGGTATATCATATTCAGATGCTAATTAATGAGCTATTTGACA 420  
 DB 361 GCTATTAATTTGGTATATCATATTCAGATGCTAATTAATGAGCTATTTGACA 420  
 QY 421 AACTGTGTATTGACAAATGAGTAACCTCCGATTTGAGCAAGAGATGAGTAATACAC 480  
 DB 421 AACTGTGTATTGACAAATGAGTAACCTCCGATTTGAGCAAGAGATGAGTAATACAC 480

QY 481 TTCACAGGAATATATACCTTTTGAATCACTTATATAAATATATGCAAGGGGATCTGTTA 540  
 DB 481 TTCACAGGAATATATACCTTTTGAATCACTTATATAAATATATGCAAGGGGATCTGTTA 540  
 QY 541 GAAAGATTTTACCTTCCCTCGGAGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600  
 DB 541 GAAAGATTTTACCTTCCCTCGGAGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600  
 QY 601 GCGTACGTACAGAGATTTGAGACCTGGGCAATGCTCGGCAATGAGAAATTCAGAGAT 660  
 DB 601 GCGTACGTACAGAGATTTGAGACCTGGGCAATGCTCGGCAATGAGAAATTCAGAGAT 660  
 QY 661 CTCCAGAGATTTAAGAGATTTTCACTTCCAGAGCTTGAAGAAATTCAGAGAGAGAG 720  
 DB 661 CTCCAGAGATTTAAGAGATTTTCACTTCCAGAGCTTGAAGAAATTCAGAGAGAGAG 720  
 QY 721 ATCCAGATGTTGAAAG 780  
 DB 721 ATCCAGATGTTGAAAG 780  
 QY 781 TTTGCTTAATTTGGGCTGAGAGCTTTCATGAGGCAACCTGAGAGAAATATATACAGT 840  
 DB 781 TTTGCTTAATTTGGGCTGAGAGCTTTCATGAGGCAACCTGAGAGAAATATATACAGT 840  
 QY 841 CCTCCACCAATGCTTCTTGGAGAGACATATATGAAAGAAATATATATATATATAT 900  
 DB 841 CCTCCACCAATGCTTCTTGGAGAGACATATATGAAAGAAATATATATATATATATAT 900  
 QY 901 AATGATACAT 960  
 DB 901 AATGATACAT 960  
 QY 961 TCAAGATATCAT 1020  
 DB 961 TCAAGATATCAT 1020  
 QY 1021 GATGAGGCAATATGTCAGAGAGAGATATATATATATATATATATATATATATATAT 1080  
 DB 1021 GATGAGGCAATATGTCAGAGAGAGATATATATATATATATATATATATATATATATAT 1080  
 QY 1081 GGTCTACAGAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140  
 DB 1081 GGTCTACAGAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140  
 QY 1141 CAGGACTTCTGGGAAAT 1200  
 DB 1141 CAGGACTTCTGGGAAAT 1200  
 QY 1201 AATATTTTGTGTGTGATATTTTCTTGGGCTATTTCTATATATATATATATATATAT 1260  
 DB 1201 AATATTTTGTGTGTGATATTTTCTTGGGCTATTTCTATATATATATATATATATATAT 1260  
 QY 1261 GT 1320  
 DB 1261 GT 1320  
 QY 1321 GAGGCGAATTTACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380  
 DB 1321 GAGGCGAATTTACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380  
 QY 1381 GAGGCAAGGCAATGCTGCAAGAGATTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440  
 DB 1381 GAGGCAAGGCAATGCTGCAAGAGATTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440  
 QY 1441 GACAGCTATCTGAG 1500  
 DB 1441 GACAGCTATCTGAG 1500  
 QY 1501 AGGAG 1560  
 DB 1501 AGGAG 1560  
 QY 1561 CAAAAATCTGAATCTGAG 1620



|    |      |   |      |
|----|------|---|------|
| Db | 1561 | CAAAAATCTGATATCTGGAGACAGATCTAGAGGAAAGTTTTCGGCTCTCCACATTGAAGG    | 1620 |
| Qy | 1621 | AACCGATTGACATATTTGAAGAGAGTACTCCCTCCCAACAGACTTTGTGAGCAATCCGT     | 1680 |
| Db | 1621 | AACCGATTGACATATTTGAAGAGAGTACTCCCTCCCAACAGACTTTGTGAGCAATCCGT     | 1680 |
| Qy | 1681 | GCGTCCCTATTTTACCAAGGCGAAATATGACAAACAGCTTTTACGCTTTAGAGGCGA       | 1740 |
| Db | 1681 | GCGTCCCTATTTTACCAAGGCGCGAAATATGACAAACAGCTTTTACGCTTTAGAGGCGA     | 1740 |
| Qy | 1741 | GCAAGGATGTGGGATCTGTGAAGACGACTTCGCGAGATGATGACACAGCACTTTAGGAT     | 1800 |
| Db | 1741 | GCAAGGATGTGGGATCTGTGAAGACGACTTCGCGAGATGATGACACAGCACTTTAGGAT     | 1800 |
| Qy | 1801 | AACGAGACCGGTAGAGATTTCTTGTGTTGTGCCCGACGACAGGAGAGAGACGCAACAGC     | 1860 |
| Db | 1801 | AACGAGACCGGTAGAGATTTCTTGTGTTGTGCCCGACGACAGGAGAGAGACGCAACAGC     | 1860 |
| Qy | 1861 | AACCTGATGACAGACCACTAGTATCCTCCGAGTGTGGCAGTGTTCACAGATGGAG         | 1920 |
| Db | 1861 | AACCTGATGACAGACCACTAGTATCCTCCGAGTGTGGCAGTGTTCACAGATGGAG         | 1920 |
| Qy | 1921 | ATGACACGACACTGTGGATTGCAATGTGTGTCTTCTGTGTGTGTGACCTTCACTTCT       | 1980 |
| Db | 1921 | ATGACACGACACTGTGGATTGCAATGTGTGTCTTCTGTGTGTGTGACCTTCACTTCT       | 1980 |
| Qy | 1981 | ACATGCGCTGTGGACAGCTTTCGACAGAGGTATTAATGATTAAGCAGCTCTGATAC        | 2040 |
| Db | 1981 | ACATGCGCTGTGGACAGCTTTCGACAGAGGTATTAATGATTAAGCAGCTCTGATAC        | 2040 |
| Qy | 2041 | AATGGAACAACCACTGAACTGAAATGAGAAAGAGGTCAAGTCTTCCACGCTTTC          | 2100 |
| Db | 2041 | AATGGAACAACCACTGAACTGAAATGAGAAAGAGGTCAAGTCTTCCACGCTTTC          | 2100 |
| Qy | 2101 | ATGACATTTCTAGAAATCTCTTCCCAAGGCAACGACAAATGATATAGCCACGATTTCA      | 2160 |
| Db | 2101 | ATGACATTTCTAGAAATCTCTTCCCAAGGCAACGACAAATGATATAGCCACGATTTCA      | 2160 |
| Qy | 2161 | ACAATATCAGTAGAAGAACTTGAAGATCCAGGACAAATAGCCACCCGTTGGATATA        | 2220 |
| Db | 2161 | ACAATATCAGTAGAAGAACTTGAAGATCCAGGACAAATAGCCACCCGTTGGATATA        | 2220 |
| Qy | 2221 | TTTTCCAACATATCTTAAATCTGGGACTGTTCATATTTGGTTAAAGTGAACATGTT        | 2280 |
| Db | 2221 | TTTTCCAACATATCTTAAATCTGGGACTGTTCATATTTGGTTAAAGTGAACATGTT        | 2280 |
| Qy | 2281 | GTCACCTGGTGTGTATGAGACCATTGTGTGACCTGGCCATCACCATCTGATTTGTCTTA     | 2340 |
| Db | 2281 | GTCACCTGGTGTGTATGAGACCATTGTGTGACCTGGCCATCACCATCTGATTTGTCTTA     | 2340 |
| Qy | 2341 | AATATCTTTTCAAGGGCAGAGGACACTATCCAAATAGGAGCAATTTCAATATGTGTT       | 2400 |
| Db | 2341 | AATATCTTTTCAAGGGCAGAGGACACTATCCAAATAGGAGCAATTTCAATATGTGTT       | 2400 |
| Qy | 2401 | ACAGTAGGAACACTGTGTTTACCTGGGATCTTTACAGCAAAATGTTTCTGAAATATT       | 2460 |
| Db | 2401 | ACAGTAGGAACACTGTGTTTACCTGGGATCTTTACAGCAAAATGTTTCTGAAATATT       | 2460 |
| Qy | 2461 | GCCATGATCCTTACTATTTATTTTCCAAAGAGCTGGAATATCTTTAGCGTTTTATGTG      | 2520 |
| Db | 2461 | GCCATGATCCTTACTATTTATTTTCCAAAGAGCTGGAATATCTTTAGCGTTTTATGTG      | 2520 |
| Qy | 2521 | ACGCTTAGCCTGTGTAACACTTGGACATCTGCCAAATGTGAAGGATATATCTGTTCTCGTTCA | 2580 |
| Db | 2521 | ACGCTTAGCCTGTGTAACACTTGGACATCTGCCAAATGTGAAGGATATATCTGTTCTCGTTCA | 2580 |
| Qy | 2581 | TTTGATATGCTGCAGATTTTCAAGTTGGCCAAATCTTGGCCAAAGCTTAAATATGCTATA    | 2640 |
| Db | 2581 | TTTGATATGCTGCAGATTTTCAAGTTGGCCAAATCTTGGCCAAAGCTTAAATATGCTATA    | 2640 |
| Qy | 2641 | AAGATCATCGGCAATTCCTGTGGGGGCTCTGGGAAATTAACCTGTCTGTGGCAATCATC     | 2700 |
| Db | 2641 | AAGATCATCGGCAATTCCTGTGGGGGCTCTGGGAAATTAACCTGTCTGTGGCAATCATC     | 2700 |

|   |      |   |      |
|---|------|---|------|
| D | 2641 | AAAGTATCGGCAATTCGGTGGGGGCTCTGGGAAATTTAACCTGTCTTGCCATCATC      | 2700 |
| Q | 2701 | GTCTTCATTTTTGGCGGTGTGGCATGCAGCTCTTGTGTAAAGCTACAAAGATTTGTGC    | 2760 |
| D | 2701 | GTCTTCATTTTTGGCGGTGTGGCATGCAGCTCTTGTGTAAAGCTACAAAGATTTGTGC    | 2760 |
| Q | 2761 | TGCAAGATCGCGAGTGATTGTCAATCCACAGCTGGCACATGATATGACTTCTTCACATC   | 2820 |
| D | 2761 | TGCAAGATCGCGAGTGATTGTCAATCCACAGCTGGCACATGATATGACTTCTTCACATC   | 2820 |
| Q | 2821 | TTCCCTGATTTGTTCGGCGCTGTGGGGAGTGGATTTGAACCATGTGGGACGTGTG       | 2880 |
| D | 2821 | TTCCCTGATTTGTTCGGCGCTGTGGGGAGTGGATTTGAACCATGTGGGACGTGTG       | 2880 |
| Q | 2881 | GAGTTGCTGTGTAAGGCATGTGCCCTTACTGTCTTCATGATGTGCATGTGTGAATC      | 2940 |
| D | 2881 | GAGTTGCTGTGTAAGGCATGTGCCCTTACTGTCTTCATGATGTGCATGTGTGAATC      | 2940 |
| Q | 2941 | CTAGTGTCTGTAATCTCTTCTGGCCTTGTGTGAGCTATTTAGTGCAGACACCTT        | 3000 |
| D | 2941 | CTAGTGTCTGTAATCTCTTCTGGCCTTGTGTGAGCTATTTAGTGCAGACACCTT        | 3000 |
| Q | 3001 | GCACCCACTATGATGATATGAAATGAATATCTCCAAATTTGCTGTGATAGATGCAC      | 3060 |
| D | 3001 | GCACCCACTATGATGATATGAAATGAATATCTCCAAATTTGCTGTGATAGATGCAC      | 3060 |
| Q | 3061 | AAAGGATAGCTTATGTGAAAGAAATATATGAAATTTATCAACAGCTCTTCATTTAG      | 3120 |
| D | 3061 | AAAGGATAGCTTATGTGAAAGAAATATATGAAATTTATCAACAGCTCTTCATTTAG      | 3120 |
| Q | 3121 | AAACAAAGATTTTATGATGAATTTAAACACTTGATGATCTTAACACAGAAAGACGT      | 3180 |
| D | 3121 | AAACAAAGATTTTATGATGAATTTAAACACTTGATGATCTTAACACAGAAAGACGT      | 3180 |
| Q | 3181 | TGTATGTCCCAATCATACARCAAGAAATTTGGGAAAGATCTTGACTATCTTAAGATGTAAT | 3240 |
| D | 3181 | TGTATGTCCCAATCATACARCAAGAAATTTGGGAAAGATCTTGACTATCTTAAGATGTAAT | 3240 |
| Q | 3241 | GGAACCTCAAGTGGTATAGCAACTGGCAGCAGTGTGAAATATACATTATTGATGAAAGT   | 3300 |
| D | 3241 | GGAACCTCAAGTGGTATAGCAACTGGCAGCAGTGTGAAATATACATTATTGATGAAAGT   | 3300 |
| Q | 3301 | GATTACATGTCAATCATAAACAACCCAGCTCTTACTGTGACTGTACCAATTTGCTGTAGA  | 3360 |
| D | 3301 | GATTACATGTCAATCATAAACAACCCAGCTCTTACTGTGACTGTACCAATTTGCTGTAGA  | 3360 |
| Q | 3361 | GAACTCACTTTGAAATTTTAAACAGGAAAGCTTTAGTAGGAATCGGATCTGGAAAT      | 3420 |
| D | 3361 | GAACTCACTTTGAAATTTTAAACAGGAAAGCTTTAGTAGGAATCGGATCTGGAAAT      | 3420 |
| Q | 3421 | AGCAAAAGAAACGATGAAAGACAGTACGTATCGAAGGTAGCACTGTGCACATCGCC      | 3480 |
| D | 3421 | AGCAAAAGAAACGATGAAAGACAGTACGTATCGAAGGTAGCACTGTGCACATCGCC      | 3480 |
| Q | 3481 | GCACCTGTAGAAAGACAGCCCGGTAGTGAACCGTGAAGAAACCTTTGAACCGAAGCTGT   | 3540 |
| D | 3481 | GCACCTGTAGAAAGACAGCCCGGTAGTGAACCGTGAAGAAACCTTTGAACCGAAGCTGT   | 3540 |
| Q | 3541 | TTTCACTGAAAGCTGTGTACAAAGATTTCAAGTGTGTCAATCAATCAATGTGGAAGAGCGA | 3600 |
| D | 3541 | TTTCACTGAAAGCTGTGTACAAAGATTTCAAGTGTGTCAATCAATCAATGTGGAAGAGCGA | 3600 |
| Q | 3601 | GGAAACAAATGTGTGAACCGTGAAGAGCTGTCCCAATAGTTGAACATTAACGTGTT      | 3660 |
| D | 3601 | GGAAACAAATGTGTGAACCGTGAAGAGCTGTCCCAATAGTTGAACATTAACGTGTT      | 3660 |
| Q | 3661 | GAGACCTTCAATTTTTCATGATTTCTCTTAGTAGTGGGCTCTGGCAATTTGAAGATTA    | 3720 |
| D | 3661 | GAGACCTTCAATTTTTCATGATTTCTCTTAGTAGTGGGCTCTGGCAATTTGAAGATTA    | 3720 |
| Q | 3721 | TATATTTATCAGCGAAAGACGATTTAAGACGATTTTGAATATGCTGACAGGTTTTCACT   | 3780 |
| D | 3721 | TATATTTATCAGCGAAAGACGATTTAAGACGATTTTGAATATGCTGACAGGTTTTCACT   | 3780 |



QY 421 AACTGCTGTTATGACAAATGACCTCTGATTGACAAAGAAATGATACACC 480  
|||||  
Db 421 AACTGCTGTTATGACAAATGACCTCTGATTGACAAAGAAATGATACACC 480  
QY 481 TTCACAGCAATATATACCTTTTGAATCACTTATATAAATTTATGCAAGGAGATTTCTTTA 540  
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Db 481 TTCACAGCAATATATACCTTTTGAATCACTTATATAAATTTATGCAAGGAGATTTCTTTA 540  
QY 541 GAAGATTTTACCTTCTGCGGATTCACATGCAAGCTGCTGATTTCACTGTATACATTT 600  
|||||  
Db 541 GAAGATTTTACCTTCTGCGGATTCACATGCAAGCTGCTGATTTCACTGTATACATTT 600  
QY 601 GCGTACGTACAGAGTTTGTGACCTGGGCAATGTCTCGGCAATGAGCAATTCACAGTT 660  
|||||  
Db 601 GCGTACGTACAGAGTTTGTGACCTGGGCAATGTCTCGGCAATGAGCAATTCACAGTT 660  
QY 661 CTCGAGCATTTGAGAGCATTTTCACTTCAGGCTGAAAAACATTTGAGGAGCCCTG 720  
|||||  
Db 661 CTCGAGCATTTGAGAGCATTTTCACTTCAGGCTGAAAAACATTTGAGGAGCCCTG 720  
QY 721 ATCCAGCTGTGAGAGAGCTCTCAGATGTATGATCCTGATCTGTCTGAGCGTA 780  
|||||  
Db 721 ATCCAGCTGTGAGAGAGCTCTCAGATGTATGATCCTGATCTGTCTGAGCGTA 780  
QY 781 TTTGCTCTATTTGGGCTGACAGCTGTTCATGAGGCACTTGAAGCAATATGATACATG 840  
|||||  
Db 781 TTTGCTCTATTTGGGCTGACAGCTGTTCATGAGGCACTTGAAGCAATATGATACATG 840  
QY 841 CCGCCACCAATGCTCTCTTGAGAGCAATGATGAAAAAGAAATTAATCTGATTTAT 900  
|||||  
Db 841 CCGCCACCAATGCTCTCTTGAGAGCAATGATGAAAAAGAAATTAATCTGATTTAT 900  
QY 901 AATGTACACTTATTAATGAAACTGTCTTGAATTTGACTGGAATCATATATTAAGAT 960  
|||||  
Db 901 AATGTACACTTATTAATGAAACTGTCTTGAATTTGACTGGAATCATATATTAAGAT 960  
QY 961 TCAAGATATCATTTATCTCTGAGAGGTTTTTATGATGACACTATGATGGAATTAAGTCT 1020  
|||||  
Db 961 TCAAGATATCATTTATCTCTGAGAGGTTTTTATGATGACACTATGATGGAATTAAGTCT 1020  
QY 1021 GATGAGGCAATGTCACAGAGGATATGATGTAAGAGCTGTGAAATCCCAATTAAT 1080  
|||||  
Db 1021 GATGAGGCAATGTCACAGAGGATATGATGTAAGAGCTGTGAAATCCCAATTAAT 1080  
QY 1081 GGTACACAGCTTTGATACCTTCAGTTGGGCTTTTGTCTGTTGAGACTAATGACT 1140  
|||||  
Db 1081 GGTACACAGCTTTGATACCTTCAGTTGGGCTTTTGTCTGTTGAGACTAATGACT 1140  
QY 1141 CAGGACTTGTGAAAAATCTTTATACACTGACATTAAGTGTCTGTGGAAGAGCTACATG 1200  
|||||  
Db 1141 CAGGACTTGTGAAAAATCTTTATACACTGACATTAAGTGTCTGTGGAAGAGCTACATG 1200  
QY 1201 AATATTTTGTGTGTGCTATTTCTGAGGCTCATTTACTATAAATTTGATCTGGCT 1260  
|||||  
Db 1201 AATATTTTGTGTGTGCTATTTCTGAGGCTCATTTACTATAAATTTGATCTGGCT 1260  
QY 1261 GTGTGTGCAATGCTCTACAGAGCAAGAAATCAGGCACTTGAAGAGAGCAAGAA 1320  
|||||  
Db 1261 GTGTGTGCAATGCTCTACAGAGCAAGAAATCAGGCACTTGAAGAGAGCAAGAA 1320  
QY 1321 GAGGCGCAATTTACAGAGATGATTAACAGCTTTAAAAAGCAAGAGAGGAGCTCAGAC 1380  
|||||  
Db 1321 GAGGCGCAATTTACAGAGATGATTAACAGCTTTAAAAAGCAAGAGAGGAGCTCAGAC 1380  
QY 1381 GAGGCAAGGCAATGCTCTCAGAGCAATTCAGAGAGCCAGTGTGAGGAGGCTCTCA 1440  
|||||  
Db 1381 GAGGCAAGGCAATGCTCTCAGAGCAATTCAGAGAGCCAGTGTGAGGAGGCTCTCA 1440  
QY 1441 GACAGCTCATTTGAGAGCTCTTAAGTTGATTTCAAGAGTGTCTAAGAGAAAGAAATTCGG 1500  
|||||  
Db 1441 GACAGCTCATTTGAGAGCTCTTAAGTTGATTTCAAGAGTGTCTAAGAGAAAGAAATTCGG 1500

QY 1501 AGGAGAAAAAGAAACAGAAAGAGACAGTCTGTGTGGGAGAGAAAGATGAGATTC 1560  
|||||  
Db 1501 AGGAGAAAAAGAAACAGAAAGAGACAGTCTGTGTGGGAGAGAAAGATGAGATTC 1560  
QY 1561 CAAAAATCTGAAATCTGAGAGACAGCATTCAGAGAGAAAGTTTGTCTTCATTTGAAGG 1620  
|||||  
Db 1561 CAAAAATCTGAAATCTGAGAGACAGCATTCAGAGAGAAAGTTTGTCTTCATTTGAAGG 1620  
QY 1621 AACGATTTGACATATGAAAAAGAGTACTCTCCACACAGCTTTGTTGAGATTCCT 1680  
|||||  
Db 1621 AACGATTTGACATATGAAAAAGAGTACTCTCCACACAGCTTTGTTGAGATTCCT 1680  
QY 1681 GGTCTCCTATTTTACCAAGAGGAAATGAGAGAAAGGCTTTTACGCTTTAGAGGCGA 1740  
|||||  
Db 1681 GGTCTCCTATTTTACCAAGAGGAAATGAGAGAAAGGCTTTTACGCTTTAGAGGCGA 1740  
QY 1741 GCAAGAGATGAGGATCTGAGAGAGCTTCTGAGATGATGAGCAGACACTTTGAGAT 1800  
|||||  
Db 1741 GCAAGAGATGAGGATCTGAGAGAGCTTCTGAGATGATGAGCAGACACTTTGAGAT 1800  
QY 1801 AACGAGAGCCGTGAGATCTCTGTTTGTGCCCCGAGACAGAGAGAGAGCAACAGC 1860  
|||||  
Db 1801 AACGAGAGCCGTGAGATCTCTGTTTGTGCCCCGAGACAGAGAGAGAGCAACAGC 1860  
QY 1861 AACCTGATGAGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920  
|||||  
Db 1861 AACCTGATGAGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920  
QY 1921 ATGACAGACACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980  
|||||  
Db 1921 ATGACAGACACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980  
QY 1981 ACATGCTCTGTGAGACAGTCTGTGAGAGAGGATGATGATGATGATGATGATGATGAT 2040  
|||||  
Db 1981 ACATGCTCTGTGAGACAGTCTGTGAGAGAGGATGATGATGATGATGATGATGATGAT 2040  
QY 2041 AATGSAACCAACCACTGAAATGAAATGAAAGAGAGGATGATGATGATGATGATGATGAT 2100  
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Db 2041 AATGSAACCAACCACTGAAATGAAATGAAAGAGAGGATGATGATGATGATGATGATGAT 2100  
QY 2101 ATGAGACTTCTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2160  
|||||  
Db 2101 ATGAGACTTCTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2160  
QY 2161 ACAAAATACAGTACAGAGAACTGAAAGATTCAGAGAGCAAGATGCCACCTGTGTATATA 2220  
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Db 2161 ACAAAATACAGTACAGAGAACTGAAAGATTCAGAGAGCAAGATGCCACCTGTGTATATA 2220  
QY 2221 TTTTCCAAATATTTCTTAATCTGGGACTGTCTCCATATGTTGTTAAAGTGAAGCAATGTT 2280  
|||||  
Db 2221 TTTTCCAAATATTTCTTAATCTGGGACTGTCTCCATATGTTGTTAAAGTGAAGCAATGTT 2280  
QY 2281 GTCAAGCTGTGTGATGAGAGCAATTTGTTGAGCTGTGCAATGATGTTAAAGTGAAGCAATGTT 2340  
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Db 2281 GTCAAGCTGTGTGATGAGAGCAATTTGTTGAGCTGTGCAATGATGTTAAAGTGAAGCAATGTT 2340  
QY 2341 AATATCTTTTTCATGAGGATGAGACACTATTCATGAGAGCAATTTCAATTAATGCTT 2400  
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Db 2341 AATATCTTTTTCATGAGGATGAGACACTATTCATGAGAGCAATTTCAATTAATGCTT 2400  
QY 2401 ACAGTACAGAACTTTGTTTCACTGAGATCTTTACAGCAAGATGTTTCTGAAATTAAT 2460  
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Db 2401 ACAGTACAGAACTTTGTTTCACTGAGATCTTTACAGCAAGATGTTTCTGAAATTAAT 2460  
QY 2461 GCAATGATCTTCTATTTATTTTTCAGAGAGGCTGAAATGCTTTGAGGCTTTTATGTTG 2520  
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Db 2461 GCAATGATCTTCTATTTATTTTTCAGAGAGGCTGAAATGCTTTGAGGCTTTTATGTTG 2520  
QY 2521 ACCTTACCTGTGATGACTGAGCTGCAATGTGAGAGATTAATCTGTTCTCCGTTCA 2580  
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Db 2521 ACCTTACCTGTGATGACTGAGCTGCAATGTGAGAGATTAATCTGTTCTCCGTTCA 2580  
QY 2581 TTTGAGTTGCTGAGAGTTTTCAGTGTGCAAAATCTTGTGCAACGTTAAATATGCTATA 2640  
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Db 2548 TTTGATGCTGCGAGTTTTCAGTTGGCAAAATCTGGCAACGTTAAATATGCTATA 2607
Oy 2641 AAGATATGCGCAATTCCTGGGGGCTGGAATTAATTAACCTCGTGGCCATCATC 2700
Db 2608 AAGATATGCGCAATTCCTGGGGGCTGGAATTAATTAACCTCGTGGCCATCATC 2667
Oy 2701 GTCCTCAATTTTGGCCGTGGGAGTCAGCTCTTTGGTAAAGCTACAAAGATTGTGC 2760
Db 2668 GTCCTCAATTTTGGCCGTGGGAGTCAGCTCTTTGGTAAAGCTACAAAGATTGTGC 2727
Oy 2761 TGCAGATGCGCAGTATGTCATCCACAGCTGGCAGCATGATGCTTCCACTCC 2820
Db 2728 TGCAGATGCGCAGTATGTCATCCACAGCTGGCAGCATGATGCTTCCACTCC 2787
Oy 2821 TTTCTGATTTGTTCCTGGCTGCTGTGGGAGTGTAGAGACATGTTGGACTATG 2880
Db 2788 TTTCTGATTTGTTCCTGGCTGCTGTGGGAGTGTAGAGACATGTTGGACTATG 2847
Oy 2881 GAGGTGCTGTGTCAGCCATGTCCTTACTGTCATGATGTCATGTCATGTCATG 2940
Db 2848 GAGGTGCTGTGTCAGCCATGTCCTTACTGTCATGATGTCATGTCATGTCATG 2907
Oy 2941 CTAGTGCTGCTGATATCTTTCTGGCTGCTTTGAGCTCATTTAGTGCAGAACCTT 3000
Db 2908 CTAGTGCTGCTGATATCTTTCTGGCTGCTTTGAGCTCATTTAGTGCAGAACCTT 2967
Oy 3001 GCAGCCATGATGATATGTAATGTAATATCTCAATGCTGTGGATAGATGACAC 3060
Db 2968 GCAGCCATGATGATATGTAATGTAATATCTCAATGCTGTGGATAGATGACAC 3027
Oy 3061 AAGAGTATGCTTATGTAAGAAATATATGTAATTTATTCACAGTCTTCATTAG 3120
Db 3028 AAGAGTATGCTTATGTAAGAAATATATGTAATTTATTCACAGTCTTCATTAG 3087
Oy 3121 AAACAAAGATTTTATGTAATTAACCACTGATGATTAACCAAGAAAGACAGT 3180
Db 3088 AAACAAAGATTTTATGTAATTAACCACTGATGATTAACCAAGAAAGACAGT 3147
Oy 3181 TGTATGCTCAATCATACACAGAAATTTGGAAAGATCTTACTATCTTAAAGATTAAT 3240
Db 3148 TGTATGCTCAATCATACACAGAAATTTGGAAAGATCTTACTATCTTAAAGATTAAT 3207
Oy 3241 GGAATCTACAGTGTATAGAACTGGCAGCAGTGTGAAATATCATTTATGATGAAGT 3300
Db 3208 GGAATCTACAGTGTATAGAACTGGCAGCAGTGTGAAATATCATTTATGATGAAGT 3267
Oy 3301 GATTCATGCTATGCTATTAACAAACCCAGTCTTACTGATGATGATGATGATGATG 3360
Db 3268 GATTCATGCTATGCTATTAACAAACCCAGTCTTACTGATGATGATGATGATGATG 3327
Oy 3361 GAATCTGATTTGAAATTTTAAACAGAGACTTATAGTATGATGATGATGATGATG 3420
Db 3328 GAATCTGATTTGAAATTTTAAACAGAGACTTATAGTATGATGATGATGATGATG 3387
Oy 3421 AGCAAGAGAACTGATGAAAGAGAGTCTCATGAAAGTATGATGATGATGATGATG 3480
Db 3388 AGCAAGAGAACTGATGAAAGAGAGTCTCATGAAAGTATGATGATGATGATGATG 3447
Oy 3481 GACAGTGTAGAGACAGCCCTAGTGAAGTCTGAAAGAACTTTAAACCAAGAGCTTGT 3540
Db 3448 GACAGTGTAGAGACAGCCCTAGTGAAGTCTGAAAGAACTTTAAACCAAGAGCTTGT 3507
Oy 3541 TTTCACTGAGAGCTGTATCAAAAGATTTCAAGTGTGTCATATCAATGATGAAAGAGCAG 3600
Db 3508 TTTCACTGAGAGCTGTATCAAAAGATTTCAAGTGTGTCATATGATGAAAGAGCAG 3567
Oy 3601 GGAAGAACTATGATGAAAGAGAGAGAGCTTTCCGAATAGTGAACATATGCTGTTT 3660
Db 3568 GGAAGAACTATGATGAAAGAGAGAGAGCTTTCCGAATAGTGAACATATGCTGTTT 3627
Oy 3661 GAGACCTCATTTGTTTCAATGATCTCCCTATAGTGTGCTGCAATTTGAAGTATA 3720

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Db 3628 GAGACCTTCATTTGTTTCATGATTCCTCTAGTAGTGTCTCTGCGCATTTGAAGTATA 3687
Oy 3721 TATATGATGAGGAAAGAGATTAAGACATGTTGAAATATGCTGCAAGGTTTACT 3780
Db 3688 TATATGATGAGGAAAGAGATTAAGACATGTTGAAATATGCTGCAAGGTTTACT 3747
Oy 3781 TACATTTTCATTTGAAAGCTTTCTTAAATTTGGGTGATGATGATGATGATGATG 3840
Db 3748 TACATTTTCATTTGAAAGCTTTCTTAAATTTGGGTGATGATGATGATGATGATG 3807
Oy 3841 ACCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3900
Db 3808 ACCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3867
Oy 3901 GCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3960
Db 3868 GCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3927
Oy 3961 CTGAGACCTCTAAGAGCTTATCTGATTTGAAGGAGTGAAGGCTGTGATGCTT 4020
Db 3928 CTGAGACCTCTAAGAGCTTATCTGATTTGAAGGAGTGAAGGCTGTGATGCTT 3987
Oy 4021 TTAGAGCAATTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 4080
Db 3988 TTAGAGCAATTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 4047
Oy 4081 TTAGAGCAATTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 4140
Db 4048 TTAGAGCAATTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 4107
Oy 4141 ACTGCTGACAGGTTTGCATGCAAGAGTGAATATCATCATCATCATCATCATCATCAT 4200
Db 4108 ACTGCTGACAGGTTTGCATGCAAGAGTGAATATCATCATCATCATCATCATCATCAT 4167
Oy 4201 GAAAGAAATGAGACTGCTGATGAAATATGTAAGTAACTTATGATGATGATGATG 4260
Db 4168 GAAAGAAATGAGACTGCTGATGAAATATGTAAGTAACTTATGATGATGATGATG 4227
Oy 4261 GGGTATCTCTCTTCTGCTCAAGTTGGCAGATTCGAAAGTATGATGATGATGATG 4320
Db 4228 GGGTATCTCTCTTCTGCTCAAGTTGGCAGATTCGAAAGTATGATGATGATGATG 4287
Oy 4321 GCAGTTGATTCAGAAAT 4338
Db 4288 GCAGTTGATTCAGAAAT 4305

RESULT 11
AAH5793
ID AAH5793 standard; cDNA; 8349 BP.
AC AAH5793;
AY 04-SEP-2001 (first entry)
DE Human adult form of SCN2A nucleotide sequence SFG ID NO:33.
KW Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;
KW diagnosis; mutation; chromosome 2q23-q31; neurological disorder;
KW anticonvulsant; neuroprotective; ss.
OS Homo sapiens.
PN MO200138564-A2.
PD 31-MAY-2001.
PE 24-NOV-2000; 2000MO-CA01404.
PR 26-NOV-1999; 99US-0167623.
PA (UWMC-) UNITV MCGILL.
XX

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1669 TTGAGCATCCGTCGCTCCCTATTTTCACCAAGCGAAATAGCAACACCTTTTACG 1728  
1783 CTGAGGATCCGTCGCTCCCTATTTTCACCAAGCGAAATAGCAACACCTTTTACG 1842  
1729 TTTAGAGGCGGAGCAAGAGATGGGATCTGAGAACGATTCGAGATGATGAGACACG 1788  
1843 TTTAGAGGCGGAGCAAGAGATGGGATCTGAGAACGATTCGAGATGATGAGACACG 1902  
1789 ACCTTTGAGGATTAACGAGACCGGATGAGATTCCTTTGTTGCCCGCAGACACGAGAG 1848  
1903 ACCTTTGAGGATTAACGAGACCGGATGAGATTCCTTTGTTGCCCGCAGACACGAGAG 1962  
1849 AGACGCAACGCAACCTGATGATGAGATGATGATGATGATGATGATGATGATGATGAT 1908  
1963 CGGCGGCGACGCAATGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 2022  
1909 GCGAATGAGGAGATGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 1968  
2023 ATGATATGAGGAGATGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 2082  
1969 CCTTCAGTTCCTACATCGCTGTTGACAGCTTCTGCCAGAGGTGATTAATGATTAAGCCA 2028  
2083 CCTTCAGTTCCTACATCGCTGTTGACAGCTTCTGCCAGAGGTGATTAATGATTAAGCCA 2121  
2029 GCTACTGATGACATGAGACACACCTGAAATCTGAAATGAGAAAGAGAGAGAGAGAGAG 2088  
2122 -----GCGACACACTACTGAAAGAGAAATTAAGAAAGAGAGAGAGAGAGAGAGAG 2166  
2089 TTCCAGCTTTCCAGGACTTTTACAGAGATTCCTTCCAAAGGACACGACGATGATTA 2148  
2167 TATCATGTTTCCAGGACTTTTACAGAGATTCCTTCCAAAGGACACGACGATGATTA 2226  
2149 GCCAGATTCCTACCAATACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTAC 2208  
2227 GCCAGATTCCTACCAATACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTAC 2286  
2209 TGTGTGATTAATTTTCCAAATATCTTAATCTGAGAGTCTCTCCATATTTGTTAA 2268  
2287 TGTGTGATTAATTTTCCAAATATCTTAATCTGAGAGTCTCTCCATATTTGTTAA 2346  
2269 GTGAACATGTTGCAACGCTGTTGATGAGACCATTTGTTGACCGGACATCAGATC 2328  
2347 GTGAACATGTTGCAACGCTGTTGATGAGACCATTTGTTGACCGGACATCAGATC 2406  
2329 TGTATGTTCTTAATATCTTTTTCATGAGGACATGAGGACATGAGGACATGAGGACAT 2388  
2407 TGTATGTTCTTAATATCTTTTTCATGAGGACATGAGGACATGAGGACATGAGGACAT 2466  
2389 AATATGTTCTTAATATCTTTTTCATGAGGACATGAGGACATGAGGACATGAGGACAT 2448  
2467 AGCAGTGTACTGTCTGTGAAACCTGTTGACAGGAGTCTTTCACAGAGAGAGAGAG 2526  
2449 CTGAATATTTTATGAGGACATGAGGACATGAGGACATGAGGACATGAGGACATGAGGAC 2508  
2527 CTGAATATTTTATGAGGACATGAGGACATGAGGACATGAGGACATGAGGACATGAGGAC 2586  
2509 GGTATTTATTTGAGGACATGAGGACATGAGGACATGAGGACATGAGGACATGAGGACAT 2568  
2587 GGTATTTATTTGAGGACATGAGGACATGAGGACATGAGGACATGAGGACATGAGGACAT 2646  
2569 GTTCTCCGTTCAATTTGATGCTGCGAGGTTTCAAGTTGCGCAAAATCTTGCGCAACGTA 2628  
2647 GTTCTCCGTTCAATTTGATGCTGCGAGGTTTCAAGTTGCGCAAAATCTTGCGCAACGTA 2706  
2629 AATATGTTCTTAATATCTTTTTCATGAGGACATGAGGACATGAGGACATGAGGACAT 2688  
2707 AATATGTTCTTAATATCTTTTTCATGAGGACATGAGGACATGAGGACATGAGGACAT 2766  
2689 TTGCGCATTCATCTCTCATTTTTCGCGGAGTGGCGGATGAGGATGAGGATGAGGATGAG 2748  
2767 TTGCGCATTCATCTCTCATTTTTCGCGGAGTGGCGGATGAGGATGAGGATGAGGATGAG 2826  
2749 AAGATTTGTCTGCAAGATGCGCAGATGATGATGATGATGATGATGATGATGATGATGAT 2808

2827 AAGAAATGTCTGCAAGATTTTCCAAATGATTTGATTTCCACGCTGCGACATGACATGAC 2886  
2809 TTTCTCATCTCTCTCATTTTTCGCGGAGTGGCGGATGAGGATGAGGATGAGGATGAG 2868  
2887 TTTTTCATCTCTCTCATTTTTCGCGGAGTGGCGGATGAGGATGAGGATGAGGATGAG 2946  
2869 TGGCATGTTATGAGGATTTGCTGCTGCAAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 2928  
2947 TGGCATGTTATGAGGATTTGCTGCTGCAAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 3006  
2929 GTGATTTGAAAGCTAGAGTCTGCAATCTCTTCTGCGCTGCTGCTGCTGCTGCTGCTGCT 2988  
3007 GTGATTTGAAAGCTAGAGTCTGCAATCTCTTCTGCGCTGCTGCTGCTGCTGCTGCTGCT 3066  
2989 GCAACACACCTTGCAGGACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3048  
3067 TCTGACATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3126  
3049 GATAGATGACAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3108  
3127 GGAAGATGACAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3186  
3109 TCTCTCATTTGCAACAAAGATTTTATGATGATGATGATGATGATGATGATGATGATGAT 3168  
3187 GCTTCTGTTAGGAGGACGAAAGCTTTGATGATGATGATGATGATGATGATGATGATGAT 3246  
3169 AAGAAAGAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3225  
3247 AAGAAAGAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3306  
3226 CTTAAAGATTTAAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3285  
3307 CTTAAAGATTTAAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3360  
3286 AATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3345  
3361 GTCGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3420  
3346 CCAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3405  
3421 CCAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3480  
3406 TCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3465  
3481 TCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3537  
3466 ACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3522  
3538 ACGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3597  
3523 CTTGAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3582  
3598 CTTGAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3657  
3583 AATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3642  
3658 AGCATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3717  
3643 GTTGAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3702  
3718 GTTGAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3777  
3703 CTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3762  
3778 CTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3837  
3763 GCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3822  
3838 GCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3897  
3823 GCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3882



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Db 3898 GGTTCCTCAAGTATATTTACCAATGCTGCTGCTGCTAGACTTCTGATGTC 3957
Oy 3883 TCATGTCAGTTTAACAGCAATGCTTGGTACTGACAACTTGAGCCATCAATCT 3942
Db 3958 TCAGTGTAGCTTAACGCAATGCTTGGTACTGACAACTTGTCCTCAATATCC 4017
Oy 3943 CTCAGACACTAAGAGCTGTGAGCTCTAAGACCTTATCTCGATTTGAAAGGATGAG 4002
Db 4018 CTCACAACTAAGAGCTGTGAGCTCTAAGAGCTTGTCTCCGCTTGAAGAAATGAG 4077
Oy 4003 GTGCTGTGAATGCTTGTAGAGCAATTCATCATCATGATGATGCTTGTGCTTGT 4062
Db 4078 GCTGTGTGAATGCTTGTAGAGCAATTCATCATCATGATGATGCTTGTGCTTGT 4137
Oy 4063 CTTATATTCCTGCTAATTTTCAGCATGAGCGTAATTTGCTGCTGCAATTCAC 4122
Db 4138 CTGATCTTTGGCTAATATTCAGTATCAGTGAAGTGAATCTTGTGCTGCAATTCAC 4197
Oy 4123 CACTGATTTAACACACACTGTGACAGGTTGACATGGAAGAGTGAATATCATCT 4182
Db 4198 CATGTATATTAATTAACACACTGTGACAGGTTGATGATGATGCTGCAATCACTAC 4257
Oy 4183 GATGCTTAAACCTAATAGAAAGAAATGAGACTGCTGATGGAAGAAATGGAAGTAAC 4242
Db 4258 GAGTCAAAAGCTCTCATTTAGAGCAATCAACTGCCAGGTGGAAGAAATGGAAGTAAC 4317
Oy 4243 TTTGATATATGAGATTTGGGATCTCTCTTTCCTCAAGTTGCCACATTCAGAGATG 4302
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Oy 4303 ATGATATATATATGACAGCACTGATTCAGAAATGGAAGTCCAGCTTAAGTATGA 4362
Db 4378 AAGGATATATATGACAGCACTGATTCAGAAATGGAAGTCCAGCTTAAGTATGA 4437
Oy 4363 GAAAGCTGATCATGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 4422
Db 4438 GAAAGCTGATCATGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 4497
Oy 4423 TTTGAACCTGTTTATGCTCATCATATATATTTCAACACAGCAAGAAAGTTTGA 4482
Db 4498 TTTGAATCTTTCAATTTGGTCTCATCATATATTTCAACACAGCAAGAAAGTTTGA 4557
Oy 4483 GGTCAAGACATCTTATGACAGAAACAGAAATCTATATGCAATGAAAAATTA 4542
Db 4558 GGTCAAGACATCTTATGACAGAAACAGAAATCTATATGCAATGAAAAATTA 4617
Oy 4543 GGATGAAAAACCGCAAAAGCTTACCTGACAGCAAGAAATTCAGAAAGTATGTC 4602
Db 4618 GGTTAAAAAACCACAAACCCATCTGACCTGCTAACAAATTCAGAAAGTATGTC 4677
Oy 4603 TTTGACTTCGTAAACAGAAAGTTTTCATATACATCATGATGATCTCATCTGCTTAAC 4662
Db 4678 TTTGATTTTGTAAACAAATCTTTGATATACATCATGATGATCTCATCTGCTTAAC 4737
Oy 4663 ATGTCACAAATGATGCTGAAACAGATGACAGAGTGAATATGCACTCAATTTTGA 4722
Db 4738 AAGGACACCATGATGCTGAAACAGATGACAGAGTGAATATGCACTCAATTTTGA 4797
Oy 4723 GGCATCAATCTGCTGATATGCTATTTACTGAGAGTGTGATGAAATCATCTCT 4782
Db 4798 TGGATTAATCTGCTGATATGCTATTTACTGAGAGTGTGATGAAATCATCTCT 4857
Oy 4783 CTACCCATTTATTTATTTACATGATGAAATTTTGTGATTTTGTGCTGCTTCTC 4842
Db 4858 CTTCCTTACTATTTACATGATGAAATTTTGTGATTTTGTGCTGCTTCTC 4917
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Oy 4903 TTTCCAGATGATGCTGCTGCTGATTTGCGCAATCTCAAGCTCATCAAGAGCAAG 4962
Db 4978 TTTCCAGATGATGCTGCTGCGAGATTTGCGCAATCTCAAGCTCATCAAGAGCAAG 5037

Oy 4963 GGGATCCGACCTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 5022
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Oy 5023 CTCCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 5082
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Oy 5083 GTTAAGAGGAAAGTTGGATGATGATGATGATGATGATGATGATGATGATGATGAT 5142
Db 5158 GTTAAGAGGAAAGTTGGATGATGATGATGATGATGATGATGATGATGATGATGAT 5217
Oy 5143 ATCTGCTATTTCCAAATTAACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5202
Db 5218 ATCTGCTATTTCCAAATTAACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5277
Oy 5203 AACCTGAAGCCACCGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 5262
Db 5278 AATAGTGACCTCCAGACTGATGATGATGATGATGATGATGATGATGATGATGAT 5337
Oy 5263 GACTGTGGAAACCATCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 5322
Db 5338 GACTGTGGAAACCATCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 5397
Oy 5323 CTGCTGTGTGTAACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5382
Db 5398 CTGCTGTGTGTAACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5457
Oy 5383 GAAAGTGCAGACCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 5442
Db 5458 GAAAGTGCAGACCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 5517
Oy 5443 TTTGATCCCGATGACCACTGATGATGATGATGATGATGATGATGATGATGATGAT 5502
Db 5518 TTTGATCCCGATGACCACTGATGATGATGATGATGATGATGATGATGATGATGAT 5577
Oy 5503 CTTGAACCGCTCTCAATCTGCAACACCAACCAACCAACCAACCAACCAACCAACCA 5562
Db 5578 CTTGAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5637
Oy 5563 CCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5622
Db 5638 CCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5697
Oy 5623 GTTCTAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5682
Db 5698 GTTCTAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5757
Oy 5683 GCTTCCAACTCTTCCAAAGCTCTCTATACGCCAATCTACTTATTAAGAAACAA 5742
Db 5758 GCATCAAAACCTCTTCCAAAGCTCTTATAGCCCATATAGAACACAGTGAAGCAACA 5817
Oy 5743 GAGGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5802
Db 5818 GAGGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5877
Oy 5803 GTTAAACAAAGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 5862
Db 5878 GTTAAACAAAGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 5937
Oy 5863 ATTAAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5922
Db 5938 ATTAAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5997
Oy 5923 CTGACCAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5982
Db 5998 ATGACGCTCTTCA---CCACGCTCTCACCTCTGATGATGATGATGATGATGATGATGAT 6054
Oy 5983 GAAAAACATGACCAAGGCAAGCAAGTAAAAAGCAAGGGAAPDA 6029
Db 6055 GAAAAATTTGAAAAAGCAATCAATCAAAAAAGAAAGCAAGGGAAGA 6101
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|    |      |  |      |
|----|------|--|------|
| Db | 1366 | TTGGCTGTGGTGGCCATGGCTCTTGGAGAACGAAATACGGCCACATTTGGAGAGGCTTAA   | 1425 |
| Qy | 1315 | CAGAAAGAGGCCGAATTTTCAGCAGATGATTTGAAACAGCTTTAAAGCAACAGAGGACACT  | 1374 |
| Db | 1426 | CAGAAAGAGGACTGAAATTTTCAGCAGATGATGTCGAAACAGTTGAAAGCAACAGAAAGACT | 1485 |
| Qy | 1375 | CAGCAGCAGCAACGG-----CACTGCCCTCAGAACATTTCCAGAGAGCCCACTGCACCA    | 1428 |
| Db | 1486 | CAGCGGCACTGACAGCCGATCGCTGATCAAGAGACCTTCAAGTGGTGGTGGATA         | 1545 |
| Qy | 1429 | GGCAGGGCTCAGACAGCTCATCTGAAAGCCTCAATTTAGTTTCCAAAGAGCTCTAAAGAA   | 1488 |
| Db | 1546 | GGAGTTTTTTCAGAGATTTTTCAGTGGCATCTTAAGTTAGCTTCCAAAGTGAAGAAAGAG   | 1605 |
| Qy | 1489 | AGAGAAATCGAGAGAAAGAAAGAAAGAAAGACAGTCTGTGTGGGAGAGAAAGAT         | 1548 |
| Db | 1606 | CTGAAAAACAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAT    | 1665 |
| Qy | 1549 | GAGATGAATTCACAAAATCTGAATCTGAGAGACAGCATGAGAGCAAAAGTTTTCGCTTC    | 1608 |
| Db | 1666 | GACAGAG---TCCTAATATTTGGATTTGAAAGACGATTAAGAAAGAAAGTTTCCGTTT     | 1722 |
| Qy | 1609 | TGCATTTAAGAGAACCGATTGACATATNGAAAGAGSTACTCTCCCCACACAGCTTTTG     | 1668 |
| Db | 1723 | TCTCTTGAAGAAAGATAGCGTGAATATGAAAGAAAGATTTTCTTCCACACAGCTCTTA     | 1782 |
| Qy | 1669 | TTGACATCCGTGGCTCCCTAATTTTTCACAAAGCGCAATATGACAGAAACCTTTTCAGC    | 1728 |
| Db | 1783 | CTGAGCATCCGTGGCTCCCTTTTCTCTCCAAAGCGCAACAGTATGGGCGAGCTTTTCAGC   | 1842 |
| Qy | 1729 | TTTAAAGGGCGAGCAAAAGATGTGGATCTGAGAAACGACTTGGCAGATATGACAGACG     | 1788 |
| Db | 1843 | TTTCAGAGTGGAGCAAAAGACATTTGGCTGTGAAATGACTTTGTATGATGACAGACG      | 1902 |
| Qy | 1789 | ACCTTATAGATTAACGAGACCGTAAAGATTCCTTTGTGTGCCCCGAGACAGACGGAAG     | 1848 |
| Db | 1903 | ACCTTATAGGACATGACAGCCGAAAGAGACCTCTCTTGTGCCCGCAGACAGATGAGAA     | 1962 |
| Qy | 1849 | AGAGCAACAGCAACCTGAGTCAAGACCAGTAGAGTCACTCCGAGTGGCAGTGTTTTCA     | 1908 |
| Db | 1963 | CGGGCCACAGCAATGTACACAGCGCAGCGCGCTCCAGGGTGTCTCCCATCTCGGCC       | 2022 |
| Qy | 1909 | GCGAATGGGAAGATGCACAGCACTGTGGATGTGCAATGTGTGGTCTTGTGGTGGTGA      | 1968 |
| Db | 2023 | ATGAAATGGGAAGATGCATACCGCTGTGTGAGTGCATATGTGTGTCTTCCCTGGTGGGGC   | 2082 |
| Qy | 1969 | CCTTCAGTTCCTACATGGCTGTGTGGACAGCTTCTGCCAGAGGTGATTAATAGATAAGCA   | 2028 |
| Db | 2083 | CCCTTCTACCCCTCAAT---CTGGTGGGCACTCTCACAGAG-----                 | 2121 |
| Qy | 2029 | GCTACTGATGACATGCAACACACACTGAAACCTGAAATGAGAAAGAGAGCTCAAGTTCT    | 2088 |
| Db | 2122 | -----GGCACACTACTGAAACAGAAATTAAGAAAGAGAGCGTCCAGTTCT             | 2166 |
| Qy | 2089 | TTTCCAGCTTCCATGAGACTTTTTCAGAAAGATCTTTCCCAAAGCAAGACCAATGAGTATA  | 2148 |
| Db | 2167 | TATCATGTTCATGATGATTTATTGGAAGATCTTACATCAAGGAAAGAGCAATGAGTATA    | 2226 |
| Qy | 2149 | GCCAGCATTTCTAACAAATACAGTGAAGAACTTGAAGAAATCCAGGCGAGAAATGCCACC   | 2208 |
| Db | 2227 | GCCAGTATTTTGAACCAACACATGGAAGAACTTGAAGAAATCCAGACAGAAATGCCACACA  | 2266 |
| Qy | 2209 | TGTTGATTAATTTTTCACACATATTCCTTAATCTGGAGACTGTTCACATTAATGTTTAAA   | 2268 |
| Db | 2287 | TGCTGTGATTAATTTTGTATTAATGTGTGTGATTTGGAGCTGTGTAAACATGTTTAAAG    | 2346 |
| Qy | 2269 | GTTGAACATGTTTGTCAACCTGTGTGTATGAGAACCAATTTGTGACTGTGGCTCAACATC   | 2328 |
| Db | 2347 | GTTGAACACCTTGTCAACCTGTGTGTATGATGAGAACCAATTTGTGACTGTGGCTCAACATC | 2406 |
| Qy | 2329 | TGTATGCTTAATTAATCTCTTTTCATGAGCCATGAGACATATTCATTAAGCAGCAATTC    | 2388 |

|    |      |  |      |
|----|------|--|------|
| Dd | 2407 | TGCATTTGCTTAATAATACATCTTCATACGCTAATAGGACACATATCCCATAGACGACAGTTCC | 2466 |
| Qy | 2389 | AATAATGGCTTACAGTAGAAGAACTGGTTTTACTGGAGTCTTTACACAGAAATGTTT        | 2448 |
| Dd | 2467 | AGCAGTAGACTGTCTGTGGAAACCTGGCTTCACAGGAGTCTTTCACACAGAAATGTTT       | 2528 |
| Qy | 2449 | CTGAAATATATGGCATAGATCCTTACTATTTATTTCCAGAAAGGCTGGAAATATCTTTGAC    | 2508 |
| Dd | 2527 | CTCAAGATTAATGGCAATGAGATCATATATTTACTTTCCAGAAAGGCTGGAAATATTTTGTAT  | 2588 |
| Qy | 2509 | GGTTTTATATGAGCGCTTACCGTGTGAGACTGGACCTGGACCTGCCAAATGGAAAGATTATAT  | 2568 |
| Dd | 2587 | GGTTTTATATGAGCGCTTACCGTGTGAGACTGGACCTGGACCTGCCAAATGGAAAGATTATAT  | 2644 |
| Qy | 2569 | GTTCTCGGTTCAATTTTCGATTTGCTGCGAGTTTTCAGATTGGCAAAATCTTGGCCAACTGTA  | 2628 |
| Dd | 2647 | GTTCTCGGTTCAATTTTCGATTTGCTGCGAGTTTTCAGATTGGCAAAATCTTGGCCAACTGTA  | 2708 |
| Qy | 2629 | AATATGCTAATAAAGATCATCGCAATTTCCGTGGGGCTCTGGGAAATTTAACTCCTGTC      | 2688 |
| Dd | 2707 | AATATGCTAATAAAGATCATTTGGCAATTTCTGTGGGGCTCTGTAGAAACCTCACTTGGTGA   | 2768 |
| Qy | 2689 | TTGGCCATACGCTTCATTTTTGGCCGTGGTGGGATGAGCTCTTGGTAAAGCTAC           | 2744 |
| Dd | 2767 | TTGGCCATACGCTTCATTTTTGGCCGTGGTGGGATGAGCTCTTGGTAAAGCTAC           | 2822 |
| Qy | 2749 | AAAGATTGTGCTCAAGATCGCACAGATGTTCACACTGCCAGCTGGACATCATATGATAC      | 2808 |
| Dd | 2827 | AAAGATTGTGCTCAAGATTTCCAAATGATTTGGAACTGCCAGCTGGACATCATATGATAC     | 2888 |
| Qy | 2809 | TTCTTTCACATCTCTTCGATTTGTGTTCCGCGTGTCTGTGGGGAGTGATAGAGCAATG       | 2868 |
| Dd | 2887 | TTCTTTCACATCTCTTCGATTTGTGTTCCGCGTGTCTGTGGAGAGTGATAGAGCAATG       | 2944 |
| Qy | 2869 | TGGGACGTATAGGAGGTGCGTGGGCAAGCATGTGCGTACATGCTTCATATGATAGTGCATG    | 2922 |
| Dd | 2947 | TGGGACGTATAGGAGGTGCGTGGGCAAGCATGTGCGTACATGCTTCATATGATAGTGCATG    | 3008 |
| Qy | 2929 | GTCATTGGAAACCTAGTGTGCTGTAATCTCTTCTGAGCTGTGTTAGAGTCATTTAGT        | 2988 |
| Dd | 3007 | GTCATTGGAAACCTAGTGTGTTCTGTAACCTCTCTTGTGGCCTGTGTTAGATTCCTTCAAT    | 3068 |
| Qy | 2989 | GCAGACAACTTGCAGCCACTGATGATGATTAATGAATGATATATCTCCAAATTCGCTGTG     | 3044 |
| Dd | 3067 | TCTGACATCTTCTGCGCACGTAGATGATGAATGAAGAAATGATATCTCCAGATTTGCTGTG    | 3122 |
| Qy | 3049 | GATGAGTGCACAAAGAGATGCTATGATGAAGAAAGAAATATATGAATTTATTCACAGG       | 3108 |
| Dd | 3127 | GGAAGAGTGCAGAAAGGAATTCGATTTGTTTAAAGAAATATGCTAAATTTATTCAGAA       | 3188 |
| Qy | 3109 | TCTCTTATTAGAAACAAAGATTTTATGATGAATTTAAACCACTTATGATATCTAAACAC      | 3168 |
| Dd | 3187 | GCCTTTGTAGAGAGCAAGAAAGCTTTTATGATGAATTTAAACCGTTTAAAGATCTAAATAT    | 3244 |
| Qy | 3169 | AAGAAAGCACTTGTATGTCCCAATCATACAR---AGAAATTTGGAAAGATCTGTGATAT      | 3222 |
| Dd | 3247 | AAAAAAGACAGCTGATTTTCCCAACATACACACCATGAAATTTAGCAAAACCTCATATAT     | 3308 |
| Qy | 3226 | CTTAAAGATGTAATGGAATCTACAAAGTGTATAGAACTGAGCAAGCTGTGAAAAATATC      | 3288 |
| Dd | 3307 | CTCAAAAGCGGAAATGGAATCTACAAAGTGTGATAT---GGCAGAGTGTAAAGAAATAT      | 3368 |
| Qy | 3286 | ATTATTTGATGAAATGATTTATCATGTCTCATTAACACACCCAGCTTACTGTGAGCTGA      | 3344 |
| Dd | 3361 | GTCGTGATGAAATGATTTATCAATCTATTTATTAACACACCTTACTGTGACAGTGA         | 3422 |
| Qy | 3346 | CCAAATTTGCTGATGAGATCTGACTTTGAAATTTTAAACACGAGAGACTTTAGTAGTGA      | 3408 |
| Dd | 3421 | CCAAATTTGCTGATGAGATCTGACTTTGAAATTTTAAATATCTGAAGAAATTTACGACGCGAG  | 3488 |
| Qy | 3406 | TGCGATCTGGAAAGAAAGCAAGAAAGCAATGAATGAAGCAATGATGCTATCAGAGTAGC      | 3468 |
| Dd | 3481 | TCAGATTTATGAGAGAAAGCAAGAAAGCAATGAATGAAGCAATGATGCTATCAGAGTAGC     | 3538 |

OY 3466 ACTGTGACATCGGCGACCTGTAGA--AGAACAGCCCGTAGTGAACCTGAAGAACT 3522  
DB 3538 ACGGTGATATGTGAGCTCCCGCGAGGAGAACAGCCTGAGGTGAACCTGAGGAATCC 3597  
OY 3523 CTGTAACCAAGAGCTGTTTCACTGAAAGCGTGTACAAAGATTCAAGTGTGCAATC 3582  
DB 3598 CTGTAACCTGAAGCCTGTTTACAGAAAGACTGTGTACGGAAGTCAAGTGTGCAATA 3657  
OY 3583 AATGTGAGAGAGCAGCAAGAAACAATGGTGAACCTGGAAGAGAGTGTTCGAAATA 3642  
DB 3558 AGCATATAGAGAGGCAAGGAAACCTGCTGGTGAATTTGAGAAACATGCTATAGATA 3717  
OY 3643 GTTGAACATACTGTTTGAAGACCTTCATGTTTTCATGATTCCTTACTAGTGTGCT 3702  
DB 3718 GTGAGACACATGTGTTGGAACCTTCATGTTGCTCATGATTCGCTGACAGAGGGGCT 3777  
OY 3703 CTGCAATTTGAATATATATATATATGATCAGGAAAGACATTAAGACATGTTGAATAT 3762  
DB 3778 CTGCACTTTGAAATATATATATATGATGACAGGAAACCAATTAAGACATGTTGAATAT 3837  
OY 3763 GCTGACAGAGTTTCACTTACATTTTCACTTCTGGAATGCTTCTAAATGGTGGCATAT 3822  
DB 3838 GCTGACAAAGTTTCACTTACATTTCACTTCTGGAATGCTTCTAAATGGTGGCATAT 3897  
OY 3823 GGTATATCAACATATTTTACCACATGCTGTGTGGTGGTGGACCTTAAATGTTGATGT 3882  
DB 3898 GGTATATCAAGTATTTTACCACATGCTGTGTGGTGGTGGACCTTAAATGTTGATGT 3957  
OY 3883 TCATTTGCTAGTTTAAACAGCAATGCTGTGGTGTACTAGAACTTGGACCATCAATCT 3942  
DB 3958 TCATTTGCTAGTTTAACTGCAATGCTGTGGTGTACTAGAACTTGGACCATCAATCT 4017  
OY 3943 CTGAGACACTAAGAGCTGTGAGACCTCTAAGACCTTATCTGATTTGAAGGATAGG 4002  
DB 4018 CTGAGAACACTAAGAGCTGTGAGACCTCTAAGACCTTATCTGATTTGAAGGATAGG 4077  
OY 4003 GTGTGTGTGATGCTCTTTTGAAGCAATTCATTCATCAATGATGTGCTTGTGTTGT 4062  
DB 4078 GCTGTGTGATGCTCTTTTGAAGCAATTCATTCATCAATGATGTGCTTGTGTTGT 4137  
OY 4063 CTATATTTGCTGATTTTTCAGCATATGAGGCTAAATTTGTTGCTGGCAATTTCTAC 4122  
DB 4138 CTGATCTTTGCTGATTTTTCAGCATATGAGGCTAAATTTGTTGCTGGCAATTTCTAC 4197  
OY 4123 CACTGTATTAACCAACACTGTTGACAGGTTTGAATCGAAGCTGAATTAATCATACT 4182  
DB 4198 CATTGTATTAATTAACCAACACTGTTGACAGGTTTGAATCGAAGCTGAATTAATCATACT 4257  
OY 4183 GATTCCTTAAACATTAAGAAAGAAATGAGACTGCTGATGAGAAATGTGAAGTAAC 4242  
DB 4258 GATTCCTTAAACATTAAGAAAGAAATGAGACTGCTGATGAGAAATGTGAAGTAAC 4317  
OY 4243 TTTGATATATGATGATTTGGGTATCTCTTCTGTTCAAGTTGCCACATTCAAAGATGG 4302  
DB 4318 TTTGATATATGATGATTTGGGTATCTCTTCTGTTCAAGTTGCCACATTCAAAGATGG 4377  
OY 4303 ATGATATTAATGATGAGAGAGTGTATTCAGAAATGTGAACTCCAGCTTAAGTAAGAA 4362  
DB 4378 ATGATATTAATGATGAGAGAGTGTATTCAGAAATGTGAACTCCAGCTTAAGTAAGAA 4437  
OY 4363 GAAAGTGTGATGATGATTTTACTTGTATTTTCAATCAATGTTGGGCTTCTTCCACC 4422  
DB 4438 GAAAGTGTGATGATGATTTTACTTGTATTTTCAATCAATGTTGGGCTTCTTCCACC 4497  
OY 4423 TTTGAACCTGTTATTTGGTGTATATATATTTTCAACAGCAAGAAAGATTTTGA 4482  
DB 4498 TTTGAATCTTTTCAATTTGGTGTATATATTTTCAACCAAGAAAGATTTTGA 4557  
OY 4483 GGTGAAGACATCTTTATGACAGAGAAAGAAATATATATATGATGAGAAAGATTTTGA 4542  
DB 4558 GGTGAAGACATCTTTTATGACAGAGAAAGAAATATATATATGATGAGAAAGATTTTGA 4617

OY 4543 GGATCGAAAAAACCAGAAACCTATATCTGACCCAGAGAAACAATTTCAAGAAATGCT 4602  
DB 4618 GGTCAAGAAAGAACCAAAAAACCATACCTGACCTGCTATCAAAATTCAGAAATGCTC 4677  
OY 4603 TTTGATCTGTAACCAACAAAGTTTGGATCAATAGCATATGATTCATCTGTCTTAC 4662  
DB 4678 TTTGATCTGTAACCAACAAAGTTTGGATCAATAGCATATGATTCATCTGTCTTAC 4737  
OY 4663 ATGTCACAAATGATGAGGAAAGAGATGACAGAGTGAATATGATCAATTTTGA 4722  
DB 4738 ATGTCACAAATGATGAGGAAAGAGATGACAGAGTGAATATGATCAATTTTGA 4797  
OY 4723 CCGATCAATCTGTTTCAATTTGCTTATTTTACTGAGAGTGTGTACTGAAACATCTCT 4782  
DB 4798 TGAATATCTGTTTATATTTATTTGTTCTGTACTGAGAAATGTGTGAAACATCTCT 4857  
OY 4783 CTACGCAATTTATTTTACCATTTGATGATGAAATATTTTGTATTTGTGTGATCTC 4842  
DB 4858 CTTCGTTACTATATTTTCAATTTGATGATGAAATATTTTGTATTTGTGTGATCTCTC 4917  
OY 4843 TCCATTTAGGATGTTTCTTGGCAGCTGATAGAAAGATTTTGTGCTCCACCTG 4902  
DB 4918 TCCATTTAGGATGTTTCTTGGCAGCTGATAGAAAGATTTTGTGCTCCACCTG 4977  
OY 4903 TTCGAGTGAATCCCTTGTGATGATTTGGCAGAAATCCATCTGATCAAGAGAGCAAG 4962  
DB 4978 TTCGAGTGAATCCCTTGTGATGATTTGGCAGAAATCCATCTGATCAAGAGAGCAAG 5037  
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DB 5038 GGGATCCGACGCTGCTTCTTGTGATGATTTGCTTGTGATGATTTGCTTGTGATGAT 5097  
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DB 5098 CTCTACTCTTCTGATGATTTGATGATTTGATGATTTGATGATTTGATGATTTGATGAT 5157  
OY 5083 GTTAAGAGGAGGATTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5142  
DB 5158 GTTAAGAGGAGGATTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5217  
OY 5143 ATCTGCTATTTCCAAATTAACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5202  
DB 5218 ATCTGCTATTTCCAAATTAACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5277  
OY 5203 AACGATAGCCACCCGACTGTGACCTAATTAATTAACCTGGAAGTCAAGTAAGGA 5262  
DB 5278 AATGATGACCTCCAGACTGTGACCTGACCAAAATCACTGGAAGTCAAGTAAGGA 5337  
OY 5263 GACTGTGGGAACCCATCTGTTGAAATTTTCTTGTGCAATTAATCAATCAATCAATCAAT 5322  
DB 5338 GACTGTGGGAACCCATCTGTTGAAATTTTCTTGTGCAATTAATCAATCAATCAATCAAT 5397  
OY 5323 CTGTTGTGTTGAACATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5382  
DB 5398 CTGTTGTGTTGAACATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5457  
OY 5383 GAAAGTCAAGAGCTCTGAGAGGAGATGATGATGATGATGATGATGATGATGATGATGAT 5442  
DB 5458 GAAAGTCAAGAGCTCTGAGAGGAGATGATGATGATGATGATGATGATGATGATGATGAT 5517  
OY 5443 TTTGATCCGATGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5502  
DB 5518 TTTGATCCGATGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5577  
OY 5503 CTGTAACCGCTCTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5562  
DB 5578 CTGTAACCGCTCTCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5637  
OY 5563 CCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5622  
DB 5638 CCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5697  
OY 5623 GTTCTAGAGAGAGATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 5682

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Db 5698 GTTTGGGCTGAGAGTGAGAGATGAGATGCTTCGATATACAGATGAGAGCGATTCAATG 5757
Oy 5683 GCTTCCAAATCCTTCCAAAGGCTCTCTATCATCAGCAATCATCTACTTAAAGCAAAACA 5742
Db 5758 GATCAAAACCCCTCCAAAGTCTCTTATGAGCCCATTTACAGCAGTGAAGCAAAACA 5817
Oy 5743 GAGAGATATCTGCTGCTATTATTCAGCGCTGTACAGACGCCACCTTTAAAGCGAACT 5802
Db 5818 GAGAGGCTGCTGCTATATATATTCAGAGAGGCTTACAGACGCTTGAAGCAAAA 5877
Oy 5803 GTAAGAACAGCTTCCTTACGTCACATTAATAAACAATAAGAGGCGGCTATCTCTT 5862
Db 5878 GTTAAAGAGTATCAAGTATATATACAGAAAGCAAGGCAAGATGTATGGAACACCC 5937
Oy 5863 ATAAAGAAAGATATATATATGACAGAAATATTAATGAAACTCTTATACAGAAAAACTGAT 5922
Db 5938 ATCAAGAAAGATATCTCTCTTATATACGATGAGAAATTCACACTCAGAAAGAAACGAT 5997
Oy 5923 CTGACCAATGTCACCTGACAGCTTGTCCACCTTCCTATGACCGGGTGCAAAAGCCAAATGTC 5982
Db 5998 ATGAGCGCTTCCA---CCACGCTCCACCCCTGTATGATAGTGTGACCAAGCAAGAAAA 6054
Oy 5983 GAAAAACATGACGACGAGGCAAGATGAAAAAGCCAAAGGCAATA 6029
Db 6055 GAAAAATTTGAAAAAGACAAATACAGAAAAAGCAAGCAAGGCAAGA 6101

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## RESULT 13

AAD32847  
ID AAD32847 standard; cDNA; 4179 BP.

AC AAD32847;  
XX 01-JUL-2002 (first entry)

DE Human ion channel cDNA #9.

XX Human; novel human protein; NHP; voltage-gated sodium channel;

KV gene therapy; bioreactor; mental disorder; biological disorder;

XX gene; medical disorder; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..4179

FT /tag= "Human ion channel protein #9"

FT /product= "Human ion channel protein #9"

FT /transl\_except= (pos:2974..2976, aa:Xaa)

FT /transl\_except= (pos:3199..3201, aa:Xaa)

FT /note= "Xaa - any amino acid"

XX WO200214496-A2.

XX 21-FEB-2002.

XX 15-AUG-2001; 2001WO-US25650.

XX 16-AUG-2000; 2000US-225989P.

XX (LEXI-) LEXICON GENETICS INC.

XX Turner CA, Mathur B, Mathur D;

XX WPI: 2002-280757/32.

XX P-PSDB: AAE20518.

XX Novel polynucleotides encoding human sodium channel proteins,

XX particularly voltage-gated sodium channel proteins useful for drug

XX screening, diagnosis and in gene therapy of biological disorders

CC The present sequence is a cDNA encoding novel human protein (NHP), ion  
CC channel protein. NHP share structural similarity with mammalian sodium  
CC channel proteins particularly voltage-gated sodium channel proteins.  
CC NHP oligonucleotides are useful as hybridisation probes for screening  
CC libraries and assessing gene expression patterns. Sequences derived  
CC from regions adjacent to the intron/exon boundaries of NHP gene can be  
CC used to design primers for use in amplification assays to detect  
CC mutations within the exons, splice sites, introns that can be used in  
CC diagnostics and pharmacogenomics. NHP nucleotide sequences are useful  
CC for drug screening effective in the treatment of symptomatic or  
CC phenotypic manifestations of perturbing the normal function of NHP in  
CC the body, and nucleotide constructs encoding NHP products are useful to  
CC genetically engineer host cells to express NHP products in vivo. These  
CC products are useful for use as bioreactors in the body  
CC delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion  
CC protein to the body. Nucleotide construct encoding NHP products are  
CC also useful in gene therapy for modulating NHP expression and to  
CC produce genetically engineered host cells to express NHP products in  
CC vivo. NHP nucleotide sequences may also be used as part of ribozyme  
CC and/or triple helix sequences that are useful for NHP gene regulation.  
CC The NHP polypeptides are useful for generating antibodies, as  
CC reagents in diagnostic assays, for identifying other cellular gene  
CC products related to NHP and as reagents in assays for screening for  
CC compounds that are useful in the treatment of mental, biological or  
CC medical disorders and diseases.

XX Sequence 4179 BP; 1239 A; 815 C; 958 G; 1164 T; 3 other;

XX Query Match 68.8%; Score 4150.8; DB 24; Length 4179;

XX Best Local Similarity 100.0%; Pred. No. 0; Mismatches 4152; Conservative 0; Indels 0; Gaps 0;

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Oy 1 ATGAGCAAAACAGTGTCTTACACAGAGAGTACAGTCTTCACTTCTTACACAGAA 60
Db 1 ATGAGCAAAACAGTGTCTTACACAGAGAGTACAGTCTTCACTTCTTACACAGAA 60
Oy 61 TCTCTGCGGCTATGTAAGAGAGAGTTCAGAGAAAGCAAAAGTCCAAACAGAC 120
Db 61 TCTCTGCGGCTATGTAAGAGAGAGTTCAGAGAAAGCAAAAGTCCAAACAGAC 120
Oy 121 AAAAAAGATGACGAGAAATGCGCCCAAGCCAAATGTGATGATGGAAGTGAAGAAC 180
Db 121 AAAAAAGATGACGAGAAATGCGCCCAAGCCAAATGTGATGATGGAAGTGAAGAAC 180
Oy 181 CTTCATTTATTTATGAGACATTCCTCAGAGATGCTGCAAGGCCCTGAGAGACTG 240
Db 181 CTTCATTTATTTATGAGACATTCCTCAGAGATGCTGCAAGGCCCTGAGAGACTG 240
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Db 361 CGGTTAGTGCACCTCTGCTGTATATTTAACTCCCTTAAAGAAATA 360
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Oy 541 GAAATTTTACTTCTTCCGAGATCAATGGAAGTCTGATTTCACTGATTTACTTACTT 600
Db 541 GAAATTTTACTTCTTCCGAGATCAATGGAAGTCTGATTTCACTGATTTACTTACTT 600
Oy 601 GCGTACGTCAAGAGTTTGTGACCTGGGCAAGTCTCGGCAATGAGACATTCAGATT 660

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Db 601 GGGTACGTACAGATTGTGGACCTGGGCAATGCTCGGCAATGGAAATTCAGAGTT 660
OY 661 CTCGAGCAATGGAAGAGATTCATCATTCAGAGCCCTGAAAAACATTTGGAGCCCTG 720
Db 661 CTCGAGCAATGGAAGAGATTCATCATTCAGAGCCCTGAAAAACATTTGGAGCCCTG 720
OY 721 ATCCAGCTGTGAGAGAGCTTCAGATGTAAATGATCCCTGACTGTCTGTGTGAGCGTA 780
Db 721 ATCCAGCTGTGAGAGAGCTTCAGATGTAAATGATCCCTGACTGTCTGTGTGAGCGTA 780
OY 781 TTTCCTCATTTGGGCTGAGGCTTCATAGGGAACCTGAGGAATTAATGATACAAATG 840
Db 781 TTTCCTCATTTGGGCTGAGGCTTCATAGGGAACCTGAGGAATTAATGATACAAATG 840
OY 841 CCTCCACCAATGCTCTCTTTGGAGAAACATAGTATAGAAAAAGATTAATCTGTAATTA 900
Db 841 CCTCCACCAATGCTCTCTTTGGAGAAACATAGTATAGAAAAAGATTAATCTGTAATTA 900
OY 901 AATGTACACTTATTAATGAATGAACCTGCTTTGAGTTGACTGGAATCATATATTCAGAT 960
Db 901 AATGTACACTTATTAATGAATGAACCTGCTTTGAGTTGACTGGAATCATATATTCAGAT 960
OY 961 TCAAGATATCATATTTCTGAGAGGCTTTTATGATGCACTACTATGTGGAATAGCTCT 1020
Db 961 TCAAGATATCATATTTCTGAGAGGCTTTTATGATGCACTACTATGTGGAATAGCTCT 1020
OY 1021 GATGCAAGCAATGCTTCAGAGGATATATGTGTGAAGAGCTGGTGAATATCCCAATTA 1080
Db 1021 GATGCAAGCAATGCTTCAGAGGATATATGTGTGAAGAGCTGGTGAATATCCCAATTA 1080
OY 1081 GGCCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTGTCTTGTTCGACTAATGACT 1140
Db 1081 GGCCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTGTCTTGTTCGACTAATGACT 1140
OY 1141 CAGGACTTTGGGAAAAATTTTATCACTGACATACGTCGCTGCGGAAAAAGCTACATG 1200
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Db 1501 AGGAGAAAAAGAAAAAGAAAGAGAGCTGTGGGGAAGAGAAANTAGAGATGAAATTC 1560
OY 1561 CAAAAATCTGAATCTGAGAGAGAGATCAGAGAGAAAGTTTTCGTTCTTCATTGAAGG 1620
Db 1561 CAAAAATCTGAATCTGAGAGAGAGATCAGAGAGAAAGTTTTCGTTCTTCATTGAAGG 1620
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Db 1621 AACCGATTGACATGAAAAAGAGTACTCTCCACACAGCTTTGTTGAGACATCCGT 1680
OY 1681 GGCTCCCTATTTTACCAAGGGGAAATAGCAGAAAGCTTTTACGCTTAAAGGCGCA 1740
Db 1681 GGCTCCCTATTTTACCAAGGGGAAATAGCAGAAAGCTTTTACGCTTAAAGGCGCA 1740

|||||
Db 1741 GCAAAGATGTGGGATCTGAGAAACGACTTGCAGATGATGAGCAGACACTTTGAGGAT 1800
OY 1741 GCAAAGATGTGGGATCTGAGAAACGACTTGCAGATGATGAGCAGACACTTTGAGGAT 1800
Db 1741 GCAAAGATGTGGGATCTGAGAAACGACTTGCAGATGATGAGCAGACACTTTGAGGAT 1800
OY 1801 AAGCAGAGCCGTAGAGATTCCTTGTGTGTGCCCCGAGCAGACAGAGAGAGAGCAACAGC 1860
Db 1801 AAGCAGAGCCGTAGAGATTCCTTGTGTGTGCCCCGAGCAGACAGAGAGAGAGCAACAGC 1860
OY 1861 AACCTGATGAGACCAATAGATGATATCCGATGCTGACATGTTTCCAGGAAATGGGAG 1920
Db 1861 AACCTGATGAGACCAATAGATGATATCCGATGCTGACATGTTTCCAGGAAATGGGAG 1920
OY 1921 ATGCAAGCAGACTGTGATTCATATGATGTGTTCCTTGTGTGTGAGACCTTCAGTTCT 1980
Db 1921 ATGCAAGCAGACTGTGATTCATATGATGTGTTCCTTGTGTGTGAGACCTTCAGTTCT 1980
OY 1981 ACATGCGCTGTGAGACAGCTTCTGCGAGAGGTGATTAATAGATTAAGCAGCTACTGATAC 2040
Db 1981 ACATGCGCTGTGAGACAGCTTCTGCGAGAGGTGATTAATAGATTAAGCAGCTACTGATAC 2040
OY 2041 AATGGAACAACCACTGAAATCTGAAATGAGAAAGAGTCAAGTTCTTTCACAGTTCC 2100
Db 2041 AATGGAACAACCACTGAAATCTGAAATGAGAAAGAGTCAAGTTCTTTCACAGTTCC 2100
OY 2101 ATGAGACTTTTAGAGATTCCTTCCAAAGGCAAGCAATGATATAGCAGACTTCTA 2160
Db 2101 ATGAGACTTTTAGAGATTCCTTCCAAAGGCAAGCAATGATATAGCAGACTTCTA 2160
OY 2161 ACAAAATACAGTAGAGAACTTGAAGAAATCCAGGAGAAATGCCACCTTGTGTATATA 2220
Db 2161 ACAAAATACAGTAGAGAACTTGAAGAAATCCAGGAGAAATGCCACCTTGTGTATATA 2220
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Db 2221 TTTTCCAAATTTCTTAATCTGGAGCTGTTCCTCAATGTGTGTTAAAGGAAACATGTT 2280
OY 2281 GTCACCTGTGTGATGAGAGCACTTGTGACCTGCGCACACATCTGATTTGCTTA 2340
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OY 2461 GCCATGATCTCTTAATTTTCCAAAGAGGCTGGAATATCTTTGACGGTTTATTTGTC 2520
Db 2461 GCCATGATCTCTTAATTTTCCAAAGAGGCTGGAATATCTTTGACGGTTTATTTGTC 2520
OY 2521 AGCCTTAGCCTGTGATGAATCTGAGCTGCCAATGTGGAAGATTAATCTGTTCCCTCA 2580
Db 2521 AGCCTTAGCCTGTGATGAATCTGAGCTGCCAATGTGGAAGATTAATCTGTTCCCTCA 2580
OY 2581 TTTGATTTGCTGAGATTTTCAAGTTGCAAAATCTTGGCAAGTTAAATATGCTAATA 2640
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OY 2641 AAGATCATCGGCAATTCGAGGAGGCTCTGGAATTTAACCTCGTGGGCAATCATC 2700
Db 2641 AAGATCATCGGCAATTCGAGGAGGCTCTGGAATTTAACCTCGTGGGCAATCATC 2700
OY 2701 GTCTTCATTTTCCCGGTGCGGATGCAATGCTTTGTTGTTAAAGCTTAAAGATTTGTC 2760
Db 2701 GTCTTCATTTTCCCGGTGCGGATGCAATGCTTTGTTGTTAAAGCTTAAAGATTTGTC 2760
OY 2761 TGCAGATGCGCAGTATGTTCAATCCAGGCTGCGACATGATGATCTTCCACTCC 2820
Db 2761 TGCAGATGCGCAGTATGTTCAATCCAGGCTGCGACATGATGATCTTCCACTCC 2820
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OY 2821 TTCCGATGTTGTTCGGGCTGCTGTGTGGAGTGGATAGAACCATGTGGACCTGTATG 2880  
 DB 2821 TTCCGATGTTGTTCGGGCTGCTGTGTGGAGTGGATAGAACCATGTGGACCTGTATG 2880  
 OY 2881 GAGGTGCGGTCAGACCATGTGCGCTTACTGCTTCATGATGATGATGATGATGATGATG 2940  
 DB 2881 GAGGTGCGGTCAGACCATGTGCGCTTACTGCTTCATGATGATGATGATGATGATGATG 2940  
 OY 2941 CTAGTGTGCTGAATCTCTTCTGCGCTTGTGCTTGTGAGCTCATTTAGTGCAGACAACCT 3000  
 DB 2941 CTAGTGTGCTGAATCTCTTCTGCGCTTGTGCTTGTGAGCTCATTTAGTGCAGACAACCT 3000  
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 OY 3361 GAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3420  
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 DB 3421 AGCAAGAGAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3480  
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 OY 3541 TTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3600  
 DB 3541 TTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3600  
 OY 3601 GGAAGAGAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3660  
 DB 3601 GGAAGAGAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3660  
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 OY 3721 TATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3780  
 DB 3721 TATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3780  
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 OY 3841 ACCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3900  
 DB 3841 ACCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3900

OY 3901 GGAATGCTGTGGCTTACTCAGAACTGGAGCCATCAATTCCTCAGACACTAGAGCT 3960  
 DB 3901 GGAATGCTGTGGCTTACTCAGAACTGGAGCCATCAATTCCTCAGACACTAGAGCT 3960  
 OY 3961 CTGAGACCTCTAAGACCTTATCTGATTTGAAGGATGAGGCTGTTGATGACCTT 4020  
 DB 3961 CTGAGACCTCTAAGACCTTATCTGATTTGAAGGATGAGGCTGTTGATGACCTT 4020  
 OY 4021 TTAGAGCAATTCATCATCATGATGATGATGATGATGATGATGATGATGATGATG 4080  
 DB 4021 TTAGAGCAATTCATCATCATGATGATGATGATGATGATGATGATGATGATGATG 4080  
 OY 4081 TTACAGATCATGAGCTAATTTGTTGCTGGAATTTACACCTGTTATACACACA 4140  
 DB 4081 TTACAGATCATGAGCTAATTTGTTGCTGGAATTTACACCTGTTATACACACA 4140  
 OY 4141 ACTGGTGACAG 4152  
 DB 4141 ACTGGTGACAG 4152

## RESULT 14

AAD32842  
 ID AAD32842 standard; cDNA; 4146 BP.

AC AAD32842;

DT 01-JUL-2002 (first entry)

XX Human ion channel cDNA #4.

XX Human; novel human protein; NHP; voltage-gated sodium channel;

KW gene therapy; bioreactor; mental disorder; biological disorder;

KM gene; medical disorder; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FH CDS 1..4146

FT /product= "Human ion channel protein #4"

FT /transl\_except= (pos:2941..2943 aa:xaa)

FT /transl\_except= (pos:3166..3168 aa:xaa)

FT /note= "Xaa = any amino acid"

XX WO200214498-A2.

PD 21-FEB-2002.

XX 15-AUG-2001; 2001WO-0525650.

PR 16-AUG-2000; 2000US-225989P.

XX (LEXI-) LEXICON GENETICS INC.

PA Turner CA, Mathur B, Mathur D;

DR WPI: 2002-280757/32.

PS P-PSDB: AAE20513.

PT Novel polynucleotides encoding human sodium channel proteins,

PT particularly voltage-gated sodium channel proteins useful for drug

CC screening, diagnosis and in gene therapy of biological disorders

CC Claim 1: Page 46-47; 83pp; English.

CC The present sequence is a cDNA encoding novel human protein (NHP), ion

channel protein. NHP share structural similarity with mammalian sodium

channel proteins particularly voltage-gated sodium channel proteins.

CC NHP oligonucleotides are useful as hybridisation probes for screening

CC libraries and assessing gene expression patterns. Sequences derived

CC from regions adjacent to the intron/exon boundaries of NHP gene can be

CC used to design primers for use in amplification assays to detect

CC mutations within the exons, splice sites, introns that can be used in  
CC diagnostics and pharmacogenomics. NHP nucleotide sequences are useful  
CC for drug screening effective in the treatment of symptomatic or  
CC phenotypic manifestations of perturbing the normal function of NHP in  
CC the body, and nucleotide constructs encoding NHP products are useful to  
CC genetically engineer host cells to express NHP products in vivo. These  
CC genetically engineered cells function as bioreactors in the body  
CC delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion  
CC protein to the body. Nucleotide construct encoding NHP products are  
CC also useful in gene therapy for modulating NHP expression and to  
CC produce genetically engineered host cells to express NHP products in  
CC vivo. NHP nucleotide sequences may also be used as part of ribozyme  
CC and/or triple helix sequences that are useful for NHP gene regulation.  
CC The NHP polypeptides are useful for generating antibodies, as  
CC reagents in diagnostic assays, for identifying other cellular gene  
CC products related to NHP and as reagents in assays for screening for  
CC compounds that are useful in the treatment of mental, biological or  
CC medical disorders and diseases.

XX Sequence 4146 BP; 1226 A; 810 C; 951 G; 1156 T; 3 other;

Query Match 67.6%; Score 4074.8; DB 24; Length 4146;

Best Local Similarity 99.2%; Pred. No. 0; Mismatches 0; Indels 33; Gaps 1;

Matches 4119; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

QY 1 ATGGAGCAAAAGTGGCTTGTACACAGACGACGCTTCACTTCCACACAGAA 60  
DB 1 ATGGAGCAAAAGTGGCTTGTACACAGACGACGCTTCACTTCCACACAGAA 60  
QY 61 TCTCTTGGGCTATTGAAAGAGCATTGCAAGAAAGCAAGAAATCCCAACAGAC 120  
DB 61 TCTCTTGGGCTATTGAAAGAGCATTGCAAGAAAGCAAGAAATCCCAACAGAC 120  
QY 121 AAAAAAGATGAGCAGCAAAATGAGCAAAAGCAAAATGAGTGAAGCTGGAAGAAC 180  
DB 121 AAAAAAGATGAGCAGCAAAATGAGCAAAAGCAAAATGAGTGAAGCTGGAAGAAC 180  
QY 181 CTTCATTTATTTATGAGAGCATCTCCAGAGATGCTCAGAGCCCTGAGAGACTG 240  
DB 181 CTTCATTTATTTATGAGAGCATCTCCAGAGATGCTCAGAGCCCTGAGAGACTG 240  
QY 241 GACCCCTACTATATCAATAAAGAACTTTATATGATTAATAAGGAGAGCCATCTC 300  
DB 241 GACCCCTACTATATCAATAAAGAACTTTATATGATTAATAAGGAGAGCCATCTC 300  
QY 301 CGGTAGAGCCACCTGCTGCTGATCACTTAACTCCCTCAATCCCTTAGAAGAAATA 360  
DB 301 CGGTAGAGCCACCTGCTGCTGATCACTTAACTCCCTCAATCCCTTAGAAGAAATA 360  
QY 361 GCTATTAGATTTTGTATCATTTATTCAGCATGCTAATTAATGTCATATTTTGACA 420  
DB 361 GCTATTAGATTTTGTATCATTTATTCAGCATGCTAATTAATGTCATATTTTGACA 420  
QY 421 AACTGTGTGTTTATGACATGAGTAACCTCTGATTTGACAAAGAAATGAGATACAC 480  
DB 421 AACTGTGTGTTTATGACATGAGTAACCTCTGATTTGACAAAGAAATGAGATACAC 480  
QY 481 TTCACAGAAATATATCTTTGAAATCACTTAATAAATTTTGCAAGGGATCTGTTTA 540  
DB 481 TTCACAGAAATATATCTTTGAAATCACTTAATAAATTTTGCAAGGGATCTGTTTA 540  
QY 541 GAAGATTTTACTTCTTGGGATGCCATGAGACCTGGCTGATTTCACTGATTAATTT 600  
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QY 721 ATCCAGTCTGTGAAGAGCTCTCAGATGTAATGATCTGACTGTCTGTGAGCGTA 780  
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QY 781 TTGCTCTATTTGGGCTGGAGCTGTCATGAGGCAACCTGAGGAATTAATATCAATG 840  
DB 781 TTGCTCTATTTGGGCTGGAGCTGTCATGAGGCAACCTGAGGAATTAATATCAATG 840  
QY 841 CTCCACCAATGCTTCTTGGAGGAACATGATATGAAAGATTAATGATTAAT 900  
DB 841 CTCCACCAATGCTTCTTGGAGGAACATGATATGAAAGATTAATGATTAAT 900  
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DB 1021 GATGAGGCCAATGCTCCAGAGGATATGATGTAAGAGCTGTAAGAAATCCCAATTAT 1080  
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QY 1141 CAGAGCTTCTGGGAAATCTTTATCAATGACATTTAGCTGCTGAGAAACGATCATG 1200  
DB 1141 CAGAGCTTCTGGGAAATCTTTATCAATGACATTTAGCTGCTGAGAAACGATCATG 1200  
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DB 1261 GTGTGCGCATGCTCAGAGAGCAAGAAATCAGGCCACTTGGAGAGCAAGCAAGAA 1320  
QY 1321 GAGCCGCAATTTACAGAGATGATTAAGCAACCTTTAAAGACAGAGAGCCATCAGAG 1380  
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DB 1741 GCAAGAGATGAGGATCTGAGAGCACTTGCAGATGATGAGAGACAGACCTTTGAGAGAT 1800  
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 DB 4108 ACTGCTGACAGG 4119

RESULT 15  
 AAD32848  
 ID AAD32848 standard; cDNA; 4197 BP.  
 AC AAD32848;  
 XX  
 DT 01-JUL-2002 (first entry)  
 XX  
 DE Human ion channel cDNA #10.  
 XX  
 KW Human; novel human protein; NHP; voltage-gated sodium channel;  
 KW gene therapy; bioreactor; mental disorder; biological disorder;  
 KW gene; medical disorder; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..4197  
 FT /tag- a  
 FT /product- "Human ion channel protein #10"  
 FT /transl\_except- (pos:2974..2976, aa:1aa)  
 FT /transl\_except- (pos:3199..3201, aa:1aa)  
 FT /note- "Xaa = any amino acid"  
 XX  
 PN WC0200214498-A2.  
 XX  
 PD 21-FEB-2002.  
 XX  
 PF 15-AUG-2001; 2001MO-US25550.  
 XX  
 PR 16-AUG-2000; 2000US-225989P.  
 XX  
 PA (LEXI-) LEXICON GENETICS INC.  
 XX  
 PI Turner CA, Mathur B, Mathur D;  
 XX  
 DR WPI; 2002-280757/32.  
 DR P-PSDB; AAE20519.  
 XX  
 PT Novel polynucleotides encoding human sodium channel proteins,  
 PT particularly voltage-gated sodium channel proteins useful for drug  
 PT screening, diagnosis and in gene therapy of biological disorders  
 XX  
 PS Claim 1; Page 78-79; 83pp; English.  
 XX

CC delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion  
 CC protein to the body. Nucleotide construct encoding NHP products are  
 CC also useful in gene therapy for modulating NHP expression and to  
 CC produce genetically engineered host cells to express NHP products in  
 CC vivo. NHP nucleotide sequences may also be used as part of ribozyme  
 CC and/or triple helix sequences that are useful for NHP gene regulation.  
 CC The NHP polypeptides are useful for generating antibodies, as  
 CC reagents in diagnostic assays, for identifying other cellular gene  
 CC products related to NHP and as reagents in assays for screening for  
 CC compounds that are useful in the treatment of mental, biological or  
 CC medical disorders and diseases.  
 XX

Sequence 4197 BP; 1232 A; 821 C; 965 G; 1176 T; 3 other;  
 Query Match 67.3%; Score 4057.8; DB 24; Length 4197;  
 Best Local Similarity 98.5%; Pred. No. 0;  
 Matches 4133; Conservative 0; Mismatches 0; Indels 64; Gaps 1;

QY 1 ATGAGCAAAACAGTGTGTTACACACGACGCTTCAACTCTTACCAGAA 60  
 DB 1 ATGAGCAAAACAGTGTGTTACACACGACGCTTCAACTCTTACCAGAA 60  
 QY 61 TCTCTTGGGCTATGAAAGCGATTCGAGAAAGGCAAGATCCCAACGAC 120  
 DB 61 TCTCTTGGGCTATGAAAGCGATTCGAGAAAGGCAAGATCCCAACGAC 120  
 QY 121 AAAAAAGATGACGACGAAATGCGCCCAAGCCAAATGATGATGGAAGGCAAG 180  
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 DB 541 GAAGATTTTACTTCTTGGGATTCAGATGGAAGCTGATTTCACTGATTAATTT 600  
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OY 901 AATGATACACTTATTAATGAAGAACTCTTATAGTTGACTGGAAGTCAATATATCAAGAT 960  
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OY 961 TCAAGATATCATATATTTCTGAGAGGTTTTTATAGTACATATATGTGGAATAGCTCT 1020  
DB 961 TCAAGATATCATATATTTCTGAGAGGTTTTTATAGTACATATATGTGGAATAGCTCT 1020  
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DB 1021 GATGACAGGCCAATGTCAGAGAGGATATATGTGTGGAAGTGTGAGAAATCCCAATAT 1080  
OY 1081 GGCTACACACACTTTGATACCTGAGTGGGCTTTTGTCTGTTTTCGACTAATGACT 1140  
DB 1081 GGCTACACACACTTTGATACCTGAGTGGGCTTTTGTCTGTTTTCGACTAATGACT 1140  
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DB 1381 GCAGCAACGCGCACTGCTCAGACATTCAGAGAGCCGAGTGCAGCGAGGCTCTCA 1440  
OY 1441 GACAGCTCATCTGAAGCTTGAAGTTGATTCAGAGAGTGGCTAAGAAAGAAATGAG 1500  
DB 1441 GACAGCTCATCTGAAGCTTGAAGTTGATTCAGAGAGTGGCTAAGAAAGAAATGAG 1500  
OY 1501 AGGAGAGAAAGAAACAGAAAGAGAGCTGTGGTGGGAGAGAAAGATGAGATGAATTC 1560  
DB 1501 AGGAGAGAAAGAAACAGAAAGAGAGCTGTGGTGGGAGAGAAAGATGAGATGAATTC 1560  
OY 1561 CAAAATATCTGATCTGAGAGACATCAGAGAGAAAGTTTCGCTTCCATTTGAAAGG 1620  
DB 1561 CAAAATATCTGATCTGAGAGACATCAGAGAGAAAGTTTCGCTTCCATTTGAAAGG 1620  
OY 1621 AACGATGACATATGAAAGAGAGAGCTGCTCCACACAGCTTTTGTGAGCAATCCG 1680  
DB 1621 AACGATGACATATGAAAGAGAGCTGCTCCACACAGCTTTTGTGAGCAATCCG 1680  
OY 1681 GGCTCCCTATTTTACAGAGGAGAAATAGCAGAACACCTTTTACGCTTTAGAGAGGGA 1740  
DB 1681 GGCTCCCTATTTTACAGAGGAGAAATAGCAGAACACCTTTTACGCTTTAGAGAGGGA 1740  
OY 1741 GCAAGAGATGTGGATCTGAGAGACATTCGAGATGATGACACAGCACTTTGAGAT 1800  
DB 1741 GCAAGAGATGTGGATCTGAGAGACATTCGAGATGATGACACAGCACTTTGAGAT 1800  
OY 1801 AACGAGACCGTAGATCTGCTGTTGTGGCCGACAGACAGGAGAGAGAGCAACAGC 1860  
DB 1801 AACGAGACCGTAGATCTGCTGTTGTGGCCGACAGACAGGAGAGAGAGCAACAGC 1860  
OY 1861 AACGAGATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1920  
DB 1861 AACGAGATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1920

OY 1921 ATGCACACACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1980  
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OY 1981 ACATGCGCTGTGTGACAGCTTCTGACAGAGGTGATATATATATATATATATATATAT 2040  
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DB 2041 AATGAGACACACTGAAATGAAATGAAAGAGAGAGCTCAATGTTCTTCCAGCTTCC 2100  
OY 2101 ATGACCTTCTGAAAGATCTTCCCAAGGAGAGAGAGAGATGATGATGATGATGATG 2160  
DB 2101 ATGACCTTCTGAAAGATCTTCCCAAGGAGAGAGAGAGATGATGATGATGATGATG 2160  
OY 2161 ACAATATAGATGAG 2220  
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OY 2221 TTTTCAACATATCTTATCTGAGCTGTTCTCCATATGTTAAAGTAAAGATGATG 2280  
DB 2221 TTTTCAACATATCTTATCTGAGCTGTTCTCCATATGTTAAAGTAAAGATGATG 2280  
OY 2281 GTCAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2340  
DB 2281 GTCAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2340  
OY 2341 AATATCTTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2400  
DB 2341 AATATCTTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2400  
OY 2401 ACAGTATGAG 2460  
DB 2401 ACAGTATGAG 2460  
OY 2461 GCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2520  
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OY 2521 ACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2580  
DB 2521 ACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2580  
OY 2581 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2640  
DB 2581 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2640  
OY 2641 AAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2700  
DB 2641 AAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2700  
OY 2701 GCTTCAATTTTGGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2760  
DB 2701 GCTTCAATTTTGGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2760  
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OY 2821 TTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2880  
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OY 3001 GCAGCCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3060

[illegible]



GenCore version 5.1.4.P5\_4578  
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OM nucleic - nucleic search, using sw model

Run on: April 22, 2003, 06:56:18 ; Search time 5065 Seconds

(Without alignments)  
19281.103 Million cell updates/sec

Title: US-09-930-871-11

Perfect score: 6030  
Sequence: 1 atggagcaacagctgtctgt.....aaaagccaaaggaataa 6030

Scoring table: IDENTITY\_NDC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 809774336 residues

Total number of hits satisfying chosen parameters: 33308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

EST:\*  
1: em\_estda:\*  
2: em\_esthm:\*  
3: em\_estln:\*  
4: em\_estmu:\*  
5: em\_estow:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score  | Query Match | Length | ID | Description        |
|------------|--------|-------------|--------|----|--------------------|
| 1          | 1039.8 | 17.2        | 1777   | 11 | BC029489 Homo sapi |
| 2          | 670    | 11.1        | 951    | 9  | AL533359 AL533359  |
| 3          | 668.2  | 11.1        | 928    | 14 | BO715936 BO715936  |
| 4          | 634.2  | 10.5        | 735    | 13 | BI488967 603021693 |
| 5          | 570.6  | 9.5         | 579    | 14 | BM718214 BM718214  |
| 6          | 557.4  | 9.2         | 674    | 12 | BC342331 BC342331  |

| Result No. | Score | Query Match | Length | ID | Description       |
|------------|-------|-------------|--------|----|-------------------|
| 7          | 555.8 | 9.2         | 562    | 14 | BM682680 BM682680 |
| 8          | 548   | 9.1         | 774    | 13 | BI488799 BI488799 |
| 9          | 518.6 | 8.6         | 618    | 10 | BB622500 BB622500 |
| 10         | 511.6 | 8.5         | 602    | 9  | AL706368 AL706368 |
| 11         | 495.8 | 8.2         | 778    | 9  | AU035605 AU035605 |
| 12         | 468.4 | 7.8         | 731    | 9  | A1796628 A1796628 |
| 13         | 454.8 | 7.5         | 716    | 14 | BQ444145 BQ444145 |
| 14         | 447.8 | 7.4         | 706    | 9  | AA984063 AA984063 |
| 15         | 438.8 | 7.3         | 547    | 12 | BF470392 BF470392 |
| 16         | 435.4 | 7.2         | 598    | 14 | BM726341 BM726341 |
| 17         | 431.8 | 7.2         | 665    | 13 | BB653350 BB653350 |
| 18         | 431.4 | 7.2         | 683    | 13 | BI667397 BI667397 |
| 19         | 421.4 | 7.0         | 689    | 12 | BF347024 BF347024 |
| 20         | 414   | 6.9         | 510    | 11 | BC023034 BC023034 |
| 21         | 413.8 | 6.9         | 561    | 12 | BF076296 BF076296 |
| 22         | 413   | 6.8         | 509    | 11 | BQ034643 BQ034643 |
| 23         | 407   | 6.7         | 708    | 14 | BQ946179 BQ946179 |
| 24         | 402.4 | 6.7         | 700    | 12 | BB631922 BB631922 |
| 25         | 399.2 | 6.6         | 873    | 12 | BF527027 BF527027 |
| 26         | 398   | 6.6         | 662    | 12 | BG253038 BG253038 |
| 27         | 397.6 | 6.6         | 952    | 13 | BI458325 BI458325 |
| 28         | 395.4 | 6.6         | 809    | 12 | BG541438 BG541438 |
| 29         | 390.6 | 6.5         | 508    | 13 | BI731882 BI731882 |
| 30         | 389.8 | 6.5         | 934    | 9  | AL517958 AL517958 |
| 31         | 388   | 6.4         | 513    | 13 | BI731739 BI731739 |
| 32         | 384.2 | 6.4         | 902    | 12 | BG761119 BG761119 |
| 33         | 374.2 | 6.2         | 608    | 10 | AM140953 AM140953 |
| 34         | 371   | 6.2         | 448    | 12 | BE864903 BE864903 |
| 35         | 366.8 | 6.1         | 450    | 9  | AL120392 AL120392 |
| 36         | 363.6 | 6.0         | 812    | 12 | BG666779 BG666779 |
| 37         | 359.2 | 6.0         | 939    | 13 | BI600029 BI600029 |
| 38         | 353   | 5.9         | 437    | 10 | AM495598 AM495598 |
| 39         | 351.2 | 5.8         | 656    | 10 | AV721039 AV721039 |
| 40         | 350.8 | 5.8         | 402    | 13 | BM484672 BM484672 |
| 41         | 350.6 | 5.8         | 547    | 12 | BE724185 BE724185 |
| 42         | 345.6 | 5.7         | 540    | 10 | BE121161 BE121161 |
| 43         | 345.6 | 5.7         | 700    | 17 | AO631408 AO631408 |
| 44         | 345.4 | 5.7         | 610    | 9  | AL588672 AL588672 |
| 45         | 338   | 5.6         | 854    | 13 | BI599275 BI599275 |

#### ALIGNMENTS

RESULT 1  
LOCUS BC029489 1777 bp mRNA linear HTC 16-MAY-2002  
DEFINITION Homo sapiens, clone IMAGE:5276436, mRNA.  
ACCESSION BC029489  
VERSION BC029489.1 GI:20809571  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 1777)  
REFERENCE  
AUTHORS Strausberg, R.  
TITLE Direct Submission  
JOURNAL Submitted (01-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
NIR-MGC Project URL: <http://mgc.ncl.nih.gov>  
Contact: MGC help desk  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Miklos Pavlovits, M.D., Ph.D.  
CDNA Library Preparation: Michael J. Brownstein (NMGRI) & Shiraki Toshitsuki and Piero Carninci (RIKEN)  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305  
Web site: <http://www-shgc.stanford.edu>  
Contact: (Dickson, Mark) [mdc@paxill.stanford.edu](mailto:mdc@paxill.stanford.edu)

Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILM at: <http://image.llnl.gov>  
Series: IRK Plate: 48 Row: h Column: 9  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA 91: 10337596  
This clone has the following problem: frame shifted.

## FEATURES

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1. 1777  
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/db\_xref="taxon:9606"  
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/lab\_host="DH10B"  
/note="Vector: pBluescript"  
BASE COUNT 526 a 333 c 395 g 523 t  
ORIGIN

Query Match 17.2%; Score 1039.8; DB 11; Length 1777;  
Best Local Similarity 81.4%; Pred. No. 1.3e-235;  
Matches 1245; Conservative 0; Mismatches 272; Indels 12; Gaps 3;

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OY 1 ATGAGCAACAGCTCTGTACACAGAGCTGACAGCTTCACCTTCACACAGAGAA 60
DB 248 ATGGACAGCTGCTGTACCCGAGAGCCGACAGCTTCGCTTCCTTACAGAGAA 307
OY 61 TCTCTGGGCGCATTTGAAAGAGCATTTGAGAAAGAAAGCAAAATCCCAACAGAA 119
DB 308 TCCCTGTGCTATTGAAACAGCAGTATGAGAAAGAAAGAGAGAGCCCAAGAGAA 367
OY 120 -CAAAAAGATGAGCAGCAAAATGAGCCCAAGCCAAATAGTACTTGGAGCTGAAAG 177
DB 368 GCGAAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 427
OY 178 AACCTTCATTTATTTATGAGAGACATTCCTCAGAGATGCTCAGAGCCCTGAGAG 237
DB 428 TCTCTTCATTTATTTATGAGAGACATTCCTCAGAGATGCTCAGAGCCCTGAGAG 487
OY 238 CTGAGCCCTACTATATCAATAAGAAACTTTATGATTTCAATTAAGAAAGGCAAC 297
DB 488 CTGAGCCCTACTATATGATTAAGAAAGCTTTATGATTAAGAAAGGCAAGCAATC 547
OY 238 TTCCGGTTCAGTGCACCTCTGCTGATCTTTTAACTCCCTTCATCTCTTAGAGAA 357
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OY 358 ATAGCTATTAGATTTGGTACATTCATTTATGAGAGCTCAATTAATGACATATTTG 417
DB 608 TTAGCTATTAGATTTGGTACATTCATTTTCAATATCTCAATTAATGAGAGCTCTT 667
OY 418 ACAACTGTGTTATGAGATGAGTAACTCCCTGATTTGAGCAAGAAATGAGAAATAC 477
DB 668 ACCAAGTGTGTTATGAGATGAGTAACTCCCTGATTTGAGCAAGAAATGAGAGTAT 727
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DB 728 ACCCTCAGAGAAATATATCTTTGATCACTTATTAATAATTAATGAGAGGATCTGT 787
OY 538 TTAGAAGATTTACTTCTCTCGGATTCAGTGAAGAGTGGCTGATTCAGTCTATTA 597
DB 788 TTAGAAGATTTACTTCTCTCGGATTCAGTGAAGAGTGGCTGATTCAGTCTATTA 847
OY 598 TTGGTGTGTCAGAGATTTGAGAGCTGGGCAATGCTCGGATTTGAGCAATTAACA 657
DB 848 TTGGTGTGTCAGAGATTTGAGAGCTGGGCAATGCTCGGATTTGAGCAATTAACA 907
OY 658 GTTCTCCGAGCATTTAGAGCATTTAGATCACTTCAAGGCTGAAAGCAATTTGGAGAG 717
DB 908 GTTCTCCGAGCATTTAGAGCATTTAGATCACTTCAAGGCTGAAAGCAATTTGGAGAG 967

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OY 718 CTGATCCAGTCTGTGAAGAAAGCTCTAGATGTAATGATCTGACTGTCTGTGAGC 777
DB 968 CTGATCCAGTCTGTGAAGAAAGCTCTGTGATGATGATGATGATGATGATGATGAT 1027
OY 778 GTATTTGCTGATTTGAGGCTGAGAGCTGATGAGGAGGAGGAGGAGGAGGAGGAGG 837
DB 1028 GTATTTGCTGATTTGAGGCTGAGAGCTGATGAGGAGGAGGAGGAGGAGGAGGAGG 1087
OY 838 TGCCCTCCGAGCATTTGAGGCTGAGAGCAAT---AGTATGAGAAAGAAATTAATCTGTG 894
DB 1088 TGCCCTCCGAGCATTTGAGGCTGAGAGCAAT---AGTATGAGAAAGAAATTAATCTGTG 1147
OY 895 AATTATTAAGTGTACCTTATTAATGAGAAAGCTCTGAGTTGATGAGTGAAGTATATAT 954
DB 1148 GATGGAGATGTGACTTACTTCAATAGAGAGTGAAGATATTAATGAGGATATATAT 1207
OY 955 CAGATTTCAAGATATATATTTTCCGAGAGGATTTTATGATGATGATGATGATGAT 1014
DB 1208 GAGGATTAAGATCACTTATTTTATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1267
OY 1015 AGCTGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1074
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OY 1075 AATTATGAGTACAAAGCTTTGATACCTTCAAGTGGGCTTTTGTCTGTTGAGACTA 1134
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OY 1135 ATGATCAGAGATCTTGGGAGAAATCTTTATCACTGATATGATGATGATGATGAT 1194
DB 1388 ATGATCAGAGATCTTGGGAGAAATCTTTATCACTGATATGATGATGATGATGAT 1447
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DB 1448 TACATGATATTTTGTGTTGATGATGATGATGATGATGATGATGATGATGATGAT 1507
OY 1255 CTGGCTGTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1314
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OY 1315 CAGAAAGAGGCGCAATTTGAGAGATGATGATGATGATGATGATGATGATGATGATG 1374
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DB 1628 CAGCAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1687
OY 1429 GCGAGGCTCTCAGACAGCTCATCTGAAAGCCTTAAGTTGAGTTCAAGAGTCTAAGAA 1488
DB 1688 GCGAGGCTCTCAGACAGCTCATCTGAAAGCCTTAAGTTGAGTTGAGTTCAAGAGTCT 1747
OY 1489 AGAAGAAATCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1517
DB 1748 CTGAGAAATCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1776

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RESULT 2  
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DEFINITION pr1me, mRNA sequence.  
ACCESSION AL533359  
VERSION AL533359.1 GI:12796852  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 951)  
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)



Db 301 TTGGCAACAGCATGATGCTGCTGTTCCAAATACCACTCTGCGGGCTGGATGACTG 360  
 OY 5188 CTAGACACCATTTCTCAACAGTAAGCCACCGAGCTGTGACCTTATTAAGTTAAAGCTTGA 5247  
 Db 361 TTGGCCCCCATCTCTCAACAGTAAGCCACCGAGCTGTGACCTTATTAAGTTAAAGCTTGA 420  
 OY 5248 AGCTCAAGTTAAGGAGACTGTGGGAACCCATCTGTTGGAATTTCTTTTGTTCAGTTAC 5307  
 Db 421 AGCTCAAGTTAAGGAGACTGTGGGAACCCATCTGTTGGAATTTCTTTTGTTCAGTTAC 480  
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RESULT 4  
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 LOCUS BI488967 603021693F1 NIH\_MGC\_114 Homo sapiens cDNA clone IMAGE:5192182 5'  
 DEFINITION mRNA sequence.

ACCESSION BI488967  
 VERSION BI488967  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 735)  
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgabbs-remail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: L14M1480 row: j column: 23  
 High quality sequence stop: 728.  
 Location/Qualifiers  
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 Site\_2: EcoRV (destroyed); RNA source anonymous pool of 6  
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 upon cloning). Average insert size 1.5 kb. Insert size  
 range 1-3 kb. Library is normalized and enriched for  
 full-length clones and was constructed by C. Gruber  
 (Invitrogen). Research Genetics tracking code 019. Note:  
 this is a NIH\_MGC library."

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 OY 4954 GGAGCAAAAGGGAGATCCGACGCTGCTCTTGGCTTTGATGATGATGATGATGATGATGATGAT 5013  
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 Db 120 AACATGCGCT 179  
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 OY 5134 AACAGCATGATCTGCTATTTCCAAATTAACAACCTCTGCTGGCTGGAGTGGATGATGATGATGAT 5193  
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 OY 5254 GTTAAGGAGACATGTGGGAACCCATCTGTTGGAATTTCTTTTGTTCAGTTATCATATC 5313  
 Db 360 GTTAAGGAGACATGTGGGAACCCATCTGTTGGAATTTCTTTTGTTCAGTTATCATATC 419  
 OY 5314 ATATCTTCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 5373  
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 Db 480 GCTACTGAAGAAAGTGCAGAGCCCTGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 539  
 OY 5434 TGGGAGAGTTGATCCCGATGCAACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 5493  
 Db 540 TGGGAGAGTTGATCCCGATGCAACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 559  
 OY 5494 GCACTGCGCTTGAACCGCTCTGCAATCTGCCACACCAACCAACCAACCAACCAACCAACCAACCA 5553  
 Db 600 GCACTGCGCTTGAACCGCTCTGCAATCTGCCACACCAACCAACCAACCAACCAACCAACCAACCA 659  
 OY 5554 ATGATTTTGGCCATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 5613  
 Db 660 ATGATTTTGGCCATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 719  
 OY 5614 ACAAGGCGGT 5624  
 Db 720 ACAAGGCGGT 730

RESULT 5  
BM718214 579 bp mRNA linear EST 01-MAR-2002  
LOCUS BM718214  
DEFINITION UI-E-EJ1-af-a-09-0-UI.r1 UI-E-EJ1 Homo sapiens cDNA clone  
ACCESSION UI-E-EJ1-af-a-09-0-UI 5', mRNA sequence.  
VERSION BM718214  
KEYWORDS GI:19036382  
SOURCE EST.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 579)  
AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.  
TITLE Normalization and subtraction: two approaches to facilitate gene  
discovery  
JOURNAL Genome Res. 6 (9), 791-806 (1996)  
MEDLINE 97044477  
COMMENT Contact: Soares, MB  
Program for Rat Gene Discovery and Mapping  
University of Iowa  
451 Eckstein Medical Research Building Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: msoares@blue.weeg.uiowa.edu  
Tissue Procurement: Dr. Gregg Hageman  
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics (www.resgen.com).  
Seq primer: M13 Reverse.  
Location/Qualifiers  
1. 579  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="UI-E-EJ1-af-a-09-0-UI"  
/clone\_lib="UI-E-EJ1"  
/tissue\_type="fetal eyes, lens, eye anterior segment,  
optic nerve, retina, Retina Foveal and Macular, RPE and  
Choroid"  
/dev\_stage="fetal and adult"  
/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
/note="Organ: eye; Vector: pVT73-Pac (Pharmacia) with a  
modified polylinker; Site\_1: Ecor I; Site\_2: Not I;  
UI-E-EJ1 is a subtracted cDNA library constructed  
according to Bonaldo, Lennon and Soares, Genome Research,  
6:791-806, 1996. First strand cDNA synthesis was primed  
with an oligo-dT primer containing a Not I site. Double  
stranded cDNA was ligated to an Ecor I adaptor, digested  
with Not I, and cloned directionally into pVT73-Pac  
vector. The oligonucleotide used to prime the synthesis of  
first-strand cDNA contains a library tag sequence that is  
located between the Not I site and the (GT)<sub>18</sub> tail. The  
sequence tags for this library are: fetal eyes, AGATACAGA  
; lens, CGATTAGCGA; eye anterior segment, AATCGCGAT;  
optic nerve, CCATTAGTG; retina, CCGCG; Retina Foveal and  
Macular, GTCC; RPE and Choroid, ACCCA. This library was  
created for the program, Gene Discovery in the Visual  
System, supported by National Eye Institute (NEI)."  
BASE COUNT 168 a 123 c 125 g 163 t  
ORIGIN  
Query Match 9.5%; Score 570.6; DB 14; Length 579;  
Best Local Similarity 99.3%; Pred. No. 2.5e-124;  
Matches 573; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
OY 5270 GGAACCAATCTGTGGAATTTCTTTTGTGAGTATCATCATATCTCTGTG 5329  
|||||  
DB 1 GGAACCAATCTGTGGAATTTCTTTTGTGAGTATCATCATATCTCTGTG 60  
|||||  
OY 5330 TGGTGAACATGTACATCGCGGTATCGAGACATCTAGTGTGTAAGAAGTCG 5389  
|||||

DB 61 TGGTGAACATGTACATCGCGGTATCGAGACATCTAGTGTGTAAGAAGTCG 120  
OY 5380 CAGACCTCTAGTATGAGATGACTTTGTAGATTTTATAGAGTTTGGAGAAGTTTATC 5449  
|||||  
DB 121 CAGAGCCCTCTAGTATGAGATGACTTTGTAGATTTTATAGAGTTTGGAGAAGTTTATC 180  
|||||  
OY 5450 CCGATGCAATCTAGTATGAGATTTGAAATATATATCTAGTTTGCAGCTGCGCTTGAAC 5509  
|||||  
DB 181 CCGATGCAATCTAGTATGAGATTTGAAATATATATCTAGTTTGCAGCTGCGCTTGAAC 240  
|||||  
OY 5510 CGCCTCTCATCTGCGCAACCAACCAACCAACCTCCAGCTTATGATGATTTGCCATG 5569  
|||||  
DB 241 CGCCTCTCATCTGCGCAACCAACCAACCAACCTCCAGCTTATGATGATTTGCCATG 300  
|||||  
OY 5570 TGAAGTGTACCGGATCCACGTCTGTGATATCTTATTTGCTTTTCAAGGGGTTTCAG 5629  
|||||  
DB 301 TGAGTGTGACCGGATCCACGTCTGTGATATCTTATTTGCTTTTCAAGGGGTTTCAG 360  
|||||  
OY 5630 GAGAGATGAGATGAGATGATGCTCTAGCAATATACATGAGAGAGGATTCAGCTTCCA 5689  
|||||  
DB 361 GAGAGATGAGATGAGATGATGCTCTAGCAATATACATGAGAGAGGATTCAGCTTCCA 420  
|||||  
OY 5690 ATCTTCCAGGTCTCTATACAGCCATCATCTACTTCTTAAACGAAACAGAGAG 5749  
|||||  
DB 421 ATCTTCCAGGTCTCTATACAGCCATCATCTACTTCTTAAACGAAACAGAGAG 480  
|||||  
OY 5750 TATCTGCTCATTTATTCAGCGTGTACAGAGCCACCTTTAAAGCACTGTAAAC 5809  
|||||  
DB 481 TATCTGCTCATTTATTCAGCGTGTACAGAGCCACCTTTAAAGCACTGTAAAC 540  
|||||  
OY 5810 AAGCTTCTCTTACGTACATTAACAAATCAATCAAG 5846  
|||||  
DB 541 AAGCTTCTCTTACGTACATTAACAAATCAATCAAG 577  
|||||

RESULT 6  
BG342331 674 bp mRNA linear EST 27-FEB-2001  
LOCUS BG342331  
DEFINITION 602374246F1 NIH\_MGC\_94 Mus musculus cDNA clone IMAGE:4481819 5',  
mRNA sequence.  
ACCESSION BG342331  
VERSION BG342331.1 GI:13148769  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 674)  
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-riemail.nih.gov  
Tissue Procurement: The Cepko laboratory  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing Arrayed by: The I.M.A.G.E. Consortium, Inc.  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: ULM10317 row: 1 column: 12  
High quality sequence stop: 672.  
Location/Qualifiers  
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/db\_xref="taxon:10090"  
/clone\_image:4481819  
/clone\_lib="NIH\_MGC\_94"  
/tissue\_type="retina"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: eye; Vector: pCMV-SPORT6; site\_1: NotI;  
site\_2: SalI; Cloned unidirectionally; oligo-dT primed.  
Average insert size 3.3 kb. Library enriched for





|                   | Matches   | 70%; Conservative | 0; Mismatches | 70; Indels | Gaps            | 10; |
|-------------------|---|-------------------|---------------|------------|-----------------|-----|
| QY 4894           | CCTACCGCTGTTCCGAGTATGCCGTCTTGTAAGA - TTGGCACCATACTTAGCTCATCA  | 4952              |               |            |                 |     |
| Dd 1              | CTTAGCTGTTTCGAGTATCCGCTTTGCACAGAGTGGGGGAATTCTTAGACTGATCAA   | 60                |               |            |                 |     |
| QY 4953           | AGGAGCAAAAGGGATCCGCAACGCTGCTCTTTGGTTTTGATGATGTCCTCCGCGTGT   | 5012              |               |            |                 |     |
| Dd 61             | GGGAGCAAAAGGGATCCGCAAGCGCTGCTTTGGCGTTGATGATGCCCTCCGCGGCG - TGT  | 119               |               |            |                 |     |
| QY 5013           | TAAACATGCGCTCTACTCTTCTCTAGTCATGTTTCATCTAGCCATCTTTGGGATGCCA  | 5072              |               |            |                 |     |
| Dd 120            | TAAACATGCGCTCTCTCTTTCTTCCGTGTCATGTTTCATCTAGCCATCTTAAAGGATGCCA   | 179               |               |            |                 |     |
| QY 5073           | CTTTGCTTAATGTAAGAGGGAAGTTGGGATGATGATGATGTTCAACTTTGAGACTTGG  | 5132              |               |            |                 |     |
| Dd 180            | TTTGCTTAATGTAAGAGGGAAG - TGggATGATGATGATGTTCAACTTTGAGACTTGG   | 238               |               |            |                 |     |
| QY 5133           | CAACACATGATCTGCCATATTCACAATTAACAACCTCTGCTGGCTGGGAYGGATGCTAGC  | 5192              |               |            |                 |     |
| Dd 239            | CACACGATATCTGCGCTGTCCAATATTACAACCTGCTGCTGGTGGATGGA - TGCTAGC  | 297               |               |            |                 |     |
| QY 5193           | ACCCATTCTCAACAGTAAGCACACCOCGACTGTGACCCCTAATAAGTTAACCTGGAAAGTC   | 5252              |               |            |                 |     |
| Dd 298            | ACCTATTCTTAATAGTGGACCTCCAGACTGTGACCTGTACAAAAGATCAACCTGGAAAGTC   | 357               |               |            |                 |     |
| QY 5253           | AGTTAAGGAGACCTGTGGGAACCCATCTGTGGAAATCTCTTTTGTGACATACATAT  | 5312              |               |            |                 |     |
| Dd 358            | AGTTAAGGAGACCTGTGGGAACCCATCTGTGGGGAATTTTCTTTTGTGACATACATAT  | 417               |               |            |                 |     |
| QY 5313           | CATATCCCTCTGCTGTGTTGTGTGAACATGTACATGCGCTCATCCGTGAGAACTTCAGTGT   | 5372              |               |            |                 |     |
| Dd 418            | CATATCCCTCTGCTGTGTTGTGTGAACATGTACATGCGCTCATCCGTGAGAACTTCAGTGT   | 477               |               |            |                 |     |
| QY 5373           | TGCTACTGAAAGAAAGTGCAGAGCCCTGTGAGTGAAGATGACTTTGAGATGTTCTATGAGCT  | 5432              |               |            |                 |     |
| Dd 478            | TGCTACTGAAAGAAAGTGCAGAGCCCTGTGAGTGAAGATGACTTTGAGATGTTCTATGAGAGCT  | 537               |               |            |                 |     |
| QY 5433           | TTTGGAGA - AGTTTGTATCCCCATGCAACTCATGTTATGGAATTTTAAAAAATTATCTCAGT  | 5491              |               |            |                 |     |
| Dd 538            | TTTGGAGACAGTTTGTATCCCAGATGGACCAATTATATGAGTTTCCAACCTT - TCTGATT  | 596               |               |            |                 |     |
| QY 5492           | TTTGACGTCGCGCTTGAACCCGCTC - TCATATCGCCACAACCAACAAACTCCAGCTCAT   | 5550              |               |            |                 |     |
| Dd 597            | TTTGACGATGCCCTGATCTCTCTCTTCTCATGCAAAAAACAAGCAAGTCCAGTCAAT   | 656               |               |            |                 |     |
| QY 5551           | GCCATGGATTTCGCCATGGTGAAGTGAACCGGATCCACTGTTTGATATCTTAATTGCT  | 5610              |               |            |                 |     |
| Dd 657            | GCCATGGATTCGCCATGGTGAAGTGAAGTGAACCGGATCCACTGTTTGATATCTTAATTGCT  | 715               |               |            |                 |     |
| QY 5611           | TTTACAAAGCCGGTCTTAGAGAGAGTGAAGAT - GGAATGCTATACAAATACACATGA   | 5669              |               |            |                 |     |
| Dd 716            | TTTACAAAGCCGGT - TTGCTGAGAGTGAAGATGAGATGGCCCTTTCGATTACGATGA   | 774               |               |            |                 |     |
| RESULT 9          |   |                   |               |            |                 |     |
| LOCUS             | BB622500  | 618 bp            | mRNA          | linear     | EST 31-ADG-2001 |     |
| DEFINITION        | BB622500 RIKEN full-length enriched, adult male olfactory brain Musculus CDNA clone 6430408L10 5', mRNA sequence.   |                   |               |            |                 |     |
| ACCESSION         | BB622500  |                   |               |            |                 |     |
| VERSION           | BB622500.1  | GI:15397780       |               |            |                 |     |
| KEYWORDS          | EST,  |                   |               |            |                 |     |
| SOURCE            | house mouse,  |                   |               |            |                 |     |
| ORGANISM          | Mus musculus  |                   |               |            |                 |     |
| REFERENCE AUTHORS | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;<br>Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.<br>1 (bases 1 to 618)<br>Arkharov,T., Carnieli,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.<br>Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Koude,<br>M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,<br>Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasak<br>.D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., |                   |               |            |                 |     |





|    |      |   |      |
|----|------|---|------|
| OY | 5242 | CCTGGAAACCTCAGTTAAGGGAAGACTGTGGGAACCATCGTGTGGAAATTTCTTTTTC      | 5301 |
| Db | 731  | CCTGGAAACCTCAGTTAAGGGAAGACTGTGGGAACCATCGTGTGGAAATTTCTTTTTC      | 674  |
| OY | 5302 | AGTTACATCATCAATAATCCCTCGTGTTMGSTGAACATGTAACATGCCGCATCCCTGAG     | 5361 |
| Db | 673  | AGTTACATCATCAATAATCCCTCGTGTTMGSTGAACATGTAACATGCCGCATCCCTGAG     | 614  |
| OY | 5362 | AACCTCACTGTGTGCTACTGGAAGAAGTGCAGAGCTCTGAGTGAAGATGACTTTGATG      | 5421 |
| Db | 613  | ACTCAAACTGTGTGCTACTGGAAGAAGTGCAGAGCTCTGAGTGAAGATGACTTTGATG      | 554  |
| OY | 5422 | TTCATGAGGTGTTGGGAGAAAGTTGATGCCGATGCACTCGATTGATGGAATTTGAAAA      | 5481 |
| Db | 553  | TTCATGAGGTGTTGGGAGAAAGTTGATGCCGATGCACTCGATTGATGGAATTTGAAAA      | 494  |
| OY | 5482 | TTATCTCAGTTTGCAGCTGCCCTTGAACCGGCTCCATCTGCACAACCAACAACATC        | 5541 |
| Db | 493  | CTTTCTGTGTTTTGGAGATGCCCTGGATCTCTCTCTCTTCATACGAAAACCAACAATC      | 434  |
| OY | 5542 | CAGCTCATTTGCCATGGAATTTGCCCATGCTGATGAGTGAACCGGATCCACTGTCTTGATATC | 5601 |
| Db | 433  | CAGCTCATTTGCCATGGAATTTGCCCATGCTGATGAGTGAACCGGATCCACTGTCTTGATATC | 374  |
| OY | 5602 | TTATTTGGTTTTTACAAAGCGGGTCTTAGSAGAGATGAGAGATGAGATGCTTACGATA      | 5661 |
| Db | 373  | TTATTTGGTTTTTACAAAGCGGGTCTTAGSAGAGATGAGAGATGAGATGCTTACGATA      | 314  |
| OY | 5662 | CAGATNGAAGAGACGATTCATGGCTTCACATCCCTTCACAGTCTCTCATCAGCAATCACT    | 5721 |
| Db | 313  | CAGATNGAAGAGACGATTCATGGCTTCACACCTTCACAGTCTCTCATCAGCAATCACT      | 254  |
| OY | 5722 | ACTACTTTAAACGAAAACAAGAGAGATATCTGCTGTCATATTATTCACGCGTCTTACGA     | 5781 |
| Db | 253  | ACCAGCTGTAACCGAAAACAAGAGAGATATCTGCTGTCATATTATTCACAGGCGTTACGA    | 194  |
| OY | 5782 | CGCCACCTTTTAAAGCGGAACGTAAACAACCTTCCTTTACGTACATAAAAAACAATC       | 5841 |
| Db | 193  | CGCTACCTCTTGAAGCAAAGTTAAAAAGATATCAAGTATATCAACMAAAGAACAAAGC      | 134  |
| OY | 5842 | AAAGGTGGGCTTAATCTTCTATATAAAGAAGACATGATAATGTGACAGATAAATGAAC      | 5901 |
| Db | 133  | AAAGATGTGATNGAAGCACCATCAAAAGAATATCTCATATTGAATTAATGAATG          | 74   |
| OY | 5902 | TCATATACAGAAAAACGTGATCTGACATGTCCACTGAGCTGTGCCACTTCCTATGAC       | 5961 |
| Db | 73   | TCAACTCCAGAGAAAACCGATATGACGCTCTCCA---CCAGTCTCCACCCCTGATAT       | 17   |
| OY | 5962 | CGGGTGCAAAAGCCA 5976  |      |
| Db | 16   | AGTGTGACCAAAACA 2   |      |

RESULT\_13  
 B0444145  
 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

B0444145 816 bp mRNA linear EST 29-MAY-2002

UT-M-EX0-bxj-d-14-0-UT.r1 NIH.BMAP-EX0 Mus musculus cDNA clone

IMAGE:5708893 5', mRNA sequence.

B0444145 B0444145.1 GI:21247257

EST.

Mus musculus house mouse.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NIH-MGC http://mgc.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapds@email.nih.gov

Tissue Procurement: Dr. James Lih, University of Iowa



Diseases (Unpublished) Stanley Neurovirology Laboratory,  
Johns Hopkins School of Medicine, Baltimore MD.\*

BASE COUNT 232 a 155 c 135 g 184 t

JOURNAL  
MEDLINE  
COMMENT

discovery  
Genome Res. 6 (9), 791-806 (1996)  
97044477  
Contact: Chih. H  
National Institute of Mental Health  
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD  
20892-9643, USA  
Tel: 301 443 1706  
Fax: 301 443 9890  
Email: mestr@nimh.nih.gov

Query Match 7.4%; Score 447.8; DB 9; Length 706;  
Best Local Similarity 79.9%; Pred. No. 3.7e-95;  
Matches 565; Conservative 0; Mismatches 137; Indels 5; Gaps 3;

538 TTAGAGATTTTACTTCTTCTGAGATCCAGTACCTGCTGATTTCTACCTGATTACCA 597  
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598 TTGGGATGCTGACAGATTTTGTGAGACCTGAGCAATGCTCGGCAATGAGAACTTACA 657  
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598 TTGGGATGCTGACAGATTTTGTGAGACCTGAGCAATGCTCGGCAATGAGAACTTACA 657  
Db TTGGGATGCTGACAGATTTTGTGAGACCTGAGCAATGCTCGGCAATGAGAACTTACA 657  
598 TTGGGATGCTGACAGATTTTGTGAGACCTGAGCAATGCTCGGCAATGAGAACTTACA 657  
Db TTGGGATGCTGACAGATTTTGTGAGACCTGAGCAATGCTCGGCAATGAGAACTTACA 657

586 GTTCCCGAGCATTTGAAAACAAATTTACATTCACGCTGAAAGACCATTTGT-GGTGC 528  
Db GTTCCCGAGCATTTGAAAACAAATTTACATTCACGCTGAAAGACCATTTGT-GGTGC 528

717 CCTGATCCAGTCTGAGAGAAAGCTCAGATGTAATGCTGAGCTGCTGCTGAG 776  
Db CCTGATCCAGTCTGAGAGAAAGCTCAGATGTAATGCTGAGCTGCTGCTGAG 776

527 CCTGATCCAGTCTGAGAGAAAGCTCAGATGTAATGCTGAGCTGCTGCTGAG 776  
Db CCTGATCCAGTCTGAGAGAAAGCTCAGATGTAATGCTGAGCTGCTGCTGAG 776

777 CGTATTTCTCTAATTTGGGCTGACCTGTTTCAAGGCACTGAGCAATTAATGATACA 836  
Db CGTATTTCTCTAATTTGGGCTGACCTGTTTCAAGGCACTGAGCAATTAATGATACA 836

467 CGTATTTCTCTAATTTGGGCTGACCTGTTTCAAGGCACTGAGCAATTAATGATACA 836  
Db CGTATTTCTCTAATTTGGGCTGACCTGTTTCAAGGCACTGAGCAATTAATGATACA 836

837 ATGGCTCCCAACCAATGCTTCTGAGAGACAT--AGTATAGAAAAGAAATTAATCTGT 893  
Db ATGGCTCCCAACCAATGCTTCTGAGAGACAT--AGTATAGAAAAGAAATTAATCTGT 893

407 ATGGCTCCCAACCAATGCTTCTGAGAGACAT--AGTATAGAAAAGAAATTAATCTGT 893  
Db ATGGCTCCCAACCAATGCTTCTGAGAGACAT--AGTATAGAAAAGAAATTAATCTGT 893

894 GAATTTATATGTAATGTAATTAATGAATGTAATGTAATGTAATGTAATGTAATGTAAT 953  
Db GAATTTATATGTAATGTAATTAATGAATGTAATGTAATGTAATGTAATGTAATGTAAT 953

347 GGATGGGATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 953  
Db GGATGGGATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 953

954 TCAAGATTCACATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 1013  
Db TCAAGATTCACATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 1013

287 TGAGATTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 1013  
Db TGAGATTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 1013

1014 TAGCTGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 1073  
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227 CAGCTCAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 1073  
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1074 CAATATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 1133  
Db CAATATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 1133

167 CAATATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 1133  
Db CAATATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 1133

1134 AATGATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 1193  
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107 CATGATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 1193  
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1194 GTACATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 1240  
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RESULT 15  
BF470392 547 bp mRNA linear EST 04-DEC-2000  
LOCUS UI-M-BH3-avc-c-07-0-UI.11 NIH\_BMAP\_M.S4 Mus musculus cDNA clone  
DEFINITION UI-M-BH3-avc-c-07-0-UI.5', mRNA sequence.  
ACCESSION BF470392  
VERSION BF470392.1 GI:11539575  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 547)  
AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.  
TITLE Normalization and subtraction: two approaches to facilitate gene

FEATURES  
source

Location/Qualifiers  
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/organism="Mus musculus"  
/strain="C57BL/6J"  
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/dev\_stage="27-32 days"  
/lab\_host="DHI08 (Life Technologies)"  
/note="Vector: pT73D-Pac (Pharmacia)"  
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NIH\_BMAP\_M.S4 library is a subtracted library of a series,  
ultimately derived from a mixture of individually tagged  
normalized libraries from ten regions of the mouse brain  
(cerebellum, brain stems, olfactory bulbs, hypothalamus,  
cortex, amygdala, basal ganglia, pineal gland, striatum,  
hippocampus) after a series of subtractions to reduce the  
representation of cDNAs from which ESTs had already been  
generated. The following serially subtracted libraries  
were generated in this process: NIH\_BMAP\_M.S3.1,  
NIH\_BMAP\_M.S3.2, NIH\_BMAP\_M.S3.3, NIH\_BMAP\_M.S4,  
NIH\_BMAP\_M.S2, NIH\_BMAP\_M.S1. The subtracted library  
(NIH\_BMAP\_M.S4) was constructed as follows: PCR amplified  
cDNA inserts from NIH\_BMAP\_M.S3.3, NIH\_BMAP\_M.S3.2, and  
NIH\_BMAP\_M.S3.1 clones from which 3' ESTs had been derived  
was used as a driver in a hybridization with a pool of  
the NIH\_BMAP\_M.S3.3, NIH\_BMAP\_M.S3.2, and NIH\_BMAP\_M.S3.1  
libraries in the form of single-stranded circles. The  
remaining single-stranded circles (subtracted library)  
was purified by hydroxyapatite column chromatography,  
converted to double-stranded circles and electroporated  
into DH10B bacteria (Life Technologies) to generate the  
NIH\_BMAP\_M.S4 library. This procedure has been previously  
described (Bonaldo, Lennon and Soares, Genome Research  
6:791-806, 1996)."

BASE COUNT 110 a 143 c 128 g 166 t

Query Match 7.3%; Score 438.8; DB 12; Length 547;  
Best Local Similarity 87.7%; Pred. No. 4.8e-93;  
Matches 479; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

4706 TGACATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 4765  
Db TGACATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 4765

4766 TACTGAAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 4825  
Db TACTGAAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 4825

62 TCGTCAAGCTTATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 121  
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122 TGTGATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 181  
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4886 TCGTCCCTACCTGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 4945  
Db TCGTCCCTACCTGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 4945



Db 182 TCGTGCCCGACCTGTTCCAGTATCCGCGCCAGATGGACGAATCTACGCC 241  
OY 4946 TGATCAAGAGGCAAGGGATCCGACGCTCTTGTGTGATGATGTCCTTCG 5005  
Db 242 TGATCAAGGGGCGCAAGGGATCCGACGCTCTTGTGTGATGATGTCCTTCG 301  
OY 5006 CGTGTGTTAACAATCGGCTCTCTACTCTTCTAGTATGTTCAATCCGATCTTTGGA 5065  
Db 302 CGCTGTTAACAATCGGCTCTCTACTCTTCTAGTATGTTCAATCCGATCTTTGGA 361  
OY 5066 TGTCCACTTGTCTATGTTAAGAGGAGTGGATGATGATGTTCAACTTTGGA 5125  
Db 362 TGTCCACTTGTCTATGTTAAGAGGAGTGGATGATGATGTTCAACTTTGGA 421  
OY 5126 CCTTGGCAACGATGATCTGCTATTCGAATTAACAATCTGCTGGGATGAT 5185  
Db 422 CCTTGGCAACGATGATCTGCTATTCGAATTAACAATCTGCTGGGATGATGAC 481  
OY 5186 TGTGAGCAACGATGATCTGCTATTCGAATTAACAATCTGCTGGGATGAT 5245  
Db 482 TGTGAGCAACGATGATCTGCTATTCGAATTAACAATCTGCTGGGATGATGAC 541  
OY 5246 GAAGCT 5251  
Db 542 GAAGCT 547

Search completed: April 22, 2003, 11:23:37  
Job time : 5117 secs

GenCore version 5.1.4\_p5\_4578  
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OM nucleic - nucleic search, using sw model

Run on: April 22, 2003, 06:57:58 ; Search time 126 Seconds  
(without alignments)  
14676.674 Million cell updates/sec

Title: US-09-930-871-11

Sequence: 1 atgagcaacaacagtgccttgc.....aaaagcaagaaggaataa 6030

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA: \*  
1: /cgn2\_6/ptodata/1/ina/5A.COMB.seq: \*  
2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq: \*  
3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq: \*  
4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq: \*  
5: /cgn2\_6/ptodata/1/ina/PCTRUS.COMB.seq: \*  
6: /cgn2\_6/ptodata/1/ina/backfile1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score  | Query Match | Length | ID | Description                         |
|------------|--------|-------------|--------|----|-------------------------------------|
| 1          | 3544.8 | 58.8        | 6404   | 3  | US-08-836-325-14 Sequence 14, Appl  |
| 2          | 3476.8 | 57.7        | 6371   | 3  | US-08-836-325-13 Sequence 13, Appl  |
| 3          | 3410.4 | 56.6        | 6452   | 3  | US-08-836-325-9 Sequence 9, Appl    |
| 4          | 2787.6 | 46.2        | 6007   | 3  | US-09-024-020B-2 Sequence 2, Appl   |
| 5          | 2787.6 | 46.2        | 6007   | 4  | US-09-425-043-2 Sequence 2, Appl    |
| 6          | 2758.2 | 45.7        | 6586   | 3  | US-09-024-020B-43 Sequence 43, Appl |
| 7          | 2758.2 | 45.7        | 6586   | 4  | US-09-425-043-43 Sequence 43, Appl  |
| 8          | 2738.8 | 45.4        | 5977   | 3  | US-09-024-020B-1 Sequence 1, Appl   |
| 9          | 2738.8 | 45.4        | 5977   | 4  | US-09-425-043-1 Sequence 1, Appl    |
| 10         | 2738.8 | 45.4        | 6556   | 3  | US-09-024-020B-7 Sequence 7, Appl   |
| 11         | 2738.8 | 45.4        | 6556   | 4  | US-09-425-043-7 Sequence 7, Appl    |
| 12         | 2674.2 | 44.3        | 6826   | 3  | US-09-024-020B-8 Sequence 8, Appl   |
| 13         | 2674.2 | 44.3        | 6826   | 4  | US-09-425-043-8 Sequence 8, Appl    |
| 14         | 1907.2 | 31.6        | 6048   | 4  | US-09-634-920-3 Sequence 3, Appl    |
| 15         | 1789.8 | 29.7        | 3033   | 3  | US-08-836-325-1 Sequence 1, Appl    |
| 16         | 1542.8 | 25.6        | 5874   | 4  | US-08-843-417-9 Sequence 9, Appl    |
| 17         | 1474.8 | 24.5        | 6527   | 4  | US-08-669-656A-7 Sequence 7, Appl   |
| 18         | 1469   | 24.4        | 6524   | 4  | US-08-669-656A-1 Sequence 1, Appl   |
| 19         | 1468.4 | 24.4        | 6344   | 4  | US-08-843-417-1 Sequence 1, Appl    |
| 20         | 1361.4 | 22.6        | 7052   | 4  | US-08-669-656A-5 Sequence 5, Appl   |
| 21         | 1046.8 | 17.4        | 6519   | 2  | US-08-808-793-24 Sequence 24, Appl  |
| 22         | 988.4  | 16.4        | 6461   | 3  | US-07-998-289B-7 Sequence 7, Appl   |
| 23         | 935.6  | 15.5        | 6318   | 2  | US-08-808-793-1 Sequence 1, Appl    |
| 24         | 935.6  | 15.5        | 6318   | 3  | US-08-772-512A-1 Sequence 1, Appl   |
| 25         | 935.4  | 15.5        | 6513   | 1  | US-08-338-702-7 Sequence 7, Appl    |
| 26         | 935.4  | 15.5        | 6513   | 1  | US-08-337-339-7 Sequence 7, Appl    |
| 27         | 935.4  | 15.5        | 6513   | 1  | US-08-724-095-7 Sequence 7, Appl    |

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|----|-------|------|------|---|-------------------------------------|
| 28 | 935.4 | 15.5 | 6513 | 5 | PCT-US95-14262-7 Sequence 7, Appl   |
| 29 | 935.4 | 15.5 | 6513 | 5 | PCT-US95-14378-7 Sequence 7, Appl   |
| 30 | 932.4 | 15.5 | 6315 | 2 | US-08-808-793-2 Sequence 2, Appl    |
| 31 | 932.4 | 15.5 | 6315 | 3 | US-08-772-512A-2 Sequence 2, Appl   |
| 32 | 762.2 | 12.6 | 930  | 3 | US-08-605-284B-21 Sequence 21, Appl |
| 33 | 761   | 12.6 | 930  | 3 | US-08-605-284B-2 Sequence 2, Appl   |
| 34 | 749.8 | 12.4 | 930  | 3 | US-08-605-284B-3 Sequence 3, Appl   |
| 35 | 748.2 | 12.4 | 930  | 3 | US-08-605-284B-1 Sequence 1, Appl   |
| 36 | 624   | 10.3 | 2573 | 4 | US-08-669-656A-3 Sequence 3, Appl   |
| 37 | 389.6 | 6.5  | 696  | 3 | US-09-024-020B-5 Sequence 5, Appl   |
| 38 | 389.6 | 6.5  | 696  | 4 | US-09-425-043-5 Sequence 5, Appl    |
| 39 | 335.8 | 5.6  | 702  | 4 | US-08-843-417-3 Sequence 3, Appl    |
| 40 | 299   | 5.0  | 1237 | 2 | US-08-808-793-26 Sequence 26, Appl  |
| 41 | 138.2 | 2.3  | 2279 | 3 | US-07-998-289B-3 Sequence 3, Appl   |
| 42 | 110.2 | 1.8  | 6232 | 4 | US-08-669-200B-11 Sequence 11, Appl |
| 43 | 110   | 1.8  | 3563 | 4 | US-09-041-886-20 Sequence 20, Appl  |
| 44 | 110   | 1.8  | 3596 | 2 | US-08-779-801-5 Sequence 5, Appl    |
| 45 | 110   | 1.8  | 3596 | 4 | US-09-298-441-5 Sequence 5, Appl    |

#### ALIGNMENTS

RESULT 1  
US-08-836-325-14  
Sequence 14, Application US/08836325  
Patent No. 6110672  
GENERAL INFORMATION:  
APPLICANT: Mandel, Gail  
APPLICANT: Halegoua, Simon  
APPLICANT: Borden, Laurence A.  
TITLE OF INVENTION: Peripheral Nervous System Specific  
TITLE OF INVENTION: Sodium Channels, DNA Encoding Thereof, Crystallization,  
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational  
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and t  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESS: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 New York Ave., N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/836,325  
FILING DATE: 2-MAY-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/14251  
FILING DATE: 02-NOV-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/482,401  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: 08/334,029  
FILING DATE: 02-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ludwig, Steven R.  
REGISTRATION NUMBER: 36,203  
REFERENCE/DOCKET NUMBER: 0917,0240002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2540  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6404 base pairs  
TYPE: nucleic acid



Db 2027 CGACCAATCAATACACAG---AAAGCGTTAGTTCCTATCTCCCTTAGAGGATTA 2083  
 Qy 2108 TTCTAGAGATCTCTCCCAAGCAAGCATAGATATAGCCAGCATTTCAACAATA 2167  
 Db 2084 TCGTAATGATCCCACTCAGACAGAGAGCATAGATAGCATATTAACAAACA 2143  
 Qy 2168 CAGTAGAAGAACTGAGAAATCAGACAGAAATGCCACCTGTTGGTAAATTTTCCA 2227  
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 Qy 3548 AAGGCTGTACAAAGATTTCAAGTTGTCAATCAATGTGAAGAGGACAGAAAC 3607  
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 Qy 3608 AATGTTGAACTGAGAAAGAGCTTTCCGATGATGATTAATCAATGATGATGATG 3667  
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 Qy 3728 ATCAGGAAACAGATTTAAGACAGATGATGATGATGATGATGATGATGATGATG 3787  
 Db 3698 AAGGAAAGAAACATTAATTAATGATGATGATGATGATGATGATGATGATGATG 3757  
 Qy 3788 TCAATTTGAAATGATTTTAAATGATGATGATGATGATGATGATGATGATGATG 3847  
 Db 3758 TCAATTTGAAATGATTTTAAATGATGATGATGATGATGATGATGATGATGATG 3817  
 Qy 3848 CCGTGTGTTGCTGACCTTTAATGATGATGATGATGATGATGATGATGATGATG 3907  
 Db 3818 CCGTGTGTTGCTGACCTTTAATGATGATGATGATGATGATGATGATGATGATG 3877  
 Qy 3908 CCTTGGTTTACTGAGAACTGAGACATCAATTTCTGAGACACTAAGACTGAGAC 3967  
 Db 3878 CTTTGGTTTACTGAGAACTGAGACATCAATTTCTGAGACACTAAGACTGAGAC 3937  
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 Db 3998 CAATTCATCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4057  
 Qy 4088 TCAATGAGCTTAATTTGTTGCTGCAATTTCAACATGATTAACACACACATGATG 4147  
 Db 4058 TCAATGAGCTTAATTTGTTGCTGCAATTTCAACATGATTAACACACACATGATG 4117  
 Qy 4148 ACAGTTTACATCAGAGCTGATTAATCAATCAATCAATCAATCAATCAATCAATCA 4207  
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 Qy 4208 ATGAGACCTGATGAGAAATGAGAAATGAGAAATGAGAAATGAGAAATGAGAAATG 4267  
 Db 4178 GTCAAAATGTGAGATGAGAAATGAGAAATGAGAAATGAGAAATGAGAAATGAGAA 4237

|    |      |  |      |
|----|------|--|------|
| OY | 4268 | TCCTCTCCCTCAAGTTCGCCACATATCAAGAGAGATGATATTAATGATATGCAGACATGG   | 4322 |
| Db | 4238 | TATCTCTGCTTCAAGTTGCGAATCTTTTAAAGGATGACGATATTAATGATATGCAGACATGG | 4292 |
| OY | 4338 | ATTCAGAAATATGGAATCTCCAGCTTAAGTATGAAGAAAGTGTGTACATGATCTTTACT    | 4387 |
| Db | 4298 | ATTCCTGTTAAATGAGACACAGACGCCAAATATATGAATATAGCTCTACATGATATATTTAT | 4357 |
| OY | 4388 | TTGTATATTTTCATATCTTTGGGTCCTCTCTACACTTTGAACCTGTTTATGGTGTATCA    | 4442 |
| Db | 4358 | TTTGCGCTTTTATATCTTTGGGTCATCTCTCACTTTGAACCTGTTCATTTGGTGTATCA    | 4412 |
| OY | 4448 | TAGATATTTTCACACACAGAAAAAGAGTTTGGAGGTCAACACATCTTATGACAGAG       | 4507 |
| Db | 4418 | TAGATATTTTCACACACAGAAAAAGAGCTTGGAGGTCAACACATCTTATGACAGAG       | 4477 |
| OY | 4508 | AACAGAAAGAAATACTATATATGCAATGAAAAATTTAGATCGAAAAACCGCAAAAGCTA    | 4567 |
| Db | 4478 | AACAGAAAGAAATACTATATATGCAATGAAAAAGCTGGGGTCCAAAGAGCCAAAGGCCAA   | 4537 |
| OY | 4568 | TACCTCCACCGAAGAAATAAATTTCAAGGAATGGTCTTTTACTTCTGTACACAGCAATTT   | 4622 |
| Db | 4538 | TTTCTCGAACCGGGAACAAAATCCAAAGAGATATATTACCTACGTGCAAAATCAAGCT     | 4597 |
| OY | 4628 | TTGACATTAAGCATATGATTCCTATCTATCTGTCTTAACTAGTCAATAGATGGTGAACAG   | 4687 |
| Db | 4598 | TTGATATTAAGTATCATGATGGTCTTATCTGTCTCAACTGTGTAAACCATGATGATGAAG   | 4657 |
| OY | 4688 | ATGACCAAGATGAATATGTCATACCAATTTTGTCAACGACAAATCTGGTGTATCTGTGC    | 4742 |
| Db | 4658 | AGGGTCAAAAGTCAACATATGATCAGAGTGAATTAATTTGATATGATGGTTTTTAATACCC  | 4712 |
| OY | 4748 | TATTTACTGGAGAGTGTGTCTGTAAGCACTATCTGTACGCCATTAATTTTACCATTG      | 4807 |
| Db | 4718 | TTTTCATCTGGAGATGTGTCTTAATCATATCTCTCCACACACTATCTTCACTGTAG       | 4777 |
| OY | 4808 | GATGGAATATTTGATTTTGTGGTGTCTCATCTCTCATTTGTAGATATGTTCTTGGCG      | 4867 |
| Db | 4778 | GATGGAATATTTGATTTTGTGGTGTCTCATCTCTCATTTGTAGATATGTTCTTACGTG     | 4837 |
| OY | 4868 | AGCTGATGAAGAAATATTTTGTGTGCCCTTAACCTGTTCGAGATGAATGCGTCTGTGATGA  | 4922 |
| Db | 4838 | ATTTGATGATGAAGCTATTTTGTGTGCCCTTAACCTGTTCGAGATGAATGCGTCTGTGATGA | 4897 |
| OY | 4928 | TTTGCCGGAATCTTACGTCGTATCAAAAGAGCAAGGGGATTCGCAACGCTGCTTTGCT     | 4987 |
| Db | 4898 | TTTGCCGGAATCTTACGTCGTATCAAAAGAGCAAAAGGGGATTCGCAACGCTGCTTTGCT   | 4957 |
| OY | 4988 | TGATGATGTCCCTTCCCTGCGTGTGTTTAAATGATGGCTCTACTCTTCTGATCATGTTCA   | 5042 |
| Db | 4958 | TGATGATGTCCCTTCCCTGCGTGTGTTTAAATGATGGCTCTGCTGCTTCCGATCATGTTCA  | 5012 |
| OY | 5048 | TCATACGCATTTTGGGATGTCACACTTTCGCCATGTTTAAAGAGGAAGTTGGGATCGATG   | 5107 |
| Db | 5018 | TCATACGCATTTTGGGATGTCACACTTTCGCCATGTTTAAAGAGGAAGTGAATTAATG     | 5077 |
| OY | 5108 | ACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATGTGCTATTTCCAAATTTACACCT   | 5167 |
| Db | 5078 | ACATGTTCAACTTTGAGACCTTTGGCAACAGTATGATTTGCTGTTCCAAATTTACACCT    | 5137 |
| OY | 5168 | CTGTGCGGTGGAGAGATTCCTAGAACCACTTCTCAAGATGAAGCACCGACGATGTGAC     | 5222 |
| Db | 5138 | CTGTGCGGTGGAGAGATTCCTAGCACATTTCTTAAAGATGAAGCACCGACGATGTGAC     | 5197 |
| OY | 5228 | CTAATTAAGTTAACCTGTGAGAGCTCAGATTAAAGGAGACTGTGGGAACCCATCTGTTGAA  | 5287 |
| Db | 5198 | CAAAAAAGTTCATCTCGGAAGATTCAGTTGGAAGAGAACTGTGTAACCCATCTGTTGGA    | 5257 |
| OY | 5288 | TTTTCTTTTTTGTAGTTAATCATATCATATCTCTCTGCTGTGGTGTGGGAACCATGATCAAG | 5342 |
| Db | 5258 | TATCTACTTTGTATATATATCATATCATCTCTCTGCTGTGGTGTGGGAACCATGATCAAG   | 5312 |

|    |      |   |      |
|----|------|---|------|
| OY | 5348 | CGGTCATCTGGAGACCTTCAGTGGTGGCTCTCTCAAAAGTGCAGAGCTGTGGATAG      | 5407 |
| Db | 5318 | CACTGATACCTGGAAATTTTAGTGTGCCACTAAABAAAGTACTGAACCTTGATGAGG     | 5377 |
| OY | 5408 | ATGACTTTGAGATCTTCTATGAGGTGGGAGAAAGTTATCCAGTCACATCGATCA        | 5467 |
| Db | 5378 | ATGACTTTGAGATCTTCTATGAGGTGGGAGAAAGTTATCCAGTCACATCGATCA        | 5437 |
| OY | 5468 | TGGAATTTGAAAAATATCTCAGTTTGCAGCTGCGCTTGAAACGCGCTCTCAATCTGCCAC  | 5537 |
| Db | 5438 | TAGAGTTCTCTAAACTCTCGATTTTGGACACTCCCTGGATCTCTCTCTCATAGCAA      | 5497 |
| OY | 5528 | AACCAACAACCTCCACTATATGGCATGGATTTGCCATGGTGAGTGAACGGATCC        | 5587 |
| Db | 5498 | AACCAACAACCTCCACTATATGGCATGGATTTGCCATGGTGAGTGAACGGATCC        | 5557 |
| OY | 5588 | ACTGCTTGATGATCTTATTTGCTTTTACAAAGGGGGTCTAGAGAGAGTGGAGAGTGG     | 5647 |
| Db | 5558 | ATTTGCTTGATGATCTTATTTGCTTTTACAAAGGGGGTCTAGAGAGAGTGGAGAGTGG    | 5617 |
| OY | 5648 | ATGCTCTACGAATTCACAGATGGAAGAGAGATATGCGCTTCCATGCTTCCAAGGTCCT    | 5707 |
| Db | 5618 | ATTTCTCTTCGTTCCACATGGAAGAAAGGTCTATGTCCTCAAAATCTTCCAAGGTCTCT   | 5677 |
| OY | 5708 | ATCAGCCAAATCACTACTACTTTTAAACGAAACAAAGAGAAATATCTGCTGTCAATTATTC | 5767 |
| Db | 5678 | ATGAACCCATCACAACCACTAAACGGAAACAAAGAGATGTGTCCTACTGTCAATTC      | 5737 |
| OY | 5768 | AGCGTCTTACAGACGCCACCTTTTAAAGGAACTGTAAACACAGCTTCTTTACGTACA     | 5827 |
| Db | 5738 | AGCGTCTTATAGACCTTACCGCTTAAAGCAAAATGTCAAAATATATCAAGTATATACA    | 5797 |
| OY | 5828 | ATTAACAACAATATGAAAGTGGGGCTTAATCTCTTAAAGAAACAGCATGATTAATGCA    | 5887 |
| Db | 5798 | TAAAGATGAGACAGAGAT--GATGATTTACTCATTAATAAATAATATGCGTTGATA      | 5854 |
| OY | 5888 | GAATTAATGAAATCTCATTTACAGAAAAAATGATGTGACATGTCCACTGAGCTGTCTC    | 5947 |
| Db | 5855 | ATGTAAATGAGAACTCAAGTCCAGAAAAAAGCAT--GCCATTCATTCACACACTCTC     | 5911 |
| OY | 5948 | CACCTTCCTATGACCGGGGTGACAAAGCCATTTGTGAAAAACATGACAGAGGCAAG      | 6007 |
| Db | 5912 | CACCTTCATATGATAGTGTACAAAGCGACAAAGAAATATGAAACAAACAGACAGACAG    | 5971 |
| OY | 6008 | ATGAAAAAGCCAAAGGGAATA 6029                                    |      |
| Db | 5972 | AAAAAGAGACAAAGGGGAAGA 5993                                    |      |

RESULT 2  
 US-08-836-325-13  
 ; Sequence 13, Application US/08836325  
 ; Patent No. 6110672  
 GENERAL INFORMATION:  
 APPLICANT: Mandel, Gail  
 APPLICANT: Halegoua, Simon  
 APPLICANT: Borden, Laurence A.  
 TITLE OF INVENTION: Peripheral Nervous System Specific  
 TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,  
 TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational  
 TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Use  
 TITLE OF INVENTION: Thereof  
 NUMBER OF SEQUENCES: 19  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
 STREET: 1100 New York Ave., N. W., Suite 600  
 CITY: Washington  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20005-3934  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/836,325  
 FILING DATE: 2-MAY-1997  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/14251  
 FILING DATE: 02-NOV-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/482,401  
 FILING DATE: 07-JUN-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/334,029  
 FILING DATE: 02-NOV-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ludwig, Steven R.  
 REGISTRATION NUMBER: 36,203  
 REFERENCE/DOCKET NUMBER: 0917.0240002  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-371-2600  
 TELEFAX: 202-371-2540  
 INFORMATION FOR SEQ ID NO: 13:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6371 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: both  
 TOPOLOGY: both  
 MOLECULE TYPE: DNA (genomic)  
 US-08-836-325-13

Query Match 57.7%; Score 3476.8; DB 3; Length 6371;  
 Best Local Similarity 75.0%; Pred. No. 0;  
 Matches 4516; Conservative 1; Mismatches 1388; Indels 117; Gaps 9;

11 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 70  
 53 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 112  
 71 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 130  
 113 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 172  
 131 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 190  
 173 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 232  
 191 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 250  
 233 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 292  
 251 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 310  
 293 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 352  
 311 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 370  
 353 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 412  
 371 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 430  
 413 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 472  
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 473 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 532  
 491 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 550  
 533 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 592  
 551 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 610

593 CTTTCTTCTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 652  
 611 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 670  
 653 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 712  
 671 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 730  
 713 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 772  
 731 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 790  
 773 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 832  
 791 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 850  
 833 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 879  
 851 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 910  
 880 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 924  
 911 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 970  
 925 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 955  
 971 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 1030  
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 1076 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 1135  
 1151 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 1210  
 1136 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 1195  
 1211 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 1270  
 1196 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 1255  
 1271 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 1330  
 1256 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 1315  
 1331 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 1390  
 1316 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 1375  
 1391 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 1450  
 1376 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 1435  
 1451 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 1510  
 1436 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 1495  
 1511 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 1567  
 1496 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 1555  
 1568 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 1627  
 1556 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 1615  
 1628 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 1687  
 1616 CAGTGTGACGACGAGCGTGAACCTTCTCAGCAGAGATCTCTCGG 1675



|    |      |   |      |
|----|------|---|------|
| QY | 1688 | TATTTCACCAAGGCAAAATAGACAAGAAAGCTTTTACAGTTTGAGGGCGACAAAG         | 1747 |
| Db | 1676 | TGTTTTCTGAAAGCCAGACAGCAGAACAAATCTTTTAGTTTCAAAGCAGAGGAAG         | 1735 |
| QY | 1748 | ATGCGGAGTCTGAAAGCAAGCTTCGAGATGATGACACAGCACTTTGAGGATAACGA        | 1807 |
| Db | 1736 | ATATAGAGTCTGAGACTGAAATTTTCCGATGATGACACAGCACTTTTGGACATATGGA      | 1795 |
| QY | 1808 | GCCGTAGAGATTCCCTGTGTTTGCCCCGACAGACAGGAGAGAGACGCAACAGCAACTGA     | 1867 |
| Db | 1796 | GCAAGAAAGGGGCTACAGTGTGTTTGCCCCACAGACCCAGAGAGGACGACAGATAACATCA   | 1855 |
| QY | 1868 | GTCAGACCAATAGGTATFCCCGGATCTGGACAGTGTGTTTCCAGCGAATGGGAATGACAA    | 1927 |
| Db | 1856 | GCCAGGCACTATAGTCTCCACCAACTGCTG-----CCGGTGAAGGGGAAATGACAA        | 1906 |
| QY | 1928 | GCACTGTGATTCGAATGATGTTGGTTTCTTGTTGGTGGAGACCTTCACTTCCATACGC      | 1987 |
| Db | 1907 | GTCGTGTGGAGCTCAACAGGTTGGTCTCCCTGTTGATGAGAGCGCTCACCTCATGCTCC     | 1966 |
| QY | 1988 | CTGTGTGACAGCTTCTGCCAGAGAGTGATATATGATAAGCACACTACTGATGACATGGA     | 2047 |
| Db | 1967 | CCATGACACGCTTCTTGCCAGAC-----GGCA 1993                           |      |
| QY | 2048 | CAACCACTGAAACTGAAATGAGAAAGAGAGGTCAAGTCTTTCACGTTTCATGAGCT        | 2107 |
| Db | 1994 | CGACCACTCAAAATACCAAG-----AAAGGCGTTGATAGTCTCATCTCTTCAGAGATA      | 2050 |
| QY | 2108 | TTCTAGAGAAATCCTTCCCAAGGCAACGACGAAATGATATACCGACATTTCAACAATA      | 2167 |
| Db | 2051 | TGCTGAATGATGCCAACTCTACAGCAAGAGCAATGATGACCAAGCAATTTAAACAAACA     | 2110 |
| QY | 2168 | CAGTAGAAGAACTTGAAGATCCAGGCAACAATAATGCCACCCGTGTGATATAATTTTCCA    | 2227 |
| Db | 2111 | CTGTGGAAGAACTTGAAGATCCAGCAACAATAATGTCCACTTGGTGTACAGATTTTGAC     | 2170 |
| QY | 2228 | ACATATTTCTTAATCTGGGACTGTTCTCCATATTTGTTAAAGTGAACATGTTGTCAAC      | 2287 |
| Db | 2171 | ACAAATTTCTTGATCTGGAATGTCTCCCAATTTGATTAATAATCAAAAAGTATCTATTT     | 2230 |
| QY | 2288 | TGGTGTGATGAGCAACCAATTTGTTGACTGTCGCAATCCATCTGATGTGCTTAATTA       | 2347 |
| Db | 2231 | TTATTTGATATGAGATCTTTTGTGTGATCTTGCAATTTACCACTTTTGCAATGTTTAAACAT  | 2290 |
| QY | 2348 | TTTTTCATGGCCATGAGCACTATCCATCATAGCAGGACATTTCAATATGCTTACAGTAG     | 2407 |
| Db | 2291 | TATTTATGAGCTATGAGAAACACCACTCAATCTAGAGAAATTTACTTGCTATAG          | 2350 |
| QY | 2408 | GAAACTGTGTTTACACTGGGATCTTTTACAGCAAGAAATGTTCTGAATAATATGCAATGG    | 2467 |
| Db | 2351 | GAAATTTGGTCTTACCTGGAATCTTTTGACGTGAATATGATTTAAACGATGTCATGG       | 2410 |
| QY | 2468 | ATTCCTTACTATTTTTCACAAGAGCGCTGGAATATCTTTTACGCGTTTATTTGACGCTTA    | 2527 |
| Db | 2411 | ATCCATATGATGATTTTTCACAAGTGAAGCGTGGAATATTTTTCACAGCCTTATTTGACTTAA | 2470 |
| QY | 2528 | GCTCTGTGATGAACCTTGGACTGCCAAATGTGGAAGAGATATCTGTTCTCGTTCATTTGCAT  | 2587 |
| Db | 2471 | GTTTATGAGGAGCTCTTCTTACGCAAGATGTGAAGAGATGTCACTGTTCTGGATCATTCACAC | 2530 |
| QY | 2588 | TGCTGCCAGATTTTCAAGTTTGGCAAAATCTTTGGCAACGTTTAATATGCAATTAAGACAA   | 2647 |
| Db | 2531 | TGCTGCCAGATCTTCAAGTTTGGCAAAATCTTGCCCAACATTTGAACATGCTGATTAAGATCA | 2590 |
| QY | 2648 | TGCGCAATTCGTTGGGGGCTCTGGGAATTTAACCTCGTCTTGCGCATCATCTGCTTCA      | 2707 |
| Db | 2591 | TGTGTAATCTAGATGAGGGGCTCTAGGTAACTCACTTATGTTGGCCATCACTGCTTCA      | 2650 |
| QY | 2708 | TTTTTGGCGTGGCGGATGACGACTCTTTGGTATTAAGGCTTACAAATAATGTGTCTGCAAGA  | 2767 |
| Db | 2651 | TTTTTGGCTGTGGTGGCATCACTCTTTTGGTATTAAGGCTTACAAATAATGTGTCTGCAAGA  | 2710 |

|    |      |   |      |
|----|------|---|------|
| OY | 2768 | TCGCACGAAATGTCACACCTCCACACGGGACATAGTAATACATCTTCCACAGCCCTTCCGA | 2827 |
| Db | 2711 | TCAAATGATGACTGACCTCTCCACGGGTGCACATGAACGACTCTTCCACTCTCTCTCGA   | 2770 |
| OY | 2828 | TTTGTTCCGCGTGTCTGTGGGAGTGTAGAGCCATGTGGGACTGTATGAGAGTTG        | 2887 |
| Db | 2771 | TTTGTTCCGCGTGTCTGTGGGAGTGTAGAGCCATGTGGGACTGTATGAGAGTTG        | 2830 |
| OY | 2888 | CTGGTCAAGCCATGTGCTTACTGTCTCTCATGATGTCTATGTGTATGGAACCTAGTGG    | 2947 |
| Db | 2831 | CTGGTCAAGCCATGTGCTTACTGTCTCTCATGATGTGTATGGAACCTAGTGTG         | 2890 |
| OY | 2948 | TTCCGAAATCTTTTCGGGCTTCTCTTTCAGGCAATTTGTGTCAACAGCAACCTGTAGCA   | 3007 |
| Db | 2891 | TTCCGAAATCTTTTCGGGCTTCTCTTTCAGGCAATTTGTGTCAACAGCAATCTTACAGCA  | 2950 |
| OY | 3008 | CTGATGATGATTAATGAAATGAAATATATCTCAATATCTGTGGATAGATGACAAAGAG    | 3067 |
| Db | 2951 | TTGGAAGAGACCCGATGACAAACAAACCTCAGATTCAGTACTGTAGATTAAGAGGAA     | 3010 |
| OY | 3068 | TAGCTTATGTGAAAAGAAAAATATATGAAATTTATTCACAGTCTTCATTAAGAAAAA     | 3127 |
| Db | 3011 | TAAATTTATGTGAAAACAAACCTTACGTAATTTATTTCAAAACATTTTCCAAAAAGCAA   | 3070 |
| OY | 3128 | AGATTTATAGATGAATTAACACCTGATGATCTTAACACAAAGAAAGACAGTGTATGT     | 3187 |
| Db | 3071 | AGATTTTCCAGGAGATATAGCAACGAGAAAGATCTGATATCTTAAGAGGAAAACTATATT  | 3130 |
| OY | 3188 | CCATATCATACACACGAATTTGGGAAAGATCTTGACATCTTAAAGATGTAATGTGAACTA  | 3247 |
| Db | 3131 | CTAACCATACACTTGTCTGAAATAGCAAAAGTCCACATTTCTCTCAAGGAAAAAGATTA   | 3180 |
| OY | 3248 | CAATGGTATAGGAACATGCGACAGATGTTGAAAATAATACATTTATGATGAAAGTATACA  | 3307 |
| Db | 3191 | TCAGTGGTT-----TGAAGCAGGGGTGGACAAACACTGTATGAGACAGATATGTC       | 3244 |
| OY | 3308 | TGTATTCATTAACACACCCACAGTCTTACTGTACTGTACCAATTCCTGTAGGACAAATGT  | 3367 |
| Db | 3245 | AATATATTAATTCACAAATCCAGGCTCACAGTGCACAGTGCATTCACCTGGGAGATCCG   | 3304 |
| OY | 3368 | ACTTGTGAAATTTTAAACAGGGAAGACTTTAGTGTAAATCCGATCTGGAGAAAGACCAAG  | 3427 |
| Db | 3305 | ATTTGGAAATATGCAATGCTGAGGAACTTACAGTGTATTCGATATGTAATACAGCAAG    | 3364 |
| OY | 3428 | AGAAACTGGAATGAAGACAGTAGCTCATACAGAAAGTAGACTGTGACATCGGCGCACCTG  | 3487 |
| Db | 3365 | TGAGATTAACCCGGTCAAGCTCCTCAGAGTGCAGCACAGTGTATACCTTTGCTGTAG     | 3424 |
| OY | 3488 | TAGAAGAACACCCGCTAGTGTGGAACCTGGAAGAACTTTTAACACAGAGCTGTTCACGT   | 3547 |
| Db | 3425 | AAGGAGAAAGACAGAGGCTGAACCTATGATTTCCGATAGGCAAGGCGCTGTTCACAG     | 3484 |
| OY | 3548 | AAGGCTGTGTCAAGATTAAGTGTGTTCAAATCAATGTGGAGAGAGGCGAGAGGAAC      | 3607 |
| Db | 3485 | ATGCTGTGTACGAGGTTCTTCATCTCTCCAAATTAACATTAAGTTCAGGGAAGGAAAA    | 3544 |
| OY | 3608 | AATGGTGAACCTGAGAGAGACGTGTTTCGATAGTGTATGACATTAACGTGTTGAGACT    | 3667 |
| Db | 3545 | TTCTGTGGAACATCAGGAAAACTGGTACAAAGATTTTGAACACAGTGTGTTGAACCT     | 3604 |
| OY | 3668 | TCATTTGTTTATGATCTCTCTTAATGATGTGTCTGTGCATTTGAAGATATATATATG     | 3727 |
| Db | 3605 | TCATTTGTTTATGATCTCTCTCTAAGATGTGTCTGTGCATTTGAAGATATATATATG     | 3664 |
| OY | 3728 | ATCAGCGAAAGACATTAACAGCATGTGTGAATATCTGACAAAGGTTTTCATTAATTT     | 3787 |
| Db | 3665 | AAAGGAAAAAGACCATTAATTAATTTATCTGTGAGATGACACAAAGATTTCACTTAACCT  | 3724 |
| OY | 3788 | TCATTTGGAATATCTCTTAAATGGGTGGCATATGGCTATTAACATATTTTACACATG     | 3847 |
| Db | 3725 | TCATTTGGAATATCTCTTAAATGGATAGCANATGTATTAACACATATTTTACACATG     | 3784 |
| OY | 3848 | CTTGGTGTGGCTGTGACTCTTAAATGTTGATGTTTCATTTGCTCACTTTAACAGCAATG   | 3907 |

||||| 3844  
Db 3765 CTTGGTGTGGCTGATTTCCATTTGATGTTCTTGGTACTTATAGGCGAACA 3844  
OY 3908 CTTGGGTTACTCAGAACTTGAGCCATCAATCTCAGACACTAGAGCTGAGAC 3967  
Db 3845 CTCTGGCTACTCAGATCTTGCGCATTAATCCCTTCGACACTGAGAGCTTTAAGAC 3904  
OY 3968 CTTAAGAGCTTATCTGATTTGAAGGATAGAGGTGGTTGTAATGCCCTTTAAGAG 4027  
Db 3905 CTCTAAGAGCTTATCTGATTTGAAGGATAGAGGTGGTTGTAATGCCCTTTAAGAG 3964  
OY 4028 CAATTCATCCATGATGATGCTTCTGTTGCTTATATCTGATTTGGAATTTTCAGA 4087  
Db 3965 CAATTCCTTCATGATGATGCTTCTGTTGCTTATATCTGATTTGGAATTTTCAGA 4024  
OY 4088 TCATGGGCTAATTTGTTGCTGGCAATTTACACCTGATTAACACCACTGGTG 4147  
Db 4025 TCATGGGCTAATTTGTTGCTGGCAATTTACACCTGATTAACACCACTGGTG 4084  
OY 4148 ACAGTTTGACATCGAAGCTGGAATATCATCTGATTTGCCATAAATAGAAAGA 4207  
Db 4085 CACGGTTCCCTGCAAGTCAAGTCCAAATCGTCCGAATGTTGGCTTATGAATGTA 4144  
OY 4208 ATGAGACTGCTGATGGAATAATGTAAGTAACTTTGATATGAGATTTGGTATC 4267  
Db 4145 GTCAAAATGCGATGGAATAATGTAAGTAACTTTGATATGAGATTTGGTATC 4204  
OY 4268 TCTCTTGGCTCAAGTTGGCCACATTCMAAGATGATGATATATATGACAGATG 4327  
Db 4205 TATCTGCTTCAAGTTGGCCACATTCMAAGATGATGATATATATGACAGATG 4264  
OY 4328 ATTCAGAAATGTGAACTCCAGCTTAACTATGAAAGAAAGTGTATCTTACT 4387  
Db 4265 ATTCGTTATATGACAAAGCAAGCCCAATATGAAATATGACCTCAATATATAT 4324  
OY 4388 TGTATTTTCAATCTTGGGCTCTGCTTCACTTGAACCTGATTTATGTTGCTATC 4447  
Db 4325 TGTGCTCTTATCATCTTGGGCTCTGCTTCACTTGAACCTGATTTATGTTGCTATC 4384  
OY 4448 TGAATATTTCAACAGCAAGAAAGATTTGGAGTCAAGACATCTTATGACAGAG 4507  
Db 4385 TGAATATTTCAACAGCAAGAAAGATTTGGAGTCAAGACATCTTATGACAGAG 4444  
OY 4508 AACAGAAATATCTATATGCAATGAAATAATAGATCGAATAACCGCAAAAGCTTA 4567  
Db 4445 AACAGAAATATCTATATGCAATGAAATAATAGATCGAATAACCGCAAAAGCTTA 4504  
OY 4568 TACCTGACAGGAATAATTTCAAGAAATGCTTTGACTCTTACACAGACAAATTT 4627  
Db 4505 TACCTGACAGGAATAATTTCAAGAAATGCTTTGACTCTTACACAGACAAATTT 4564  
OY 4628 TTGACATTAAGCATGATCTTCATCTGCTTAAACATGTCACAAATGATGTTGAAAC 4687  
Db 4565 TTGATTTTATGATCATGTTCTTATCTGCTTAAACATGTCACAAATGATGTTGAAAC 4624  
OY 4688 ATGACAGAGTGAATATGACTACATTTTGCAGCATCATCTGCTTATGTTGC 4747  
Db 4625 AGGCTCAAGTCAACATGACTGAAGTTTATATGGAATAATGCTTTTATATATCC 4684  
OY 4748 TATTTCTGAGAGTGTACTGAAACTCATCTCTACAGCATTTATTTATTTACATG 4807  
Db 4685 TTTTCTGAGAGTGTACTGAAACTCATCTCTACAGCATTTATTTATTTACATG 4744  
OY 4808 GATGAATATTTTGAATTTGTTGCTGCTATCTCTCATCTTATGATGTTTCTGCC 4867  
Db 4745 GATGAATATTTTGAATTTGTTGCTGCTATCTCTCATCTTATGATGTTTCTGCC 4804  
OY 4868 AGCTATAGAAAGTATTTGCTGCTCCCTACCTGTTCCAGTATCCGTTCTGTAAGA 4927  
Db 4805 ATTTGATTAAGAGTATTTGCTGCTCCCTACCTGTTCCAGTATCCGTTCTGTAAGA 4864  
OY 4928 TTGGCGAATCTAGCTGATCAAGAGGAGCAAGGAGATCCGACGCTCTCTTGGCT 4987  
|||||

Db 4865 TTGGCGAATCTAGCTGATCAAGAGGAGCAAGGAGATCCGACGCTCTCTTGGCT 4924  
OY 4988 TGAATATGCTCTCTGCTGCTGTTTAAACATCGGCTCTCTCTCTCTCTCTCTCTCT 5047  
Db 4925 TGAATATGCTCTCTGCTGCTGTTTAAACATCGGCTCTCTCTCTCTCTCTCTCTCT 4984  
OY 5048 TCTAGCCATCTTTGGATGTCACACTTTCATGTTTAAAGAGGAATGGATGATGAT 5107  
Db 4985 TCTAGCCATCTTTGGATGTCACACTTTCATGTTTAAAGAGGAATGATGATGAT 5044  
OY 5108 ACATGTTCAATTTGAGACTTTGCAACAGATGATGCTCTTATTCATTAACAACCT 5167  
Db 5045 ACATGTTCAATTTGAGACTTTGCAACAGATGATGCTCTTATTCATTAACAACCT 5104  
OY 5168 CTGCTGCTGGATGATGTTGCTAGCACCCTTCTCAACATTAAGCCACCGACTGTGAC 5227  
Db 5105 CTGCTGCTGGATGATGTTGCTAGCACCCTTCTCAACATTAAGCCACCGACTGTGAC 5164  
OY 5228 CTATTAAGTTAACCTGAGCTCAAGTTAAAGGAGACTGTGGAAACCATGTTGGA 5287  
Db 5165 CAAAAAAGTTCACTCTGAGTTCAAGTTAAAGGAGACTGTGGAAACCATGTTGGA 5224  
OY 5288 TTTCTTTTGTCACTTACATCATATCTCTCTGTTGTTGTTGTTGTTGTTGTTGTT 5347  
Db 5225 TATCTACTTGTATGATATATCATATCTCTCTGTTGTTGTTGTTGTTGTTGTTGTT 5284  
OY 5348 CGCTATCTGCAAACTTCACTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5407  
Db 5285 CAGTCACTGCAAACTTCACTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5344  
OY 5408 ATGACTTGTGATGTTCTATGAGTTTGGAGAAAGTTGATCCGATGCAACTGATCA 5467  
Db 5345 ATGACTTGTGATGTTCTATGAGTTTGGAGAAAGTTGATCCGATGCAACTGATCA 5404  
OY 5468 TGAATTTGAATAATATCTCACTTGTGACCTGCTGCTGCTGCTGCTGCTGCTGCT 5527  
Db 5405 TAGATTTCTAAGCTCTGATTTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5464  
OY 5528 AACCAAAACATCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5587  
Db 5465 AACCAAAACATCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5524  
OY 5588 ACTGCTGATCTTATTTGCTTTTAAAGGAGGTTCTAGAGAGAGTGAAGTGG 5647  
Db 5525 ATGCTCTGATCTTATTTGCTTTTAAAGGAGGTTCTAGAGAGAGTGAAGTGG 5584  
OY 5648 ATGCTCTGATCTTATTTGCTTTTAAAGGAGGTTCTAGAGAGAGTGAAGTGG 5707  
Db 5585 ATGCTCTGATCTTATTTGCTTTTAAAGGAGGTTCTAGAGAGAGTGAAGTGG 5544  
OY 5708 ATGACCATCACTACTTATTAACGAAACAGAGAGATATCTGCTCATTTATTC 5767  
Db 5645 ATGACCATCACTACTTATTAACGAAACAGAGAGATATCTGCTCATTTATTC 5704  
OY 5768 AGGCTGCTTACAGGCTGCTTAAAGGAGGTTCTAGAGAGGTTCTGCTTACGTA 5827  
Db 5705 AGGCTGCTTACAGGCTGCTTAAAGGAGGTTCTAGAGAGGTTCTGCTTACGTA 5764  
OY 5828 ATAAAAACAATCAAGTGGGCTATCTCTTATTAAGAGAGATGATTAATGCA 5887  
Db 5765 TAAAAAGTGAAGAGAT ---GATGATTTACTCAATTAAGAGAGATGATTAATGCA 5821  
OY 5888 GAATTAATGAAGTGAAGAGATTAAGAGAGATTAAGAGAGATTAAGAGAGATTAAG 5947  
Db 5822 ATGTTATGAGAACTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 5878  
OY 5948 CACCTCTCTGACCGGCTGCAAGGATGTTGAGAAATGTTGAGAAAGAGAGAGAG 6007  
Db 5879 CACCTCTCTGATGATGATTAAGAGAGATTAAGAGAGATTAAGAGAGATTAAGAG 5938  
OY 6008 ATGAAAAAGCAAGGAGATA 6029  
Db 5939 AAAAGAGAGCAAGGAGATA 5960



Db 1476 TGGTATTTTTCCTGGGCTCCTTTTACCTGATTAACCTGATCCTGGCTGTGGTACCATG 1535  
OY 1274 CCTAGAGAACAGATCAGGCCACCTTGGAGAAAGACAGAAAGAGCCGGAATTC 1333  
Db 1536 CATTAGAGAACAGAACAGCCCAATCGAAGAACTTAACAGAAAGAGTTAGAAATTC 1595  
OY 1334 AGCAATATATTGAACGCTTAAAGCAACAGAGGAGCTCAGCAGGACAGCAACGGCA 1393  
Db 1596 AGCAATATATTGAACGCTTAAAGCAACAGAGGAGCTCAGCAGGACAGCAACGGCA 1655  
OY 1394 CTGCTCAGAACATTCACAGAGAGCCAGTGCAGCAGGAGCTCTCAGACAGCTCATG 1453  
Db 1656 CTGCTCAGAACATTCAGAGATTAAGGCGGAGCAGATCATGGAGCTCTCTGAGAGCTTCAG 1715  
OY 1454 AAGCTCTAAGTTGAGTTCCAGAGTGTAAAGAAAGAAAGAAATCGAGAGAAAGAA 1513  
Db 1716 AATCTCCAGGCTGAGCTCAAAAGAGTGCACAGAGAAAGAAAGAAAGAAAGAAAGAA 1775  
OY 1514 AACAGAAAGAGAGTCTGGTGGGAGAAAGAAAGATGAGAGTGAATTCACAAAATCTGAT 1573  
Db 1776 AACAGAAAGATGTCAGAGCGGAGAAAGAGGTGAGAGATGAGAGGTGTCACAGTACAGAT 1835  
OY 1574 CTGAGAGACATTCAGAGAGAAAGTTTTCCTTCATTAAGAGAAAGCAAGTTCAGAT 1633  
Db 1836 CAGAGAAAGATTCAGAGAAAGAAAGTTCATCTGCTGTGAGAAAGGACACACCGGACCC 1895  
OY 1634 ATGAAAGAGTACTCTCCACACACAGTCTTTTGTGAGCATCCGTGGCTCCCTATTTT 1693  
Db 1896 GGGAAAGAGGCTGTCACACCCCAACAGTCCACTCAGCATTTGGCGGTCCCTGTTT 1955  
OY 1694 CACCAAGCGGAATAGCAGAACACAGCTTTTCACTTTAGAGGCGAGCAAGATGAG 1753  
Db 1956 CTGCGCAGCGGAGCAGAGAGAGTCTTCTTCAAGTTTAAAGGCGAGAGAGATGAG 2015  
OY 1754 GATGTAGAGACATTCGAGATGATGAGACAGACCTTTAGAGTAAAGAGAGCCGTA 1813  
Db 2016 GATGTAGAGACATTCGAGATGATGAGACAGACCTTTTGGAGACAGAGAGAGAGAG 2075  
OY 1814 GATGTCTCTGTTTGTGCCCGCAGACAGAGAGAGAGAGCAACCACTGAGTACAG 1873  
Db 2076 GGGTTCTACTATTCGATACCCCATAGACCCCGGAGCGGAGAGTACATCAGTCAG 2135  
OY 1874 CCAAGTAGTATCCCGAGTGTGCGAGAGTTCCTCAGCAGATGAGAAAGATGACAGAC 1933  
Db 2136 CCAAGTAGTATCCCGAGTGTGCGAGAGTTCCTCAGCAGATGAGAAAGATGACAGAC 2186  
OY 1934 TGGATTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1993  
Db 2187 TGGATTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2246  
OY 1994 GACACCTTCAGAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 2053  
Db 2247 GACACCTTCAGAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 2306  
OY 2054 CTGAACTGAATGAGAAAGAGAGTCAAGTTCTTCCAGCTTTCATGACTTCTAG 2113  
Db 2307 ATCACA---TGGCAAAAGAAAGCTCTAGTCTTACTTCTGCTGAGCAATGCTCA 2363  
OY 2114 AAGATCTTCCAAAGGAGAGAGATGATGATGATGATGATGATGATGATGATGATG 2173  
Db 2364 ATGACCCGATCAG 2423  
OY 2174 AAGACTTGAAGATCAG 2233  
Db 2424 AAGACTTGAAGATCAG 2483  
OY 2234 TCTAATCTGGAGTGTCTCCATATGTTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 2293  
Db 2484 TCTAATCTGGAGTGTCTCCATATGTTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 2543  
OY 2294 TGAATGACCATTTGATGACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2353  
Db 2544 TGAATGACCATTTGATGACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2603  
  
OY 2354 TGGCATGAGACATATCCATATGAGACCATTTCAATATATGCTTACAGTAAAGTACT 2413  
Db 2604 TGGCATGAGACATATCCATATGAGACCATTTCAATATATGCTTACAGTAAAGTACT 2663  
OY 2414 TGGTTTACAGTGGATCTTTACAGAGAAAGTCTTGAATTTATGTCATGATGATG 2473  
Db 2664 TGGTTTACAGTGGATCTTTACAGAGAAAGTCTTGAATTTATGTCATGATGATG 2723  
OY 2474 ACTATTTTCCAAAGAGCTGGAATATCTTGAAGTATTTATGTCAGTCTTACCTG 2533  
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OY 2714 CCGTGTGCGCATGACGCTTTTGTAAAGTACAAAGATGCTGTCAGATGCGCA 2773  
Db 2964 CCGTGTGCGCATGACGCTTTTGTAAAGTACAAAGATGCTGTCAGATGCGCA 3023  
OY 2774 GTGATTTGCACTCCAGCTGTCAGATGATGATGATGATGATGATGATGATGATG 2833  
Db 3024 GTGATTTGCACTCCAGCTGTCAGATGATGATGATGATGATGATGATGATGATG 3083  
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Db 3084 TCCGCTGCTGTGTGGGAGTGTAGAGAGATGAGAGATGAGAGATGAGAGATGAGAG 3143  
OY 2894 AAGCATGTGCTTACTGCTTTCATGATGATGATGATGATGATGATGATGATGATG 2953  
Db 3144 AAGCATGTGCTTACTGCTTTCATGATGATGATGATGATGATGATGATGATGATG 3203  
OY 2954 ATCTCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 3013  
Db 3204 ATCTCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 3263  
OY 3014 ATGATTAAGTAATGATATCTTCAATGCTGTGATGATGATGATGATGATGATGATG 3073  
Db 3264 ATGATTAAGTAATGATATCTTCAATGCTGTGATGATGATGATGATGATGATGATG 3323  
OY 3074 ATGTAAGAAAGAAATATATGATTAATTAATTAATTAATTAATTAATTAATTAAT 3133  
Db 3324 ATGTAAGAAAGAAATATATGATTAATTAATTAATTAATTAATTAATTAATTAAT 3383  
OY 3134 TAGATGAATTAACACCTGATGATGATGATGATGATGATGATGATGATGATGATG 3193  
Db 3384 TAGATGAATTAACACCTGATGATGATGATGATGATGATGATGATGATGATGATG 3443  
OY 3194 ATACAGAGAAATTTGGAAAGATCTTGAATCTTAAAGATTAATTAATTAATTAAT 3253  
Db 3444 ATACAGAGAAATTTGGAAAGATCTTGAATCTTAAAGATTAATTAATTAATTAAT 3503  
OY 3254 GTATAGAGATGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATG 3313  
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Db 3558 TCAATAACACCCAGTCTTACTGAGCTGTACCAATGTCTGTAGAGATGATGATGATG 3617  
OY 3374 AATATTTAAACAGGAGAGTGTAGAGATGATGATGATGATGATGATGATGATGATG 3433  
Db 3618 AATATTTAAACAGGAGAGTGTAGAGATGATGATGATGATGATGATGATGATGATG 3677



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01 DB 5835 TGGACATCTGTTTGTTCCTTTTACAAGAGCGGGGTCTGTGGTGAGAGGGTGAGAGATGCATTCCTC 5894
02 OY 5654 TAGCAATACAGATGGAAGAAGCGATTCCATGCGCTTCCAATCTCTCCAAAGCTCTCTATACAGC 5713
03 Db 5895 TTCGTACACAGATGGAAGAAAGGTTTCAATGTCAGGCCAATCTCTTAAGTGTCTCTATGAAAC 5954
04 OY 5714 CAATACGATCTCTTTAAAGAACAAAACAAGAGATATGCGTCTCATTTATTCAGCGTG 5773
05 Db 5955 CCATACACACCCACTGTAAGAGAAAAACAAGAGAGGTGTCCGCGACTATCATCTACGCGTG 6014
06 OY 5774 CTTACAGACGCGCACCTTTTTAAAGCGAAGCTGTAAACAAAGCTCTCTTATAGTACATAAA 5833
07 Db 6015 CTTACAGAGCGATATGCCCTCAGACACAACAGCTCAAGATATATGAGTATATACATAAAG 6074
08 OY 5834 ACAAAATCAAAGGTGGGGCTTAATCTCTTATATAAAGAAAGACATGTATTAATGACAGATAA 5893
09 Db 6075 ATGGAGACA---GGGATGATGATTTTGCCCAATAAAGAAGATACAGTCTTTTGTAAACGTGA 6131
10 OY 5894 ATGAAATCTTATTTACAGAAAAAATGATCTACCATGTCCACTGACGCTGTCCACTT 5953
11 Db 6132 ACGAAGACTCAAGTCCGCGAAAGACAGATGTAAC--TGCCCAACGATCTCGCCACTT 6188
12 OY 5954 CCTATGACCGGTGACAAAGCCAAATTTGTGA AAAACATGAGCAAGAGCAAGATGAA 6013
13 Db 6189 CCTATGACGTGTACAAAAGCCAGATCAAGAGAAATATGAACACAGCAAAAACGAGAAAG 6248
14 OY 6014 AACCCAAAGGGAATA 6029
15 Db 6249 AAGACAAGAGAAAG 6264
16 RESULT 4
17 US-09-024-020B-2
18 Sequence 2, Application US/09024020B
19 Patent No. 6030810
20 GENERAL INFORMATION:
21 APPLICANT: DELGADO, STEPHEN G.
22 APPLICANT: DIETRICH, PAUL S.
23 APPLICANT: FISH, LINDA M.
24 APPLICANT: HERMAN, RONALD C.
25 APPLICANT: SANGAMESWARAN, LAASHMI
26 TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
27 TITLE OF SEQUENCES: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
28 NUMBER OF SEQUENCES: 43
29 CORRESPONDENCE ADDRESS:
30 ADDRESSEE: JANET PAULINE CLARK
31 STREET: 3401 HILAVIEW AVENUE, MS A2-250
32 CITY: PALO ALTO
33 STATE: CA
34 COUNTRY: U.S.A.
35 ZIP: 94304-1397
36 COMPUTER READABLE FORM:
37 MEDIUM TYPE: Floppy disk
38 COMPUTER: IBM PC compatible
39 OPERATING SYSTEM: PC-DOS/MS-DOS
40 SOFTWARE: Patent Release #1.0, Version #1.30
41 CURRENT APPLICATION DATA:
42 APPLICATION NUMBER: US/09/024.020B
43 FILING DATE: 16-FEB-1998
44 CLASSIFICATION: 536
45 PRIOR APPLICATION DATA:
46 APPLICATION NUMBER: US 60/039,447
47 FILING DATE: 26-FEB-1997
48 ATTORNEY/AGENT INFORMATION:
49 NAME: CLARK, JANET P.
50 REGISTRATION NUMBER: 34,799
51 REFERENCE/DOCKET NUMBER: R0020B-REG
52 TELECOMMUNICATION INFORMATION:
53 TELEPHONE: (650) 852-3097
54 TELEFAX: (650) 852-3522
55 INFORMATION FOR SEQ ID NO: 2:
56 SEQUENCE CHARACTERISTICS:
57 LENGTH: 6007 base pairs

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|                       | STRAND        | EDNESS  | nucleic acid    | single      |
|-----------------------|---------------|---|-----------------|-------------|
|                       | TOPOLOGY      | Linear  |                 |             |
|                       | MOLECULE TYPE | DNA (genomic)   |                 |             |
| US-09-024-0208-2      |               |   |                 |             |
| Query Match           | 46.28         | Score 2787.6  | DB 3            | Length 6007 |
| Best Local Similarity | 69.99         | Pred. No. 0   |                 |             |
| Matches 4086          | Conservative  | 3   | Mismatches 1597 | Indels 162  |
|                       |               |   |                 | Gaps        |
| QY                    | 14            | TGCTGTTTCACACGAGCACTGACAGCTTCAACTTCTACACAGAGAAATCTTGGGCTA   | 73              |             |
| DB                    | 35            | TGCTGACACACGAGGCGCTATGTTTCAAGCCTTTACCCCTGATCTCTGCGACACA     | 94              |             |
| QY                    | 74            | TTGAAAGACGATTCGACAGAAAGGCAAAAGTCCAAACGAG-----ACA            | 121             |             |
| DB                    | 95            | TGAGAGGCGTATTCGCGAGAGCAATCAAGAAACCAAGAGGCGAGTGCAGCCACC      | 154             |             |
| QY                    | 122           | AAAAAGATGAGAGAAATGGCCCAAAAGCCAAATATGACTTGGAGAGTGGAAAGAAC    | 181             |             |
| DB                    | 155           | GAGAGAGAGATGAAGACAGCAAGCCCAAGCCAAAGCTGACAGCTGGAGAGAGATT     | 214             |             |
| QY                    | 182           | TTTCATTTATTTATGAGAGATTCCTCCAGAGATGCTGACAGAGCCCTGGAGAGCTTG   | 241             |             |
| DB                    | 215           | TGCCCTTATCTACGGGGACATCCCGCAAGGCTGCTTGGGCTTCCCTGAGAGACTTG    | 274             |             |
| QY                    | 242           | ACCCTTACTATATCAATTAAGAAACCTTTATATGATTTGAATTAAGGAGAGCCATCTCC | 301             |             |
| DB                    | 275           | AACCTTACTATTTAGCGAGAGAAACCTTTGATTTAAACAGAGGAGAAACCTCTTCA    | 334             |             |
| QY                    | 302           | GGTCAGTGCACCTCTGCGCTGACATTTTAACCTCTTCAATCTCTTAGAGAAATAG     | 361             |             |
| DB                    | 335           | GATTTAGTGCACACCTGCGCTTGTACATTTTAAACCTTTTAACTATTAAGAAATAG    | 394             |             |
| QY                    | 362           | CTATTAAATTTTGGTACATTCATTTACAGATGCTAATATGTCATTTATTTGACAA     | 421             |             |
| DB                    | 395           | CTATTAAATTTTGTATACACTCACTTTTACAGATGATCATATGTGACCATCTTGACA   | 454             |             |
| QY                    | 422           | ACTGTGCTTATATGACATGATGAACCTCTGATTTGGACAAAGATGATGAATACCT     | 481             |             |
| DB                    | 455           | ACTGTGCTTATGACCTTTGATGAACCTCTGATTTGGACAAAGATGATGAATACCT     | 514             |             |
| QY                    | 482           | TCACAGAAATATATCTTTTGAATCACTTATTAATTAATTTGCAAGGGATCTGTTAG    | 541             |             |
| DB                    | 515           | TCACAGGATTTTACACATTTTAACTACAGTGAAGAAATCATCGCAAGGTTTCTGCAATG | 574             |             |
| QY                    | 542           | AAGATTTTACTTCTTCCTGGGATTCATGAGAACTGGCTGCATTTCACTTATTCATTTG  | 601             |             |
| DB                    | 575           | AAGGCTTACCTTCTTCTGGAAGCCGCTGGAATCTGTTAGCTTATGATCTCTATGATGG  | 633             |             |
| QY                    | 602           | CGTACGTACAGAGTTTGTGACCTGGGCAATGCTCGGCATTTGAGAAATTCAGACTTC   | 661             |             |
| DB                    | 635           | CATATGTACAGAGTTTGTGACCTGGGCAATGCTCGGCATTTGAGAAATTCAGACTTC   | 699             |             |
| QY                    | 662           | TCCGAGCATGGAAGCGATTTCACTCATTTCCAGGCTGAAAAACATTTGGGAGCCCTGA  | 721             |             |
| DB                    | 695           | TCCGAGCTTTGAAAACTATCTCTGTAATTTCCAGGCTGAAACATCTGGGCGCCCTAA   | 754             |             |
| QY                    | 722           | TCCAGTCTGTGAAGAAGCTCTCAATGTAATGATCTGACTGTCTTCTGTAGAGCTAT    | 781             |             |
| DB                    | 755           | TCCAGTCTGTGAAGAAGCTCTCAATGTAATGATCTGACTGTCTTCTGTAGAGCTAT    | 814             |             |
| QY                    | 782           | TTGCTCTAATTTGGGCTGAGCTGTTCAATGGGCAACCTGAGAGAAATATTAACAAAGGC | 841             |             |
| DB                    | 815           | TGCGCTTATTTGGCTGAGCTGTTCAATGGGCAACCTTCCAAACAAAGTGTCTGTGCGC  | 874             |             |
| QY                    | 842           | CTCCACCAATGCTTCTTGGAGAGACATGATATGAAAGAAATATTAACGTGTAATTATA  | 901             |             |
| DB                    | 875           | CCA-----TAACTCA   | 888             |             |
| QY                    | 902           | ATGTCACATTAATTAATGAACCTGCTTTGAGTTTGAATGCAATCATATTTCAAAATT   | 961             |             |
| DB                    | 887           | ACGAGAGTCTACGTGAGAGGCAACGACAGAGCTTTGATGGGAGAGATATATCAACATA  | 948             |             |



OY 962 CAGATATCATATTTCTGAGGGTTTTTAGATGACTACTAGTGGAAATAGCTGTG 1021  
DB 947 AAAAAAACTTTACATGTTCTCGAGCTAGAAACCTTGGCTCGGGAAACAGTTCTG 1006  
OY 1022 AAGCAGGCCAATGTCAGAGGATATATGTGTGAAGACTGTGAAATCCCAATTATG 1081  
DB 1007 AATGCTGGCAATAGCCAGAGGATTCAGATGATGAACAGAGAAAGAAACCCCACTAG 1066  
OY 1082 GCTACACAGCTTTGTATGATCTTCACTGAGGCTTTTGTCTTGTCTGACTAATGACTC 1141  
DB 1067 GTTACACAGCTTTGACACTTCACTGAGGCTTTCTGCTATTTATTCCTTATGACCC 1126  
OY 1142 AAGACTTGTGAGAAATCTTATCACTGATTAAGTCTGCTGTGGAAAGCTATGTA 1201  
DB 1127 AAGACTATTTGGAGAACTATTAACAGCTGACCTTAGAGCCCTGGGAAAGCTATGTA 1186  
OY 1202 TATTTTGTGTGTGATTTCTTGGGCTCATTCTTACTTAATTAATTGATCTGTG 1261  
DB 1187 TCTTCTTGTGTGATCTTCTGCTGCTTCTTCTTCTTCTGATGACTTGTGCTG 1246  
OY 1262 TGTGAGCCATGCTCTGAGAGAAACAGATCAGGCCACTTGGAGAGAGCAAGAAAG 1321  
DB 1247 TGTGTGCTATGCTTATGAGAGACAGAAACAGCACTGAGAGAGAGCAAGAAAG 1306  
OY 1322 AAGCCGAATTTGAGAGATGATTAAGACTTAAAGAGCAGAGAGAGAGCTCAGCAG 1381  
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OY 1382 CAGCAAGGCACTGCTC-----AGAACATTCAGAGAGAGAGAGAGAG 1424  
DB 1367 CTGCAATGAGCCCTCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1426  
OY 1425 AAGCAGAGAGCTCTGAGA-CAGCTATCTGAAGCTCTAAGTTGAGTTCCAGAGAGCTA 1483  
DB 1427 AATGGGTAGGCTCTCGAGAGAGCTCTTCTGAACTGTCTAATCTCACTTCCAGAGAG 1486  
OY 1484 AAGAAAGAAATGAG 1543  
DB 1487 AAGAGCGGAG 1546  
OY 1544 AAGATG---GGATGAATTCAGAAATCTGATCTGAGAGAGAGAGAGAGAGAG 1600  
DB 1547 AAGGAG 1606  
OY 1601 TTTGCTTCCATTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1660  
DB 1607 TCGGCTGCGACAG 1654  
OY 1661 AATCTTTTGTGAGCATCCGTGCTCCATATTTTACAGAGAGAGAGAGAGAGAG 1720  
DB 1655 AATCTCTGCTCAGCATTTCCAGAGCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 1714  
OY 1721 TTTTCAAGCTTTG-----AGGGCAGAGAGAGAGAGAGAGAGAGAGAGAG 1774  
DB 1715 TCTTCAAGCTTTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1774  
OY 1775 AATGATGAG 1834  
DB 1775 AAGATGAG 1834  
OY 1835 AAGCAG 1879  
DB 1835 TCGGAG 1894  
OY 1880 GGTCAATCCGAGATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1939  
DB 1895 GCTGCTGCGAGATCTTCCAGAGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 1954  
OY 1940 GCAATGCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1999  
DB 1955 GCAAG 2002

OY 2000 TTTGCGAGAGAGAGAT 2059  
DB 2003 TCTGCTGAG 2056  
OY 2060 CTGAATATGAG 2119  
DB 2057 TGGAAATTAAG 2116  
OY 2120 CTTCAG 2176  
DB 2117 AAG 2176  
OY 2177 AACTGAG 2236  
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DB 3017 AAGGAG 3076  
OY 3077 TGAAG 3136

Db 3077 CCAAGGTAGAGTGCACGCTTCATGCAGGCTCACCTC-----AAGCAGCGGAGGCGG 3130  
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Db 3131 ATGAATTAACACCTTATGATCTAAACACAGAAAGACGTTGTATGTCATCATCA 3190  
Qy 3197 C---ARCAGAAATTCGGAAGATCTTGTATCTTAAGATGTAAATGAGTACAAAGT 3253  
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Qy 3254 GTATAGAACTGCGACAGTGTGAAAAATACATTATGATGAAGTATTCATGTCAT 3313  
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Qy 3914 GTTACTGAACTTGAAGCATCAATCTCTAGAGACATAGAGTCTGAGACCTTAA 3973  
Db 3899 GCTACTGAACTTGAAGCATCAATCTCTAGAGACATAGAGTCTGAGACCTTAA 3958  
Qy 3974 GAGCTTATCTGATTTGAAGGATGAGGTTGTTGATGATCCCTTTAGAGCAATTC 4033  
Db 3959 GAGCTTATCTGATTTGAAGGATGAGGTTGTTGATGATCCCTTTAGAGCAATTC 4018  
Qy 4034 CATTCATCATGATGCTCTCTGTTGTTGTTATATCTGCTAAATTTCAACATCAG 4093  
Db 4019 CTTCTCATCATGATGCTCTCTGTTGTTGTTATATCTGCTAAATTTCAACATCAG 4078  
Qy 4094 GCGTAAATTTGTTGCTGGCAATTTCAACATGATGATTTAAACCAACATGCTGAGCT 4153  
Db 4079 GAGTTAACTCTGTTGCTGGCAATTTCAACATGATGATTTAAACCAACATGCTGAGCT 4138  
Qy 4154 TTGACATGAGAGCTGATATATCATGATGCTTAAACCAATGAGAAAGAAATGAGA 4213

Db 4139 TCGAATGCAATTTGTCACAAATTAACAGACTGTGAGAGCTCATGAGGCAACAGCA 4198  
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Db 4199 CGGAGATCGGATGAGAAATGTAAGTAATTTGATTAATGATGATTTGGGTATCTCT 4258  
Qy 4271 CTGCTCTCAAGTGTGCAATTCAGAGATGATGATTAATGATGATGATGATGAT 4330  
Db 4259 CCTCTTCAATGAGCAACCTTCAAGAGCTGATGATGATGATGATGATGATGATGAT 4318  
Qy 4331 CCAGAAATGAGACTCCAGCTTAAGTATGAAGAAAGTGTGATGATGATGATGATGAT 4390  
Db 4319 CCCGAAAGCTAGAGAGAGAGCTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 4378  
Qy 4391 TTAATTTATCATCTTTGGCTCTCTTCACTTCACTTCACTTCACTTCACTTCACT 4450  
Db 4379 TCAATTTATCATCTTTGGCTCTCTTCACTTCACTTCACTTCACTTCACTTCACT 4438  
Qy 4451 ATAAATTTCAACAG 4510  
Db 4439 ACAATTTCAACAG 4498  
Qy 4511 AGAAGAAATCTATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4570  
Db 4499 AGAAGAAATCTATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4558  
Qy 4571 CTGACACAG 4630  
Db 4559 CCGGACCTTGAACAAATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4618  
Qy 4631 ACATAGAGATCTATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4690  
Db 4619 ACATAGAGATCTATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4678  
Qy 4691 ACCAGAGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4750  
Db 4679 CTCAG 4738  
Qy 4751 TTAAGTGAAG 4810  
Db 4739 TCACTGAG 4798  
Qy 4811 GGAATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4870  
Db 4799 GGAATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4858  
Qy 4871 TGATGAG 4930  
Db 4859 TGATGAG 4918  
Qy 4931 GCGAATCTACGCTGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4990  
Db 4919 GCGAATCTACGCTGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4978  
Qy 4991 TGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5050  
Db 4979 TGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5038  
Qy 5051 ACCGATCTTGTGAG 5110  
Db 5039 TCTCATTTTGTGAG 5098  
Qy 5111 TGTTCAATTTGAG 5170  
Db 5099 TGTTCAATTTGAG 5158  
Qy 5171 CTGCTGAG 5230  
Db 5159 CTGCTGAG 5215  
Qy 5231 ATAAAGTAAACCTGAG 5290  
Db 5216 ACAAG 5275

|    |      |   |      |
|----|------|---|------|
| QY | 5291 | TCTTTTGTGAGTTACATTCATCATCCTCTCGTGTTGTGGTAACATGTACATCGGG         | 5350 |
| Db | 5276 | TCTTCTTTGTGAGCTACATCAATCATCTCTCCCTTGATTGTGGTAACATGTACATCGCCA    | 5335 |
| QY | 5351 | TCTACTCTGGAAACTTCAGTGTGTGCTACTGAAGAAGTCAGAGCCTTGAGTGAAGATG      | 5410 |
| Db | 5336 | TCATCTCTGGAAACAATTCAGCTGGCCACCAGAGAGAGCGCCGACCTCTGAGTGAAGATG    | 5395 |
| QY | 5411 | ACTTTGAGATGTTCTATGAGTTTGGGGGAAGTTGATCCCGATGCACATCAGTTTCATNG     | 5470 |
| Db | 5386 | ACTTCGACACTTTCATGAGATCTGGGGGAAGTTGACCCAGAGGCCAACCCAGTTTCATCG    | 5455 |
| QY | 5471 | AATTTGAAAATAATATCTCAGTTTGGCAGCTGGCGCTTGAACCCGCTCTCATCTGCACAAAC  | 5530 |
| Db | 5456 | AGTACTGTAACTGGCACAGCTTTGCCGAGCGCCTGGAGACACCCTGCGAGTTACCCAAAGC   | 5515 |
| QY | 5531 | CAAAACAACTCAGCTCATTTGCCATGATGATTTGCCCATGGTAGTGATGACCGATCCACT    | 5590 |
| Db | 5516 | CAAACACATCGAGCTCATCCGATCCATGACGATGCCCATGTGTAGCGGAGATGCGATCCACT  | 5575 |
| QY | 5591 | GCTCTGATATCTTATTTCTTTTACAAAGCGGGTCTTAGGAGAGAGTGGAGAGATGATG      | 5650 |
| Db | 5576 | GCTTGGACATCTTCTTCCCTTCCACCAAGCCAGTCTTGGGAGACAGTGGGGAAGTTGGACA   | 5635 |
| QY | 5651 | CTTCAAGAAATCAGATGGAAGAGGATTCATGAGGCTCCAAATCCTTCAAAGGTCTCTATC    | 5710 |
| Db | 5636 | TCTTCGGCGACAGATGAGAGAGCGGTTCTGTGGATTCCAATCTTCCAAAGTGTCTTACG     | 5695 |
| QY | 5711 | AGCCATCACTACTACTTAAACAGAAAAAAGAGAGATGCTCTGCTCATTTATTCAGC        | 5770 |
| Db | 5696 | AGCCATATCAACAACACTCTGGGGGCCAAGAGAGAGAGAGTGTCTGCAATGGTCTCCGACAGC | 5755 |
| QY | 5771 | GTCGTTACAGAGCCACTTTTAAAGCG                                      | 5798 |
| Db | 5756 | GTCGCTACAGGGGACACTTGGCTAGGCG                                    | 5783 |

RESULT 5  
 US-09-425-043-2  
 Sequence 2, Application US/09425043  
 Patent No. 6535172  
 GENERAL INFORMATION:  
 APPLICANT: DELGADO, STEPHEN G.  
 APPLICANT: DIETRICH, PAUL S.  
 APPLICANT: FISH, LINDA M.  
 APPLICANT: HERMAN, RONALD C.  
 APPLICANT: SANGAMESWARAN, LAKSHMI  
 TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE  
 TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICED VARIANT THEREOF  
 NUMBER OF SEQUENCES: 43  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: JANET PAULINE CLARK  
 STREET: 3401 HILLYER AVENUE, MS A2-250  
 CITY: PALO ALTO  
 STATE: CA  
 COUNTRY: U.S.A.  
 ZIP: 94304-1397  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/425,043  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 09/024,020  
 FILING DATE: 16-FEB-1998  
 APPLICATION NUMBER: US 60/039,447  
 FILING DATE: 26-FEB-1997  
 ATTORNEY/AGENT INFORMATION:

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: TYPE: nucleic acid
:
: STRANDEDNESS: single
:
: TOPOLOGY: linear
:
: MOLECULE TYPE: DNA (genomic)
:
: US-09-425-043-2

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|----|---|--------|------------------|-------------|--------------|
|    | Query Match   | 46.2%  | Score 2187.6;    | DB 4;       | Length 6007; |
|    | Best Local Similarity   | 69.9%; | Pred. No. 0;     |             |              |
|    | Matches 4086; Conservative  | 3;     | Mismatches 1597; | Indels 162; | Gaps 18;     |
| OY | 14 TGCCTGTACACAGGACTGTGACACTTTCATCTTTCCACGAGAAATCTTGCGGGCTA         | 73     |                  |             |              |
| Db | 35 TGCTCGAACACCAGGCCCTGTATGTTTCAACCTTTACCCCCGTGAGTGGCAGAAACA        | 94     |                  |             |              |
| OY | 74 TTGAAGAAGCATTCGACAGAAAAAGCAAAGATCCAAACAG-----ACA                 | 121    |                  |             |              |
| Db | 95 TCAGAGGGGGTTTTGCCGAGAACAGCTCACAAAACCAACAAAGGGGATGGACAGCAC        | 154    |                  |             |              |
| OY | 122 AAAAAGATGACACAGAAATATGGCCCAAGGCCAAATATGACTTTGGAACTGGAAAGAAC     | 181    |                  |             |              |
| Db | 155 GGGAGAGAGATTAAGACACAGAACCCCAAGCAGAGTACTGGAGGGCTGGAAAGATT        | 214    |                  |             |              |
| OY | 182 TTCATTTATTTATGGAAGACATTCCTCCAGAGATGGTGTCAAGAGCCCCTGGAGACCTGG    | 241    |                  |             |              |
| Db | 215 TGCCCTTTCATCTACGGGGGACATCCGGCAAGGCGTGGTTCGGTTCCTCCCTGGAGACTTGG  | 274    |                  |             |              |
| OY | 242 ACCCTTACTATTCATAATAGAAACCTTTATATGATATGAATTAAGSAGAGCCATCTTCC     | 301    |                  |             |              |
| Db | 275 ACCCTTACTATTTAGACGCAAAACCTTTGTAGTATTAACAGAGAGGAAACCTCTCTTCA     | 334    |                  |             |              |
| OY | 302 GGTTTAGTGCCACCTCTGCCCCTGTACATTTTAACTCCCTTCATCCCTCTTAGAAATATG    | 361    |                  |             |              |
| Db | 335 GATTTAGTGCCACACCTGCTGTACATTTTAAAGCCCTTTAACTGATTAAGAAATATG       | 394    |                  |             |              |
| OY | 362 CATTAAGATTTTGTGACATTCATATATTCAGATGCTATTTATGTGACATATTTTGACA      | 421    |                  |             |              |
| Db | 395 CATTAAGATTTTGTGACATTCATATATTCAGATGCTATTTATGTGACATATTTTGACA      | 454    |                  |             |              |
| OY | 422 ACTGTGTGTTTATGACAATGAGTAACCCCTCGATTTGGACAAGATATGAGATATACACT     | 481    |                  |             |              |
| Db | 455 ACTGTGTGTTATGACCTTTAGTAACCCCTCGAATATGATTCGAAGATATGAGATATACACT   | 514    |                  |             |              |
| OY | 482 TCACAGGAATATATCTTTGAAATCACTTATATAAANTATTCGAAGGGGATTCGTGTAG      | 541    |                  |             |              |
| Db | 515 TCACAGGGGATTTTACATTTGAAATCACTATGATAAATATTCGAAGGGGATTCGTGTAG     | 574    |                  |             |              |
| OY | 542 AAGATTTTACTTCTTCGCGATTCATGGAACCTGGCTCATTTCACTGATTAACATTTG       | 601    |                  |             |              |
| Db | 575 ACGGTTTACCTTCTTCGCGAGAACCCCTGGAACCTGGTATGACTTCACTGATTAACATTTG   | 634    |                  |             |              |
| OY | 602 CGTACGTCACAGAGTTTGTGACCTGGGCAATGTCTCGGACTTGAAGACATTCAGAGTTC     | 661    |                  |             |              |
| Db | 635 CATAATGTGACAGAGTTTGTGAGACCTGGGCAATGTCTCAAGCCCTGGAACATTCAGAGTTC  | 694    |                  |             |              |
| OY | 662 TCCGAGCAATGGAAGAGATTTTCAAGCATTTCCAGGCCCTGAAACCAATGTGGGAGGCCCTGA | 721    |                  |             |              |
| Db | 695 TCCGAGCAATGGAAGAGATTTTCAAGCATTTCCAGGCCCTGAAACCAATGTGGGAGGCCCTRA | 754    |                  |             |              |
| OY | 722 TCCAGTCTGTGGAAGAGCTCTCAGATGTATATGATACCTGACTGTGTCTGTGACAGCTAT    | 781    |                  |             |              |
| Db | 755 TCCAGTCTGTGGAAGAGCTCTGAGACGTATGATCTGCACTGTGTTCTGCGCTGAGATGTTT   | 814    |                  |             |              |
| OY | 782 TTGGCTTATTTGGGGGCGAGCTGTCATGAGGGCAACTGAGAAATTAAGTATNCAATGGC     | 841    |                  |             |              |

Db 815 TCGCCGATGTCGCTGAGCTCTTCATGAGGAGACCTTCGAAACAAGTGTGTGTGTC 874  
QY 842 CTCGCCACCAATGCTTCTTGGAGACATAGTATGAAAAAGATTAATCTGCAATTATA 901  
Db 875 CCA-----TAACTTCA 886  
QY 902 ATGTGACCTTATAAATGAACTGTCTTGAATTTGACGTGAATCATATTAATTCAGATT 961  
Db 887 ACGAGAGCTACCTGGAGAACGCGACACAGAGCTTTGACTGGAGGAATATATCAACAATA 946  
QY 962 CAAGATATCATATTTCTCTGAGAGGTTTTTATGATGCACTACTATGTGGAATAAGCTG 1021  
Db 947 AAACAACCTTTTACATGGTTCCTGGACATGAAACCTTGTCTCGCGGGAACAGTTCTG 1006  
QY 1022 ATGACGCCATGTCACAGAGCATATATGTGTGAAGCTGTGGAATATCCCATTTATG 1081  
Db 1007 ATGCTGGGCAATGCCAGAGGATTCATGATCATGAACACAGAGGAACCCCACTAG 1066  
QY 1082 GCTACACAAGCTTGTATACCTTCATGTGGGCTTTTGTCTTGTGCACTAATGATC 1141  
Db 1067 GTTACACAGCTTTTACACCTTACCTGAGCTGGCTTCTGCAATTAATTCGCTTATGACC 1126  
QY 1142 AGGACTTCTGGGAAATCTTTATCACTGACATTAAGTCTGCTGGGAAAGCTACATGA 1201  
Db 1127 AGGACTATTTGGAGAACTTATACAGCTGACCTTACAGCCGCTGGGAAAGATACATA 1186  
QY 1202 TATTTTGTGTGCTCATTTTCTGTGGCTCATTTCACTTAATTAATTTGATCTGTG 1261  
Db 1187 TCTTTCTGTGTGCTCATTTTCTGTGGCTCATTTCACTTAATTTGATCTGTG 1246  
QY 1282 TGTGTGCACTGCTTACAGAGGAACAAATACAGGCACTTGTGAGAGAGAGAAAG 1321  
Db 1247 TGTGTGCACTGCTTATGTGAGAAACAAACAGGCACTTGTGAGAGAGAGAAAG 1306  
QY 1322 AGGCGCAATTTTACAGAGATTTGAACAGCTTAAAGCAAGAGAGAGCTACAGAG 1381  
Db 1307 AGGCGGAGTTCAAGGCAATGCTGAGCACTCAAGAGAGAGAGAGAGAGAGAGAG 1366  
QY 1382 CAGCAAGGCAACTGCTC-----AGAACATTCAGAGAGAGAGAGAGAGAG 1424  
Db 1367 CTGCAATGCGCACCTACAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1426  
QY 1425 AGCAGGAGAGCTTACAG--CAGCTCATGAGAGAGCTTAAGTTGATTCAGAGAGAG 1483  
Db 1427 ATGTGTGTGCTCTCTGAGAGAGCTTCTGAAGCTGTCACTCACTTCAAGAGAGAG 1486  
QY 1484 AGCAAGAAGATGAG 1543  
Db 1487 AGGAGCGGAG 1546  
QY 1544 AAGATGA--GGATGAATTCAAAAATCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1600  
Db 1547 AAGGAG 1606  
QY 1601 TTCCGCTTCCATTTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1660  
Db 1607 TCCGCTGCGAGACACAGAGATAGG-----AGGAAATTTTCAATCATATCAAT 1654  
QY 1661 ACTCTTTTGTGAGCATCTGCTGCTCTTATTTTACCAAGAGAGAGAGAGAGAGAGAG 1720  
Db 1655 AGTCTGCTGCTGAGCATCTGAGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1714  
QY 1721 TTTTCACTTTAG-----AGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1774  
Db 1715 TCTTCACTTTCTGAG 1774  
QY 1775 ATGATGAG 1834  
Db 1775 AGGATGAG 1834  
QY 1835 GAGGAG 1879  
Db 1835 TCCGCGCCCGGAG 1894  
QY 1880 GGTATCCCGAGAGCTGGAGAGTGTTCACAGAGATGAGAGAGAGAGAGAGAGAGAG 1939  
Db 1895 GCTGTGCGGAGATCTTCCAGCCTGCGGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 1954  
QY 1940 GCATGAGTGTGTCTTCTGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1999  
Db 1955 GCAAGGCGAGAGT 2002  
QY 2000 TTCTGCGAGAGT 2059  
Db 2003 TCTGCGCTGAGT 2056  
QY 2060 CTGAATGAG 2119  
Db 2057 TGGAAATTTAAG 2116  
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Db 2117 ACGAG 2176  
QY 2177 AACTGAG 2236  
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QY 2237 TATCTGAG 2296  
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QY 2357 CCATGAG 2416  
Db 2357 CAATGAG 2416  
QY 2417 TTTTCACTGAG 2476  
Db 2417 TGTTCACCGGAG 2476  
QY 2477 ATATTTTCCAG 2536  
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QY 2537 AACTGAG 2596  
Db 2537 AGCTGAG 2596  
QY 2597 TTTTCAAGTGTGCAAAATCTTGGCAACGTTAAATATGCTAATTAATCAATGAGAGAG 2656  
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QY 2657 CCGTGGGAG 2716  
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QY 2717 TGTGTGCGAG 2776  
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QY 2777 ATGTGCACTTCCAG 2836  
Db 2777 AGTGAAG 2836  
QY 2837 GCGT 2896  
Db 2837 GAGT 2896  
QY 2897 CCATGTGCTTACTGTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATG 2956  
Db 2897 CCATGTGCTTACTGTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATG 2956

|    |      |  |      |
|----|------|--|------|
| QY | 2957 | TCCTTCGGCCCTTCCTTTCAGCTCAATTTAGTGCAGACAACTTCACCACTGATGATG          | 3016 |
| Db | 2957 | TATTCCTGGCCCTTCCTTCAGCTCCTTCAAGCCAGACAACTTCGCGCCAGACGACG           | 3016 |
| QY | 3017 | ATATAGAAATGAATTAATCTCCAAATTCCTGTGGATAGATGCACAAAGAGATAGCTTATG       | 3076 |
| Db | 3017 | ACGGGGAAATGAACAACTTCAGATCTCAGTGATCCGGATCAAGAAAGGGCGTGGCTTGG        | 3076 |
| QY | 3077 | TGAAAGCAAAAATATATGAAATTTATTCACAGTCTCTCATTTAGGAACAAAAGATTTTGA       | 3136 |
| Db | 3077 | CCAAAGTGAAGGTGACAGCCCTTCATCCAGGCTCACTTC-----AAGCAGGGGAGGCGG        | 3130 |
| QY | 3137 | ATGAAATTAACACATGATGATCTTAACAAAGAAAGACAGTTGTATGTCCATCTCA            | 3136 |
| Db | 3131 | ATGAAAGTGAAGCCCTTCGAGACCTGTATGAGAAAGGCCAACTGCATCCGCAACCA           | 3190 |
| QY | 3197 | C---ATCAGAAATTTGGGAAAGATCTTGACTATCTTAAATGTAAATGGAATCAACATG         | 3253 |
| Db | 3191 | CGGGCGGTGATATCCACCGGAGACGGGACTTCCAGAAAGACGGGAACCGAACACACGCG        | 3250 |
| QY | 3254 | GATATAGGAATGCGACAGTGTGAAAATTAACATTTATGATGAAGATTAACATGTCAT          | 3313 |
| Db | 3251 | GCAT-----CGCAGACAGGCTGGAGAAATCATCATCGACGA-----GGACCAATGTCT         | 3301 |
| QY | 3314 | TCATAAACAAACCCCACTGCTTACTGTGACGTACGTACCAATTCCTGTACGAAATCTGACTTG    | 3373 |
| Db | 3302 | TCATTAACAAACCAACCTGACAGCTCGGGGTGCCATTCCTGTGGGCAATGCTGACTTCG        | 3361 |
| QY | 3374 | AAATTTAAACACGGAAGATTTATGATAGTAATCCGATCTGGAAACAAAGCAAGAAC           | 3433 |
| Db | 3362 | AGAACTCAACACAGAGAGATTTAGAGCAAGAACCACTGTAAGGACGCAAAAGATTAAC         | 3421 |
| QY | 3434 | TGATGAAACACAGTATGCTCATCGAAGGTAGACAGTGTGGACATCGGCGACACTGTAGAG       | 3493 |
| Db | 3422 | TGAGCATATCC---AGTCTCTCGAAGGAAGTATCATCATGACATCAAGCTGAGTGGAG         | 3478 |
| QY | 3494 | AACAGCCCGTAGTGGAACTCGAAGAAATCTGTGAACCAAGACTTGTTCACCTGAGAGCT        | 3553 |
| Db | 3479 | AAGTTCCTGGAGACACCTGAGAGATTAATCTGGATCCGAGACCTCTTTCAGAGGGT           | 3538 |
| QY | 3554 | GTCATCAAAATTCAGTGTGTCTCAATCAATGTGAAGAAAGGACAGGAAACAAATGCT          | 3613 |
| Db | 3539 | GCCTCCAGCGGTTCAAGTGTCTGCCAGGTCAACATCGAGGAAGACTGAGCAATGCTGTGT       | 3598 |
| QY | 3614 | GGAACCTGAGAAAGGACGTGTTCCTCCAGATAGTTGAACATTAATGCTTGAAGACTTCATG      | 3673 |
| Db | 3599 | GGATCTTGGGGAAGAACTGCTCTCTCATGTGTGAGACAAATTTGTTTGAACCTTCA           | 3658 |
| QY | 3674 | TTTTCATGATTCCTCTTAAGTAGTAGTGGTCTCTGGCATTTGAAGATATATATATGATCAGC     | 3733 |
| Db | 3659 | TCCTCATGATTCCTGCTACGACAGTGGGCGCTTGCCCTTTGAGGACATCTACATATGAGCAGA    | 3718 |
| QY | 3734 | GAAAGACGATTAAGACGATCTTGGAAATATGCTGACAAAGGTTTCACTTAACATTTTCATC      | 3793 |
| Db | 3719 | GGAAGACCAATCCGACCAATCTTGAGATATGCGACAAAGGTCTTCACTACATCTTCATCC       | 3778 |
| QY | 3794 | TGGAATATGCTTCAAAAATGGGTGGCATATGCGATCAAAACATATTTTACCAATGCTCGT       | 3853 |
| Db | 3779 | TGGAGATGTTGCTCAAGTGGACAGCCTACAGGCTTGTCTCAAGTTCTTCAACAAATGCTGTGT    | 3858 |
| QY | 3854 | GTTGGCTGACACTTCTTAATTTGATGTGATGTTTCATTTGGTCAGTTTAAACAGCAAAATGCTTGG | 3913 |
| Db | 3899 | GCTACTCGGAACATGAGGCCATTAAGTCCCTTAAGGACCTTAAGACCTTTGAGACCTTTAA      | 3958 |
| QY | 3974 | GAGCCTTATCTCGATTTTGAAGGGATAGAGGTGGTTTGTGATCCCTTTTGAAGGACATTC       | 4033 |
| Db | 3959 | GAGCCTTATCAACATTTGAAGGGATAGAGGTGGTGTGATATCCCTTTGGTGGGCGCATCC       | 4018 |
| QY | 4034 | CATCCATCATGATGTGCTTCTGGTTTGTCTATATTTCTGGCTAAATTTTCAGCATATGG        | 4093 |

|    |      |  |      |
|----|------|--|------|
| Db | 4019 | CTTCACATCATGAATGTCTCTCTGGTGTCTCATCTCTGGCTGATTTTCACATCAATGG         | 4078 |
| QY | 4094 | GCCTAAATTTTGTGTCTGGCAAAATTTCTACCACTGATATTTAACACCAACTGGTGCACAGT     | 4153 |
| Db | 4079 | GAGTTAACCTGTGTGGCGGGAAATTAACACTACTGCTTTAATGAGACTTCTGAAATCCGGT      | 4138 |
| QY | 4154 | TTGACATCGAAGACGTGTAAATATATCATACGTGATTGCTTAATAATATAGAAAGAAATGAGA    | 4213 |
| Db | 4139 | TGCAAAATCGAATATATGTCCAAATAATTAACGAGACTGTGAGAAAGCTCATGGAGGGCAACAGCA | 4198 |
| QY | 4214 | CTG---CTCAATGGAAGAAAATGTAAAGTAACTTGTATATGTAGAGATTTGGGTATCTCT       | 4270 |
| Db | 4199 | CGGAGATCCCATGTGAAAGATGTCAACATCAACTTTTGACATGTTCGAGACAGGTAACCTGG     | 4258 |
| QY | 4271 | CTTGTCTTCAAGTGTGCACATTTCAAGTAAAGATGATTAATGTATATGACAGCATTTGATT      | 4330 |
| Db | 4259 | CCCTCTTCAAGTGGCAACTTCAAAAGCGGTGAGTACATATGATATGGGTGTAGATT           | 4318 |
| QY | 4331 | CCGAAATGTGGAACTCCAGCTTAAGTATGAAAGAAAGTGTACATGTATCTTAACTTTG         | 4390 |
| Db | 4319 | CCCGAAAGCCAGACGAGACCTGACTAGAGGGCAACATCAATGATACATCTACTTCG           | 4378 |
| QY | 4391 | TTATTTTCATCATCTTTGGGTCTTCTTCACTTGAACCTGTTATTTGGTGTACATCAG          | 4450 |
| Db | 4379 | TCATCTTCATCATCTTGGGTCTTCTTCACTTGAACCTGTTATTTGGTGTACATCAG           | 4438 |
| QY | 4451 | ATAATTTCAACGACGAGAAAAGATTTGAGAGGTAAACATCTTTTATGACAGAGAAC           | 4510 |
| Db | 4439 | ACAATTTCAACGACGAGAAAAGATTTGAGAGGTAAACATCTTTTATGACAGAGAAC           | 4498 |
| QY | 4511 | AGAGAATATCTATTAATGCAATGAAAAAATTTAGATCGAAAAAACCAGAAAGCTATAC         | 4570 |
| Db | 4499 | AGAGAATATCTATTAATGCAATGAAAAAATTTAGATCGAAAAAACCAGAAAGCTATAC         | 4558 |
| QY | 4571 | CTGACCAAGGAAACAATTTCAAAGGAATGTCTTTGACTTGTGTAACGACAAAGTTTGG         | 4630 |
| Db | 4559 | CCCGACCTTGAACAAATTTCAAAGGAATGTCTTTGACTTGTGTAACGACAAAGCTTGG         | 4618 |
| QY | 4631 | ACATTAACATCATGATTCATCTATCTGTCTTAAACATGTGTCAATGATGAGTGAACAGATG      | 4690 |
| Db | 4619 | ACATTTGATCATGATTCATCTATCTGTCTTAAACATGTGTCAATGATGAGTGAACAGATG       | 4607 |
| QY | 4691 | ACGAGATGAATATGTGACTACCAATTTGTCAACCATCATCTGTGTTCATTTGTCTAT          | 4750 |
| Db | 4679 | CTCAGACCAAGACAGATGAGAACATTTCTTACAGATTAATCTGGCTTGTGCATCTCT          | 4738 |
| QY | 4751 | TTACTGAGAGTGTGTACTAACAATCTATCTCTACCATTAATTTTACCAATGGAT             | 4810 |
| Db | 4739 | TCACCTCGAGTGTGTCTCAAAATCTTTGGCTTGGACATCAATTAATTCACCAATGGCT         | 4798 |
| QY | 4811 | GGAAATTTTTGATTTTGGGTGTGATCTATCTTCCCATTTGTAGTAAATTTCTTGGCGAGC       | 4870 |
| Db | 4799 | GGAAATTTTTGATTTTGGGTGTGATCTATCTTCCCATTTGTAGTAAATTTCTTGGCGAGC       | 4858 |
| QY | 4871 | TGATAGAAAATATTTCTGTCTCCCTACCTGTCTCGATGTATCCGTCTGTAGATTTG           | 4930 |
| Db | 4859 | TCATTTAGAAAGTACTTGTCTCTCCCAACCTTATTCGAAATTTTCGATTTGGCCGATTTG       | 4918 |
| QY | 4931 | GGCGAATCTACGTGTGATCAAGAGCAAAAGGGATCCGACAGCTGCTCTTGTCTTGA           | 4990 |
| Db | 4919 | GGCGAATCTACGTGTGATCAAGAGCAAAAGGGATCCGACAGCTGCTCTTGTCTTGA           | 4978 |
| QY | 4991 | TGATGTCCCTCTCGGTGTGTTTAAATAGGCTCTACTCTTCTTCAAGCATTTGATCT           | 5050 |
| Db | 4979 | TGATGTCCCTCTCGGTGTGTTTAAATAGGCTCTACTCTTCTTCAAGCATTTGATCT           | 5038 |
| QY | 5051 | ACCGCATCTTTGGAGATCCCACTTTGGCTATGTTAAAGAGGAAATTTGGATTCATGATCA       | 5110 |
| Db | 5039 | TCATCATTTTGGCATGTCCAACTTTGCAATAGCTAGAACGAGCCGCAATTAACAGCA          | 5098 |
| QY | 5111 | TGTTCAACTTTGAGACCTTTGGCAACAGATGATGCTTATTTCCAAATTTACAACTTGG         | 5170 |

Db 5099 TCTTCACTTCGAGACATTTGGACACAGCATGATCTGTTTTCACAGATCAACAGCTG 5158  
 Oy 5111 CTGGCTGGAGTGGATGCTAGACACCATTCCTAACAAGTAAAGCCACCTGACCCCA 5230  
 Db 5159 CTGGCTGGAGTGGATGCTAGACACCATTCCTAACAAGTAAAGCCACCTGACCCCA 5215  
 Oy 5231 ATAAAGTAAAGCCACCTGACCCCAAGTAAAGCCACCTGACCCCAAGTAAAGCCACCT 5290  
 Db 5216 ACAAAGTAAAGCCACCTGACCCCAAGTAAAGCCACCTGACCCCAAGTAAAGCCACCT 5275  
 Oy 5291 TCTTCTTGTGAGTAAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 5350  
 Db 5276 TCTTCTTGTGAGTAAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 5335  
 Oy 5351 TCACTTGGAGAACCTTCAAGCTGCTGCTAGTAAAGTAAAGTAAAGTAAAGTAAAGT 5410  
 Db 5336 TCACTTGGAGAACCTTCAAGCTGCTGCTAGTAAAGTAAAGTAAAGTAAAGTAAAGT 5395  
 Oy 5411 ACTTGAAGATGTTATGAGTGGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 5470  
 Db 5396 ACTTGAAGATGTTATGAGTGGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 5455  
 Oy 5471 AATTGAAATATATCTGAGTGGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 5530  
 Db 5456 AGTACTGTAAGCTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 5515  
 Oy 5531 CAACAAATCTGAGTGGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 5590  
 Db 5516 CCACAAATCTGAGTGGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 5575  
 Oy 5591 GTCCTGATATCTTATGCTTTTACAAAGCGGTTCTGAGAGAGTGGAGTGGAGTGGAGT 5650  
 Db 5576 GCTTGAACATCTTCTGCTTCCACAGAGTGGTGGAGTGGAGTGGAGTGGAGTGGAGT 5635  
 Oy 5651 CTCACGATACGATGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 5710  
 Db 5636 TCTTGGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 5695  
 Oy 5711 AGCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5770  
 Db 5696 AGCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5755  
 Oy 5771 GTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5798  
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RESULT 6

Sequence 43, Application US/090240208  
 Patent No. 6030810  
 GENERAL INFORMATION:  
 APPLICANT: DELGADO, STEPHEN G.  
 APPLICANT: DIEHRICH, PAUL S.  
 APPLICANT: FISH, LINDA M.  
 APPLICANT: HERMAN, RONALD C.  
 APPLICANT: SANGAMESWARAN, LAKSHMI  
 TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE  
 NUMBER OF SEQUENCES: 43  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: JANET PAULINE CLARK  
 STREET: 3401 HILLYTEW AVENUE, MS A2-250  
 CITY: PALO ALTO  
 STATE: CA  
 COUNTRY: U.S.A.  
 ZIP: 94304-1197  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 OPERATING SYSTEM: IBM PC compatible  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/024,0208  
 FILING DATE: 16-FEB-1998  
 CLASSIFICATION: 536  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/039,447  
 FILING DATE: 26-FEB-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: CLARK, JANET P.  
 REGISTRATION NUMBER: 34,799  
 REFERENCE/DOCKET NUMBER: R0020B-REG  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (650) 852-3097  
 TELEFAX: (650) 855-5322  
 INFORMATION FOR SEQ ID NO: 43:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6586 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 US-09-024-0208-43

Query Match 45.7%; Score 2758.2; DB 3; Length 6586;  
 Best Local Similarity 69.4%; Pred. No. 0;  
 Matches 4050; Conservative 3; Mismatches 1646; Indels 136; Gaps 17;  
 Oy 14 TCTGTGTACACAGAGCTGACAGCTTCACTTCTTCAACAGAGATCTCTGGAGCTA 73  
 Db 182 TCTGTGTACACAGAGCTGACAGCTTCACTTCTTCAACAGAGATCTCTGGAGCTA 241  
 Oy 74 TGAAG 121  
 Db 242 TGAAG 301  
 Oy 122 AAAAGATGACAGCAAAATGAGCCCAAGCAAAATGAGCTTGAAGCTGGAAGAGAGAG 181  
 Db 302 GGGAGAGAGATGAG 361  
 Oy 182 TTTCAATTTTATGAGAGATCTCTCAAGAGATGCTGAGAGAGAGAGAGAGAGAGAGAG 241  
 Db 362 TTTCAATTTTATGAGAGATCTCTCAAGAGATGCTGAGAGAGAGAGAGAGAGAGAGAG 421  
 Oy 242 ACCCTTAT 301  
 Db 422 ACCCTTAT 481  
 Oy 302 GGTTCAGTCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 361  
 Db 482 GATTTAGTCCACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 541  
 Oy 362 GATTTAGTCCACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 421  
 Db 542 GATTTAGTCCACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 601  
 Oy 422 ACTGCTGCTTATGAG 481  
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 Oy 482 TCACAGAGATTTATGAGATTTGATGATGATGATGATGATGATGATGATGATGATGATG 541  
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 Oy 542 AAGATTTACTTCTCTGAG 601  
 Db 722 AAGATTTACTTCTCTGAG 781  
 Oy 602 CGTACGACAG 661  
 Db 782 CATATGACAG 841  
 Oy 662 TCCGAGATTTGAAGAGATTTGATGATGATGATGATGATGATGATGATGATGATGATG 721  
 Db 842 TCCGAGATTTGAAGAGATTTGATGATGATGATGATGATGATGATGATGATGATGATG 901



|    |      |  |      |
|----|------|--|------|
| Oy | 722  | TCGACGTGTGAACACTCTCGAGGTATGATGATCTGACTGCTGCTCTGACGAT             | 781  |
| Db | 902  | TCGACGTGTGAACACTCTCGAGGTATGATGATCTGACTGCTGCTCTGACGAT             | 961  |
| Oy | 782  | TTGCTCTAATTTGGGCTGCACTGCTTCATGCGGCACCTGAGAAATATATACATGAC         | 841  |
| Db | 962  | TCGCGCTGATTTGGCTGCACTGCTTCATGCGGCACCTGAGAAATATATACATGAC          | 1021 |
| Oy | 842  | CTCCCAACCAATGCTTCTCTTGAGAGAACATAGTATAGAAAGAATATACTGTGAATTATA     | 901  |
| Db | 1022 | CCA-----TAAACTTCA  | 1033 |
| Oy | 902  | ATGTGACTATTAATAATGAACACTGCTTTGAGTTGACTGGAAGTCATATTTACAAGATT      | 961  |
| Db | 1034 | ACGAGAGCTACTGTGAGAACGGCAGCAGACGAGGCTTTTACTGTGGAGAAATATATACAAATA  | 1093 |
| Oy | 962  | CAAGATATCATTTATTTCTCTGAGGGTTTTTTTAAAGTGCATACTATGTGGAAATAGCTGTG   | 1021 |
| Db | 1094 | AAACAAACTTTTATCATAGTTGCTCTGGCACTGCTAAGAACCTTGTCTGCGGGAGCAACTTCTG | 1153 |
| Oy | 1022 | ATGAGAGCAATGTCCAGAGGAGATATATGTGTGTGAACCTGTGTAGAAATCCCATTTATG     | 1081 |
| Db | 1154 | ATGCTGGGCAATGCCCAGAGGGATTCAGAGTCATGAAACAGAGAAAGAAACCCCAACTACG    | 1213 |
| Oy | 1082 | GCTACACAGAGCTTTGAAATCCTTACAGTTGGGCTTTTGTCTGTGTTTCACATAAAGCTC     | 1141 |
| Db | 1214 | GTTTACACAGCTTTGACACCTCTACAGCTGGGCCCTTTGGGCAATTTATCCGCTTATGACC    | 1273 |
| Oy | 1142 | AGCACTTCTGGGAAATCTTTATCATACTGACATTAACGTGCTGCTGGGAAACGTACATGA     | 1201 |
| Db | 1274 | AGGCACTTTGGGAAACCTTTATACAGCTGACCTTTACAGACCCCTGGGAAACGTACATGA     | 1333 |
| Oy | 1202 | TATTTTGTGTGTGCTCATTTTCTGTGGGCTCATTTACACTAATTAATTTGATCCAGGCTG     | 1263 |
| Db | 1334 | TCTTCTTTGTGTGTGCTCATTTTCTGTGGGCTCATTTACACTAATTAATTTGATCCAGGCTG   | 1393 |
| Oy | 1322 | AGGCGCAATTTACACAGATGATTTGAACAGCTTAAAGAAACAAGAGGAGCAGCTCAGAG      | 1383 |
| Db | 1454 | AGCGCGAATTTACACAGATGATTTGAACAGCTTAAAGAAACAAGAGGAGGAGCAGGCTG      | 1513 |
| Oy | 1382 | CAGCAACGGCAACTGCTC-----AGAACTATCCAGAGACCCCACTGTC                 | 1424 |
| Db | 1514 | CTGCATATGGCCACTCAGCGGGCACTGCTCGGAAAGACCCATTTGAAGAAAGGGAAG        | 1573 |
| Oy | 1425 | AGCAGCAGAGCTCTCAAA-CAGCTCATCTGAAAGCTCTTAAGTTGAGTTCTCAAGAATGCTA   | 1483 |
| Db | 1574 | ATGGGATAGGCTCTCCAGAGAGGCTCTTGTGAATGCTTAATCTCAGTTTCCAAAGACCGGA    | 1633 |
| Oy | 1484 | AGGAAAGAAATATCGGAGAGAGAAAGAAACAGAAAGACAGCTGTGTGGGAAAGAGA         | 1543 |
| Db | 1634 | AGGAGCGGCGGAAACCGAGAGAGAAAGAGAGAGAGAGAGAGCTCTCTGAAGCGAGAGAGA     | 1693 |
| Oy | 1544 | AAGATGA---GATGAATTCCAAAATCTGAATCTGAGAGACAGATCAGAGAGAAAGTT        | 1600 |
| Db | 1694 | AAGGGAGACCGGAGAAAGGTGTTTAAGTCAGAGTCGGAAGACGGTATGAAAGAAAGGCTT     | 1753 |
| Oy | 1601 | TTTCCTTCTCATTTGAAGGGAACCGAATGACATNTAAGAAAGAGTACTCTCCCAACAC       | 1666 |
| Db | 1754 | TCGCGCTGCCAGACACAGAGATAGG-----AGGAAGTTTTCATCATGAAATC             | 1801 |
| Oy | 1661 | AGCTTTGTTGAGAGCTCCGTGCTCCCTATTTTTCACCAAGGCGGAATATGACAAATACACC    | 1720 |
| Db | 1802 | AGTGCCTGCTCAGCATTTCCAGGCTCGGCCCTTCTCTCCGACATTAACAGCAAAACAGACA    | 1861 |
| Oy | 1721 | TTTTTCACTTTAG-----AGGCGAGCAAAAGATGTGGGATCTGAGAAACGACTTGCAG       | 1774 |
| Db | 1862 | TCTTCAAGCTTCCGGGAGCCGGTGTGGTCCGGGAGCCGGGCTGTAGAAATGATGTGGAG      | 1921 |

|    |      |  |      |
|----|------|--|------|
| QY | 1775 | ATGATGACACAGGACACCTTTGAGATGATTAACAGAGACCGGTGAGATTTCCTGTTTGAGCC | 1834 |
| Db | 1922 | ACGATGACACACGACACCGTGGAGGAGCGAGGGCCGCGGTGCTCGCTCTTCACTCCGA     | 1981 |
| QY | 1835 | GACGACACGGAGAGACGACAAACGCAACCTGTGATGACAGAC--TAGGTCAATCCGGAT    | 1892 |
| Db | 1982 | TCCGGGCCCGGAGCGCGGACGACGACGTACAGTGGCTACAGCGGCTACAGCCAGTGCACCC  | 2041 |
| QY | 1893 | GCTGGCACTGTTTCCAGCGAAATGGGAAGATGCACAGCACTGTGGATTCGAATGCTGTGGT  | 1953 |
| Db | 2042 | GCTGCTCCGCTGAAATAAGATTAAGGCAAGCTACAGGACGGCACTCTTCCCACTCGCGGC   | 2101 |
| QY | 1953 | TTTCCTGGTTGGTGGACCTTCAGTCTTCATATCGCTGTGTGGACAGCTTCTGCCAGAGT    | 2012 |
| Db | 2102 | GCACGTCGAACCGCAACGACGCGTGACTGCACACGCGCTAGTGTCACTCATCGGGCCCG    | 2161 |
| QY | 2013 | GATATATAGATTAAGCCAGCTACTGTATGACATGGAACAAACCTGTAACCTGAATATAGAA  | 2072 |
| Db | 2152 | GCTCACACATGGGGCGGCTCTG-----CCTGAGGCAACAGACTGAGGTGGAAATTAAGA    | 2216 |
| QY | 2073 | GAGAAAGTCAAGTTCCTTTCCACGTTTCCATGAGCTTTTACAGAAATCTTCCCAAGGCA    | 2132 |
| Db | 2217 | GAAAGGCCCTGGATCTCTTTAGTTTCTATAGACAACTCGGCTCTACAGGACGGAAGA      | 2276 |
| QY | 2133 | ACGACCAATAGATTAAGCAGCAATCTACAAATAC--AGTAGAAGAACTGAAGAAATC      | 2189 |
| Db | 2277 | CAGATTCACACGCAATTAATGAGCGGTGCACAAACAGCAATGAGAAAGCTGGAAGATGC    | 2336 |
| QY | 2190 | CAGGAGAAATGGCCACCGCTGGTGTATTAATTTCACATATCTTAATCTGGAGCTG        | 2249 |
| Db | 2337 | TCAGGAAATGGCCACCGCTGGTGTATTAATTTCACAACTTCTCATCTGGAGCTG         | 2366 |
| QY | 2250 | TTTCTCATATTTGTTTAAAGTGAACAACTGTGTGCACCTGGTGTGATGAGACCCATTTGT   | 2309 |
| Db | 2397 | TCACCCCTACCTGATTAACACTGAAAGAGATCGGAACCTTAATCGTCAATGAGACCTTTGT  | 2456 |
| QY | 2310 | TGACCTGGCCATCAACATCTGATATGTCTTAAATCTCTTTCAATGCCATGAGACATA      | 2369 |
| Db | 2457 | AGACTTACCCATTCACATCTGCATCTGTGATAGCGATTAATTAAGCAATGAGACCA       | 2518 |
| QY | 2370 | TCCATGACGGACCATTTCAATATAGCGCTACAGTAGAAACTGTGTTTACATCGGAT       | 2429 |
| Db | 2517 | TCCATGACACCACTTCACACCGCTTGGCGGTAGAAATCTGTGTTCACCGGAT           | 2576 |
| QY | 2430 | CTTTACAGCAGAAATGTTTCTGAAATTAATTAATGCGACGATCTTACTATTAATTTCCAGA  | 2489 |
| Db | 2577 | CTTACGCGCGGAATGTGTTGGAAGCTCAATAGCAATGAGACCCCTATTAATTTCCAGA     | 2636 |
| QY | 2490 | AGCCTGGAAATCTTTAGACGTTTATTTGTGACGCTTAAGCCTGTGAAACTTGAACCTGC    | 2549 |
| Db | 2637 | AGGCTGGAACTTTTACGGAATTAATGTCTCCCTCACTTAATGAGACCTAGCTCGC        | 2696 |
| QY | 2550 | CAATGTGGAAGGATTAATCTCTCTCCGTCATTTGCAATGTGCTGCGAGTTTCAATGTGGC   | 2609 |
| Db | 2697 | AGATGTGGAAGGCGCTCAGTGTGTGGGCTTTTCCAGCTGTCCAGATCTTCAACTGCG      | 2756 |
| QY | 2610 | AAATCTTGGCGCACTTTAAATATAGCAATTAAGATCAATCGGCATTCGTTGGGGGCTCT    | 2669 |
| Db | 2757 | CAAGTCTGCGCCCAACCTGGAACATGCTGATCAAGATCAATCGGAACTCGTGGGTGCTCT   | 2816 |
| QY | 2670 | GGGAAATTAACCTGCTGTGGCCATCATCGTCTTCATTTTGGCGGTGCGGATGCA         | 2729 |
| Db | 2817 | GGGCAACCTGCCTGTGGTGGCCATCATCGTCTTCATCTTCCGCGGTGGGGATGCA        | 2876 |
| QY | 2730 | GCTCTTGTGTAAGCTACAAATATGTGTCTGCAAGATGCGCAATGTGTCAACTGCC        | 2789 |
| Db | 2877 | GCTGTTTGGAAAGATTACAAAGGATGCGCTGTATGATCAACACAGGAGTGCAGACTGCC    | 2936 |
| QY | 2790 | ACGCTGGCAATGATATCACTTTCACATCTCCATCTCGATTTGTGTTCCGCGGTGCTGTGG   | 2849 |
| Db | 2937 | GCGCTGGCAATGAGCACTTCTTCCATCTCTTCCATCTGCTTCCAGTGTCTGTGG         | 2996 |
| QY | 2850 | GGAATGATAGACCAATGTGGGACTGTATGAGAGTTGCTGTGTCAGGCATGTGCTTAC      | 2909 |

||||| 2997 GGAGGATTCAGACCAATGTTGGAGTGGAGTGGCGGCGGACGATGCTCAT 3056  
2910 TGTCTTCATGATGTCATGATGTAAGAACCTAGTGTCTGTAATCTCTTGGCCCT 2969  
3057 TGTCTTCATGATGTCATGATGTAAGAACCTAGTGTCTGTAATCTCTTGGCCCT 3116  
2970 GCTTGTGATGTCATGATGTAAGAACCTAGTGTCTGTAATCTCTTGGCCCT 3029  
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3030 TAATCTTCATGATGTCATGATGTAAGAACCTAGTGTCTGTAATCTCTTGGCCCT 3089  
3177 CAACCTGATGTCATGATGTAAGAACCTAGTGTCTGTAATCTCTTGGCCCT 3236  
3090 ATATGATGTCATGATGTAAGAACCTAGTGTCTGTAATCTCTTGGCCCT 3149  
3237 GCAGGCTTCATGATGTCATGATGTAAGAACCTAGTGTCTGTAATCTCTTGGCCCT 3290  
3150 ACTGATGTCATGATGTAAGAACCTAGTGTCTGTAATCTCTTGGCCCT 3206  
3291 COTGATGTCATGATGTAAGAACCTAGTGTCTGTAATCTCTTGGCCCT 3350  
3207 TGGGAAATGTCATGATGTAAGAACCTAGTGTCTGTAATCTCTTGGCCCT 3265  
3351 CCACGGAAGGCTTCATGATGTCATGATGTAAGAACCTAGTGTCTGTAATCTCTTGGCCCT 3404  
3267 CAGCAGTGTGAAATGTCATGATGTAAGAACCTAGTGTCTGTAATCTCTTGGCCCT 3326  
3405 CAGCAGTGTGAAATGTCATGATGTAAGAACCTAGTGTCTGTAATCTCTTGGCCCT 3461  
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3522 AGAGATGTCATGATGTCATGATGTAAGAACCTAGTGTCTGTAATCTCTTGGCCCT 3579  
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3927 TGGAGCTATGTCATGATGTCATGATGTAAGAACCTAGTGTCTGTAATCTCTTGGCCCT 3986

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Db 722 ACGGCTTCACCTCTTTCGGAGACCCGTTGTAAGTTCAGTTCATCATCATGATG 781  
OY 602 CGTACGTACAGAGTTTGTGACCTGGCCATGTCTCGGCATTGAGAACATTCCAGAGTTC 661  
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OY 2490 TCGAG 2549  
Db 2637 TCGAG 2696  
OY 2550 TCGAG 2609  
Db 2697 TCGAG 2756  
OY 2610 TCGAG 2669  
Db 2757 TCGAG 2816  
OY 2670 TCGAG 2729  
Db 2817 TCGAG 2876







QY 482 TCACAGGATATATATCTTTTGAATCACTATATAAATATATGCAAGGAGATCTGTTAG 541  
DB 515 TCACAGGATATATATCTTTTGAATCACTATATAAATATATGCAAGGAGATCTGTTAG 574  
QY 542 AGATTTTACTTCTCTGGGATCAGTGAAGCTGCTGATTCATGCTATTAACATTTG 601  
DB 575 ACAGCTTACCTCTCTGGGATCAGTGAAGCTGCTGATTCATGCTATTAACATTTG 634  
QY 602 CGACAGCAGATGTTGAGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATG 661  
DB 635 CATATGAGAGAGATGTTGAGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 694  
QY 662 TCCGAGATGAGAGATGTTGAGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 721  
DB 695 TCCGAGATGAGAGATGTTGAGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 754  
QY 722 TCCAGTCTGAGAGATGTTGAGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 781  
DB 755 TCCAGTCTGAGAGATGTTGAGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 814  
QY 782 TCCAGTCTGAGAGATGTTGAGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 841  
DB 815 TCCAGTCTGAGAGATGTTGAGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 874  
QY 842 CTCACCAATGCTCTCTGGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 901  
DB 875 CCA-----TAACTTCA 886  
QY 902 ATGATCACTATATATATGAACTGCTTGAATGAGTGAAGTGAAGTGAAGTGAAGTGAAG 961  
DB 887 ACAGAGCTATGAGAGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 946  
QY 962 CAAGATATCTATATATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 1021  
DB 947 AAACAACTTATATATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 1006  
QY 1022 ATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 1081  
DB 1007 ATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 1066  
QY 1082 GCTACACAGCTTATGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 1141  
DB 1067 GTTACACAGCTTATGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 1126  
QY 1142 AGGATCTGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 1201  
DB 1127 AGGATCTGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 1186  
QY 1202 TATTTTGTGATGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 1261  
DB 1187 TCTTCTGTGATGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 1246  
QY 1262 TGTGATGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 1321  
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DB 1307 AGGATCTGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 1366  
QY 1382 CAGCAAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 1424  
DB 1367 CAGCAAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 1446  
QY 1425 AGGATCTGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 1483  
DB 1427 ATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 1486  
QY 1484 AGGATCTGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 1543  
DB 1487 AGGATCTGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 1546

QY 1544 AGATGA-----GATGAATTCAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 1600  
DB 1547 AAGGAGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 1606  
QY 1601 TCCGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 1660  
DB 1607 TCCGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 1654  
QY 1661 AGATGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 1720  
DB 1655 AGATGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 1714  
QY 1721 TTTTCACTTATG-----AGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 1774  
DB 1715 TTTTCACTTATG-----AGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 1774  
QY 1775 ATGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 1834  
DB 1775 ATGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 1834  
QY 1835 GAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 1879  
DB 1835 TCCGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 1894  
QY 1880 GGTATCTGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 1939  
DB 1895 GGTATCTGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 1954  
QY 1940 GCAATGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 1999  
DB 1955 GCAATGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 2002  
QY 2000 TTTTCACTTATG-----AGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 2059  
DB 2003 TTTTCACTTATG-----AGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 2026  
QY 2060 CTGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 2119  
DB 2027 TGTGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 2086  
QY 2120 CTGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 2176  
DB 2087 AGGATCTGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 2146  
QY 2177 AACTGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 2236  
DB 2147 AACTGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 2206  
QY 2237 TATCTGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 2296  
DB 2207 TATCTGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 2266  
QY 2297 TGTGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 2356  
DB 2267 TGTGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 2326  
QY 2357 CAGTGAAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 2416  
DB 2327 CAGTGAAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 2386  
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DB 2387 TGTGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 2446  
QY 2477 ATATGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 2536  
DB 2447 ATATGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 2506  
QY 2537 AACTGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 2596  
DB 2507 AACTGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 2566  
QY 2597 TTTTCACTTATG-----AGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 2656

Db 2567 TCTTCAAGCTGGCCAGTCCGCGCCACCCGGAACATGTCATCAAGATTCATCGGAACT 2626  
OY 2657 CCGTGGGGGCTCTGGGAAATTAACCTCGTCTGGCCATCATGCTCTCAATTTTGGCG 2716  
Db 2627 CCGTGGGGGCTCTGGGAAATTAACCTCGTCTGGCCATCATGCTCTCAATTTTGGCG 2686  
OY 2717 TGGTGGGATGACAGCTCTTGGTGAAGATTAAGATTAAGATTAAGATTAAGATTAAG 2776  
Db 2687 TGGTGGGATGACAGCTCTTGGTGAAGATTAAGATTAAGATTAAGATTAAGATTAAG 2746  
OY 2777 ATGTCACTCCCAAGCTGGGACATGATGATGATGATGATGATGATGATGATGATGATG 2836  
Db 2747 AGTCAAGCTCCGCGGTGGGACATGAACGATCTTCCATCTCCCTCCATCTCCCTCC 2806  
OY 2837 GCGTGTGTGTGGGAGTGTATGAGACATGTGGGAGTGTATGAGAGTGTGTGTGTGT 2896  
Db 2807 GAGTGTGTGTGGGAGTGTATGAGACATGTGGGAGTGTATGAGAGTGTGTGTGTGT 2866  
OY 2897 CCATGTGCTTACGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATG 2956  
Db 2867 CCATGTGCTTACGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATG 2926  
OY 2957 TCTTGTGGGCTCTTGTGAGTCTATGATGATGATGATGATGATGATGATGATGATGATG 3016  
Db 2927 TATTCCTGGCTCTTGTGAGTCTATGATGATGATGATGATGATGATGATGATGATGATG 2986  
OY 3017 ATATGAATGAATATATCTCCAAATGCTGTATGATGATGATGATGATGATGATGATG 3076  
Db 2987 ACAGGGAATGAATATATCTCCAAATGCTGTATGATGATGATGATGATGATGATGATG 3046  
OY 3077 TGAATAAATAATATATGATTTATGATGATGATGATGATGATGATGATGATGATGATG 3136  
Db 3047 CCAATGAAGTGTACGCTCTTATGATGATGATGATGATGATGATGATGATGATGATGATG 3100  
OY 3137 ATGAATAAATAATATGATTTATGATGATGATGATGATGATGATGATGATGATGATGATG 3196  
Db 3101 ATGAAGTGAATATATCTCCAAATGCTGTATGATGATGATGATGATGATGATGATGATG 3160  
OY 3197 C---ARCAAGAAATGGAAGATCTTGATGATGATGATGATGATGATGATGATGATG 3253  
Db 3161 CGGGGCTGTGATATCCACCGGAACGCGCTCCAGAAAGGAGGAGGAGGAGGAGGAGGAG 3220  
OY 3254 GTATAGGAAGTGTGAGAGTGTGAATAATGATGATGATGATGATGATGATGATGATGATG 3313  
Db 3221 GCAT-----CGCAGACGCTGTGAGATGATGATGATGATGATGATGATGATGATGATG 3271  
OY 3314 TCATTAACCAACCCAGTCTTACTGTGATGATGATGATGATGATGATGATGATGATGATG 3373  
Db 3272 TCATTAACCAACCCAGTCTTACTGTGATGATGATGATGATGATGATGATGATGATGATG 3331  
OY 3374 AAAATTTAAACAGGAAGATTTAGTATGATGATGATGATGATGATGATGATGATGATG 3433  
Db 3332 AGAAGCTCAACACAGAGATTTAGTATGATGATGATGATGATGATGATGATGATGATG 3391  
OY 3434 TGAATGAAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3493  
Db 3392 TGGAGCATAC---AGTCTCCAGAGAGATGATGATGATGATGATGATGATGATGATGATG 3448  
OY 3494 AACAGCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3553  
Db 3449 AAGTTCCTGTGAGCAACCTGATGATGATGATGATGATGATGATGATGATGATGATG 3508  
OY 3554 GTGTACAAAGATTAAGTGTGTCAAAATGATGATGATGATGATGATGATGATGATGATG 3613  
Db 3509 GCGTCCAGCGGTCAAGTGTGCGAGGCAATCGAGAGAGAGAGAGAGAGAGAGAGAGAG 3568  
OY 3614 GGAACCTGAG 3673  
Db 3569 GGAATCTTGGCAAAACCTGCTCTCATGATGATGATGATGATGATGATGATGATGATGATG 3628  
OY 3674 TTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3733  
Db 3629 TCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3688  
OY 3734 GAAAGCATTAAGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3793  
Db 3689 GAAAGCATTAAGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3748  
OY 3794 TGAATAATCTTAAATAGGAGTGTATGATGATGATGATGATGATGATGATGATGATGATG 3853  
Db 3749 TGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3808  
OY 3854 GTTGGCTGAGCTCTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3913  
Db 3809 GCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3868  
OY 3914 GTTACTGAACTTGGAGCCATCAATCTTCAGAGACATTAAGACCTTGAACCTCTTA 3973  
Db 3869 GCTACTCGAACTAGTGTCCATTAAGTCCCTTAAGACCTTAAGACCTTGAACCTCTTA 3928  
OY 3974 GAGCTTATCTGATTAAGGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 4033  
Db 3929 GAGCTTATCTGATTAAGGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 3988  
OY 4034 CATCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4093  
Db 3989 CCTCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4048  
OY 4094 GCGTAAATTTTGTGCTGGCAATTTCAACACTGATTAACCAACACTGCTGACAGGT 4153  
Db 4049 GAGTAACTCTGTTGGGGGAAATACACTACTGCTTAATGATGATGATGATGATGATG 4108  
OY 4154 TTGACATGAGAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4213  
Db 4109 TCGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4168  
OY 4214 CTG---CTGATGAGAAATGATGAAAGTATGATGATGATGATGATGATGATGATGATG 4270  
Db 4169 CGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4228  
OY 4271 CTTTGTCTCAAGTGTGCAATTAAGAGATGATGATGATGATGATGATGATGATGATGATG 4330  
Db 4229 CCGTCTTCAAGTGTGCAATTAAGAGATGATGATGATGATGATGATGATGATGATGATG 4288  
OY 4331 CCAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4390  
Db 4289 CCGGAAACCGAGACAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATG 4348  
OY 4391 TTATTTTATCATCTTTGGTCTCTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 4450  
Db 4349 TCATCTTATCATCTTTGGTCTCTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 4408  
OY 4451 ATATTTCAACCGAGAGAAAGATTTGAGGTCAAGACATCTTATGATGATGATGATGATG 4510  
Db 4409 ACAACTTCAACCGAGAGAAAGATTTGAGGTCAAGACATCTTATGATGATGATGATGATG 4468  
OY 4511 AGAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4570  
Db 4469 AGAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4528  
OY 4571 CTCGACCGAGAAACAAATTTAAGAGATGCTTGAATCTGATCAACAGACAAAGTTTGG 4630  
Db 4529 CCGGACCTTGAACAAATTTAAGAGATGCTTGAATCTGATCAACAGACAAAGTTTGG 4588  
OY 4631 ACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4690  
Db 4589 ACATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4648  
OY 4691 ACCAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4750  
Db 4649 CTCAGAGCAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4708  
OY 4751 TTACTGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4810  
Db 4709 TCACCTGCGAGTGTGTCTCAAAATGTTGCTTGAACACACTACTACTACTACTACTACT 4768

|    |      |  |      |
|----|------|--|------|
| OY | 4811 | GGAATATTGATTTGGTGTGTAATTCACATTTGAGTAGTATGTTTTCTTGCCAGC         | 4870 |
| Dd | 4769 | GGAAATCTTGTACTTTGTGTGTGTCAATCTCCATTTGTGGAAATGTTCTCGGTGTATA     | 4828 |
| OY | 4871 | TGATAGAAAAGTATTTGTTGCCCTTACCCTGTTCCGATGTATCCGTATGCATAGATTG     | 4930 |
| Dd | 4829 | TCATTTGAGAAGTACTTGTCTCTCCCAACCCATATCCGATTTATCCGATTTGGCCCCATATG | 4888 |
| OY | 4931 | GCCGAACTCATGCTGTGATCAAAGAGCAAAAGGGATCCGACAGCTGCTCTTTGCTTTGA    | 4990 |
| Dd | 4889 | GGCCGACTCTGGCGCTGTATCAAGGGGGCCAAAGAGATCCGACACCCTGCTTTGGCTTAA   | 4948 |
| OY | 4991 | TGATGTCCCCTCCGGGTGTTTTAACAATGGGCCCTCTACTCTCTCCAGCAATGTTAACCT   | 5050 |
| Dd | 4949 | TGATGTGCTGCCCGCCCTGTTCACAACTGGCTCTCTGCTCTCTCGCATGTTCATCT       | 5008 |
| OY | 5051 | AGCCGACTTTTGGGATGATCCCAACTTTTGCCATGTTTAAAGAGGAATTTGGATTCATGACA | 5110 |
| Dd | 5009 | TCTCCATTTTGGGATGATCCCACTTTGSCANTAGCTGAAGCAGAGGCCGGCANITGACGACA | 5068 |
| OY | 5111 | TGTTCACTTTGAGACTTTTGGCAACAGATGATCTGCTATTTCCAATTTACAACCTGTG     | 5170 |
| Dd | 5069 | TGTTCACTTTGAGACATTTTGGCAACAGATGATCTGTTTGTTCAGATFACAACAGTCTG    | 5128 |
| OY | 5171 | CTGGCTGGAGTGAATTTCTAGCAACCCATTTCTMAAGTAAAGCACCCGACCTGTGACCTTA  | 5230 |
| Dd | 5129 | CTGGCTGGAGTGGCTCTCTCTGCTGCANATCTTGAAACG---CCCCCTGACTGCACTTGG   | 5185 |
| OY | 5231 | ATPAAAGTTAACCTCGAAGCTCAGTTTAAAGGAGACTGTGGGAACCATCTGTTGGAAATT   | 5290 |
| Dd | 5186 | ACAAAGAGACACCCAGGGAGTGGCTTAAAGGGGACTGTGGGAACCCCTCGGGGGCACT     | 5245 |
| OY | 5291 | TCTTTTGTGCAATTATATATATATCTCTCTGTTGTGTGAACATGATCATCGCG          | 5350 |
| Dd | 5246 | TCTTTTGTGAGGTATCATATCATCTCTCTCTGTTGTGTGAACATGATCATCGCA         | 5305 |
| OY | 5351 | TCATCTCGAGAACTTCAGTGTGTGCTATCTACNTAAAGTAAGTACAAGCTCTGAGTGAAGT  | 5410 |
| Dd | 5306 | TCATCTCGAGAACTTCAGCGTGGCCACGAGAGAGCGCCACCTCTGATGTAGGATG        | 5365 |
| OY | 5411 | ACTTGGAGATTTCTATGAGGTTTGGGAGAAGTTTGATCCCATGCATCACTCACTTCATG    | 5470 |
| Dd | 5366 | ACTTGGAGACTTTCTATGAGATCTGGGAGAAAGTTTGAACCAAGCCACCCAGTTTCATG    | 5425 |
| OY | 5471 | AATTTGAAAAATTTCTCAGTTTGGAGCTGCGTTTAAACCCGCTCTCATCTGCCACAA      | 5530 |
| Dd | 5426 | AGTACTGTAACTGGCAGACTTTTGGCCAGACCCCTGGAGAACCCGCTCGAGATCAACAA    | 5485 |
| OY | 5531 | CAAAACAATCTCAGCTATTTGCCATGGATTTTGGCCATGTGTGATGTGATGACCGATCACT  | 5590 |
| Dd | 5486 | CCAAACCATCTGACCTATGCGCATGSACTGCGCATGTTGAGCGGAATGCAATCCACT      | 5545 |
| OY | 5591 | GCTCTGATATCTTATTTTGGCTTTTCAAAGCGGGTTTACGAGAGAGTGGAGATGTGATG    | 5650 |
| Dd | 5546 | GCTTGGAGATCTTTTGGCTTCAACCAAGAGATCTCTGGGAGACAGTGGGGAGTTTGGACA   | 5605 |
| OY | 5651 | CTTACAGAAATCACATGGAAGAGAGATATAGGCTTCCAAATCTTCAAAGGCTCTATTC     | 5710 |
| Dd | 5606 | TCTCTGGCGCAGATGTGAGAGAGCGGTGTGTGSCATTCATCTTCCAAATGTCTTACG      | 5655 |
| OY | 5711 | AGCCAACTCACTTACTTTTAAAAAGAAAAGAGGAAGTATCTGCTGTATTTATTCAG       | 5770 |
| Dd | 5666 | AGCCATCAACAACACTCTCGCGGCAAGAGAGAGAGGTGTCGACAGTGGTCTGAGC        | 5725 |
| OY | 5771 | GTCGTTACAGACGCACTTTTAAACG                                      | 5798 |
| Dd | 5726 | GTCGTTACAGGCGACACTTGGCTTAAAGG                                  | 5753 |

RESULT 9  
US-09-425-043-1  
; Sequence 1, Application US/09425043

Patent No.6535172  
GENERAL INFORMATION:  
APPLICANT: DELGADO, STEPHEN G.  
APPLICANT: DIETRICH, PAUL S.  
APPLICANT: FISH, LINDA M.  
APPLICANT: HERMAN, RONALD C.  
APPLICANT: SANGMESMARAN, LAKSHMI  
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE  
TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: JANET PAULINE CLARK  
STREET: 3401 HILLVIEW AVENUE, MS A2-250  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94304-1397  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/425,043  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/024,020  
FILING DATE: 16-FEB-1998  
APPLICATION NUMBER: US 60/039,447  
FILING DATE: 26-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: CLARK, JANET P.  
REGISTRATION NUMBER: 34,799  
REFERENCE/DOCKET NUMBER: R020B-BEG  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 852-3097  
TELEFAX: (650) 855-5322  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5977 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-425-043-1

|                       |              |              |                 |             |
|-----------------------|--------------|--------------|-----------------|-------------|
| Query Match           | 45.4%        | Score 2738.8 | DB 4            | Length 5977 |
| Best Local Similarity | 69.5%        | Pred. No. 0  |                 |             |
| Matches 4063          | Conservative | 3            | Mismatches 1590 | Indels 192  |
|                       |              |              | Gaps            | 18          |

  

|    |     |             |  |     |
|----|-----|-------------|--|-----|
| OY | 14  | TGCTGTACCA  | CAGACGACCTGACAGCTTCAACTTCTCCACGAGAAATCTCTGGCGCTA         | 73  |
|    |     |             |  |     |
| Db | 35  | TGCTGCGACAC | ACAGGCCCTGATAGTTTTCAGACCTTTCACCCCTGATGCTGCGACAAACA       | 94  |
|    |     |             |  |     |
| OY | 74  | TTGAAGAAGCA | TTGTCAGAGAAAGGCAAGAAATCCCAACCCAG-----ACA                 | 121 |
|    |     |             |  |     |
| Db | 95  | TCGAGAGCGG  | TTTCCCGAGACAGCTCAGAAACACCAAGCGGATGGCAAGCCACC             | 154 |
|    |     |             |  |     |
| OY | 122 | AAAAAGATGAC | GACGAAAAATGGCCCAAGGCCAAATAGTGTGACTTGGAAAGTGGAAAGACC      | 181 |
|    |     |             |  |     |
| Db | 155 | GAGAGGAGAT  | GAAGACAGCAAGCCCAAGCCCAACAGTGCCTGGAGGCTGGGAAGACTT         | 214 |
|    |     |             |  |     |
| OY | 182 | TTTCATTTAT  | TATATGAGAAATTCCTCCAGAGATGGTGTCAAGAGCCCTTGGAGAGACTGG      | 241 |
|    |     |             |  |     |
| Db | 215 | TGCTTTATAT  | CATCGGGGACATCCCGCAAGGCTGTGGCTGCTCCCTGGAGGACCTTGG         | 274 |
|    |     |             |  |     |
| OY | 242 | AACCCCTACT  | ATATATCATAATAGAAACCTTTTATATAGTATGAATTTAAAGGAGAGGCATCTTCC | 301 |
|    |     |             |  |     |
| Db | 275 | AACCTTACTA  | TTTGGACGAGAAACCTTTGTAGTATTTAAACGAGAGGAAACCTCTCTCA        | 334 |
|    |     |             |  |     |
| OY | 302 | GGTTCAGTGC  | CACTCTGCGCTGTATCAATTTTAACTTCCTTCAATCTCTTAAAGAAATAG       | 361 |
|    |     |             |  |     |

Db 335 GATTATGACACACCTGCTGTACATTTTAAGCCCTTTAACTGATAGAGAATAG 394  
 QY 362 CATTATAGATTTGGTACATTAATTTGACATGCTAATTAATGTCATATTTTACAA 421  
 Db 395 CTAATTAATTTGATACATGATTTTACATGATATCATATGTCACATCTCCACA 454  
 QY 422 ACTGTGTGTTTACAAATGATTAACCTTCCTGATGAGCAAAAGATAGATACCT 481  
 Db 455 ACTGTGTGTTACATGATTTAGTAACTTCACCAATGTCGCAAGATGAGAGTACAT 514  
 QY 482 TCACAGAAATATATCTTTTGAATCACTATATAAATTAATGCAAGGATTCCTGTTAG 541  
 Db 515 TCACAGAGATTTACATTTGAATCACTATGTAATTAATCAATCCAGAGGTTCTGCATAG 574  
 QY 542 AAGATTTTACTTCTTGGGATCCATGCACTGGCTGCATTTCTCATTTACATTG 601  
 Db 575 ACGGCTCACTCTTTCGACAGACCCGTCGAACTGGTATGACCTGATCATCATATAG 634  
 QY 602 CGTACGTACAGATTTGTCGACCTGGGCAATGTCGCGCATTTGAGACATTCAGATTC 651  
 Db 635 CATATGTACAGATTTGTCGACCTGGGCAATGTCGCGCATTCAGACATTCAGGTTTC 694  
 QY 662 TCCGACATTTGAGACATTTTCACTTCAGTCCAGGCTGAAACCATTTGGAGCCCTGA 721  
 Db 695 TCCGACATTTGAAACTATCTGTATTTCCAGGCTGAAAGCAATCGTGGGCGCCCTAA 754  
 QY 722 TCCAGTCTGTGAAGAGCTCTCAGATGTATGATCTGATGCTGTCTGTCTGAGCGTAT 781  
 Db 755 TCCAGTCTGTGAAGAGCTCTCAGATGTATGATCTGATGCTGTCTGTCTGTGATGTT 814  
 QY 782 TTTGCTATTTGGGCTGACGCTGTCATGAGGCACTGAGAACTAATTAATATATATGTC 841  
 Db 815 TCCGCTGATTTGGCTGACGCTGTCATGAGGCACTGAGAACTAATTAATATATATGTC 874  
 QY 842 CTCGCCACATGCTCTTGGAGGAATAGTATAGAAAGATATATAGTGTGAATATTA 901  
 Db 875 CCA-----TAACTTCA 886  
 QY 902 ATGTACACTTATTAATGAACTGTCTTGAATTTGATGAGAAATCATATATTCAGAT 961  
 Db 887 ACAGAGCTTACCTGAGGAACGACACAGAGGCTTGTACTGGGAGATATATACAAATA 946  
 QY 962 CAAGATATCTATTTCTGAGAGGTTTTTTAGATGACATCATATGGAATATAGCTG 1021  
 Db 947 AATCAAACTTTTACATGTTCTGTGATGTAACCTTGTCTCTCGGGAAGATGTTG 1006  
 QY 1022 ATGACGCAATGTCAGAGGATATATGTTGTAAGCTGTAGAAATCCCAATTAAG 1081  
 Db 1007 ATGCTGGCAATGCCAGAGGATTTCCAGTGCATGAAACAGAGAAAGAACCCACTAG 1066  
 QY 1082 GCTACCAAGCTTTGATACCTTCAGTTGGCTTTTGTCTTGTTCGACTAATGATC 1141  
 Db 1067 GTTACACAGCTTTGACCTTCAGCTGGGCTTCTTGGCATATATTCGCGCTATAGACC 1126  
 QY 1142 AGGACTTTCGGGAAATCTTATCACTGACATTAAGTCTGCTGGGAAACCTAATGA 1201  
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 QY 1202 TATTTTGTGTCATTTCTTGGGCTCATTTACCTAATTAATTTGATCTGCTGCTG 1261  
 Db 1187 TCTTCTTGTGTCATTTCTTGGGCTCATTTACCTAATTTGATCTGCTGCTGCTG 1246  
 QY 1262 TGTGTCATGCTGCTGACGAGGACAGATTCAGGCACTTGGAGAGAGAGCAAGAAAG 1321  
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 QY 1322 AGGCGCAATTTTCAGAGATGATTTGAACAGTTTAAAGCAACAGAGGACGCTCAGAG 1381  
 Db 1307 AGGCGCAATTTTCAGAGATGATTTGAACAGTTTAAAGCAACAGAGGACGCTCAGAG 1366  
 QY 1382 CAGCAAGGCACTGCTC-----AGACATTTCCAGAGAGCCAGTGC 1424  
 Db 1367 CTGCAATGCGCACCTCAGCGGCGACATGCTCTCGAAGACGCAATTTGAAGAAAGGGAG 1426

QY 1425 AGCAGGAGGCTCTCAGA-CAGCTCATTCGAGGCTCTAAGTTGAGTCCAGAGTCTA 1483  
 Db 1427 ATGGGTAGGCTCTCCGAGGAGCTCTTGAATGTTAATCTAGTCTCCAGAGGCGCA 1486  
 QY 1484 AGGAAAGAAATTCGAGAGAGAAAGAAAGAAAGAGAGAGAGTGTGGGAGAGAG 1543  
 Db 1487 AGGAGGAGGAG 1546  
 QY 1544 AAGATGA---GGATGAATTCGAAATTCGATCTGAGAGACGATCAGAGAGAAAGTT 1600  
 Db 1547 AAGGAGAGGAG 1606  
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 QY 1661 AGCTTTGTTGAGATCCGAGCTGCTCTATTTTACCAAGGCGAAATAGAGAAAGAGC 1720  
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 Db 1895 GCTGCTGCGGAG 1954  
 QY 1940 GCAATGCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1999  
 Db 1955 GCAACGCGGAG 2002  
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 Db 2003 TCTGCTGCTGAG-----CAACACTGAG 2026  
 QY 2060 CTGAAATGAGAAAG 2119  
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2477 ATATTTTCCAGAGAGCTGGAAATATCTTTGACGGTTTATTTGACGCTTAGCCTGTAG 2536  
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2537 AATTGGACCTGGCAATGTGGAAGATATCTCTCCCTTCACTTCGATGTGTGGAG 2556  
2507 AGCTGAGTCTGCAAGATGTGGAAGGCTGAGCTGCTCTTCCGATCTCCGAG 2566  
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2777 ATGTCAACTCCACGCTGGACATGATGATCTTCCACTCTCTGATTTGTTC 2836  
2747 AGTCAAGCTCCGCGCTGGACATGACGATCTTCCACTCTCTGATTTGTTC 2806  
2837 GCGTCTGTCTGGGAGTGGATAGAGACATGTGGACGTATGGAGTTGCTGTCAAG 2896  
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3167 CCGGCGGATGATTCACCGGAGCGGATCTCCAGGAAGAGGGAACGGAACGACGAGCG 3220  
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3314 TCAATGAATTAATTAATGATTTATTCACAGCTCTTCAATAGGAACCAAAAGTTTATG 3373  
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3434 TGAATGAATTAATTAATGATTTATTCACAGCTCTTCAATAGGAACCAAAAGTTTATG 3493  
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3449 AATTTCCCTGAGAGAGATCTGAAAGAACTTTGAATCCGAGAGCTGTTTCAAGTGAAGCT 3508  
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3509 GCGTCCAGCGCTTCAAGTGTGCGAGCTCAACATCGGAGAGGCTAGGCAAGTGTGCT 3568  
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3674 TTTTCATGATCTCTTATGATGATGCTCTGCAATTTGGAAGAAATTAATTAATGATG 3733  
3629 TCTTCAATGATCTCTTATGATGATGCTCTGCAATTTGGAAGAAATTAATTAATGATG 3688  
3734 GAAAGAGATTTAAAGAGATTTGGAATGCTGCAAGAGTTTCACTTAATTTCAATTC 3793  
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3854 GTTGGCTGAGCTCTTAAATGATGATGCTGCAATTTGGAAGAAATTAATTAATGATG 3913  
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3914 GTTACTGAGATCTTCAATGATGATGCTGCAATTTGGAAGAAATTAATTAATGATG 3973  
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3974 GAGCTTATCTGATTTGAAGAGATGAGGTTGTTGATGATGCTTGAAGCAATTC 4033  
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4034 CATCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4093  
3989 CTTCCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4048  
4094 GCGTAAATTTGTTGCTGCGAAATTTACACGATGATTAACACCAACGATGATGATG 4153  
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4154 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4213  
4109 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4168  
4214 CTTG---CTGATGGAATTAATGATGATGATGATGATGATGATGATGATGATGATG 4270  
4169 CCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4228  
4271 CTTGCTTCAAGTGTGCAATTAAGATGATGATGATGATGATGATGATGATGATGATG 4330  
4229 CCGTCTTCAAGTGTGCAATTAAGATGATGATGATGATGATGATGATGATGATGATG 4288  
4331 CCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4390  
4289 CCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4348  
4391 TTTATTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4450  
4349 TCAATTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4408  
4451 ATATTTCAACAGAGAGATTTAGTGAATGATGATGATGATGATGATGATGATGATG 4510  
4409 ACAATTTCAACAGAGAGATTTAGTGAATGATGATGATGATGATGATGATGATGATG 4468  
4511 AGAAGATTTCAACAGAGAGATTTAGTGAATGATGATGATGATGATGATGATGATG 4570  
4469 AGAAGATTTCAACAGAGAGATTTAGTGAATGATGATGATGATGATGATGATGATG 4528  
4571 CTTGAGAGAGATTTCAACAGAGATTTAGTGAATGATGATGATGATGATGATGATGATG 4630  
4529 CCGGAGATTTCAACAGAGAGATTTAGTGAATGATGATGATGATGATGATGATGATG 4588  
4631 ACATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4690

[illegible]

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| OY | 5771 | GTCCTTACAGACGCCAECTTTTAAGCG | 5798 |
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| Db | 5726 | GTGCTTACAGGGGACACTTGCGTAGCG | 5753 |

RESULT 10  
US-09-024-020B-7

; GENERAL INFORMATION:

APPLICANT: DIETRICH, PAUL S.

APPLICANT: SANGAMESWARAN LAKSHMAN, RONALD C.

TITLE OF INVENTION: SODIUM CHA

CORRESPONDENCE ADDRESS:

STREET: 3401 HILLVIEW AVENUE

STATE: CA  
COUNTRY: U S A

COMPTON READABLE FORM.

COMPUTER: IBM PC compatible

SOFTWARE: PatentIn Release #

APPLICATION NUMBER: US/09/02

CLASSIFICATION: 536  
PRIOR ADDITION DATE:

APPLICANT NUMBER: US 60/033  
FILING DATE: 26-FEB-1987

NAME: CLARK, JANET P.

REFERENCE/DOCKET NUMBER: R002

TELEPHONE: (650) 852-3097

7: INFORMATION FOR SEQ ID NO: 7:

TYPE: nucleic acid

TOPOLOGY: linear

US-09-024-020B-7

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Matches 4063; Conservative 3;

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[illegible]

182 TTCCATTATTAATGGAGCAATTAC

362 TGCCTTTCATCTACGGGACATCCCGC

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RESULT 10
US-09-024-020B-7
: Sequence 7, Application US/09024020B
: Patent No. 6030810
: GENERAL INFORMATION:
: APPLICANT: DELGADO, STEPHEN G.
: APPLICANT: DIERFICH, PAUL S.
: APPLICANT: FISH, LINDA M.
: APPLICANT: HERMAN, RONALD C.
: APPLICANT: SANGAMESWARAN, LAKSHMI
: TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
: TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPICE VARIANT THEREOF
: NUMBER OF SEQUENCES: 43
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: JANET PAULINE CLARK
: STREET: 3401 HILLVIEW AVENUE, MS A2-250
: CITY: PALO ALTO
: STATE: CA
: COUNTRY: U.S.A.
: ZIP: 94304-1397
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/024,020B
: FILING DATE: 16-FEB-1998
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/039,447
: FILING DATE: 26-FEB-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: CLARK, JANET P.
: REGISTRATION NUMBER: 34,799
: REFERENCE/DOCKET NUMBER: R0020B-RBG
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (650) 852-3097
: TELEFAX: (650) 855-5322
: INFORMATION FOR SEQ ID NO: 7:
: LENGTH: 6556 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
US-09-024-020B-7

Query Match      45.4%; Score 2738.8; DB 3; Length 6556;
Best Local Similarity 69.5%; Pred. No. 0;
Matches 4063; Conservative 3; Mismatches 1590; Indels 192; Gaps 18;

    14 TGCTGTACCAACAGACCCTGACGCCTTCAACTTCCTCACCAGAAATCTCTGGCGTA 73
       ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   182 TGCITGCCACCCAGCGCCCTGATAGTTCAAGCCCTTACCCCTGACCTGTCGAACA 241

    74 TTGAAGAAGCATTGACAGAGAAAAGAAAGAAAGTATCCCAAACAG-----ACA 121
       ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   242 TCGAGAGGCGATTGTCGAGAGCAAGCTCAAGAAACCAACCAAGGCGATGCAACACC 301

    122 AAAAAGTAGAGCAAGAAATGCCCCAAAGCCAAATTAAGTGAAGTGAAGCAAGCAACC 181
       ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   302 GGAGAGAGCATGAAGACAGCAAGCAAGCCCAAGCAACATGACTGAGGCTGGGAAAGATT 361

    182 TTCATTATTTATGAGACATTCCTCCAAGATGGGTGAGAGAGCCCTGGAGAGCTGG 241
       ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   362 TGCTTCATCATCAAGGGGAGCATCCCGCAAGAGGCTGGTGGTGGTGGTGGTGGTGGTGG 423

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Db 2474 CATGAGAGACCATCCCATGACACACAGTTGAAACAGCTTGGCGGTGGAATCTGG 2533  
 QY 2417 TTTTCACTGGGATCTTTACAGACAGAAATGTTTGAATAATTTGCCATGATCTTACT 2476  
 Db 2534 TGTTCACCGGACCTTACAGCGGCAATTTCTTGAAGTCATAGCATGAGCCCTTACT 2593  
 QY 2477 ATTATTTCCAAAGAGGCTGGAATATCTTGAAGTTTATTTGAGCCTTAGCCTGTAG 2536  
 Db 2594 ATTATTTCCAAAGAGGCTGGAATATTTGAGCCTTAGCCTGTAGCCTGTAG 2633  
 QY 2537 AACTTGGACTGCGGCAGAGAGATATCTTCTCCGTCATCTTGCATTTGCTGCGAG 2596  
 Db 2654 AGGTGATGTCGCGAGATGAGAGGCGCTCATGCTGCGGCTCTTCCAGCTGTGCGAG 2713  
 QY 2597 TTTTCAAGTTGGCAAAATCTTGGCCAAAGTTAATATCTTAATAGATCATCGCAATT 2656  
 Db 2714 TCTTCAAGTTGGCAAAATCTTGGCCAAAGTTAATATCTTAATAGATCATCGCAATT 2773  
 QY 2657 CCGTGGGGGCTTGGGAAATTTAACCTGCTTGGCCATCATGCTTCAATTTTGGCG 2716  
 Db 2774 CCGTGGGGGCTTGGGAAATTTAACCTGCTTGGCCATCATGCTTCAATTTTGGCG 2833  
 QY 2717 TGGTGGCATGACAGCTCTTGTGTAAGTACAAAGATGTTGTCGAGATGCGCAGTG 2776  
 Db 2834 TGGTGGGAGTACAGCTGTTTGAAGAGTTACAAGAGTGCCTGTGTAATCAACAGG 2893  
 QY 2777 ATTGTCACTCCAGCGCTGGCAGATGATGATCTTCCATCTCTTCAATTTGTCTC 2836  
 Db 2894 AGTGAAGCTCCGCGCTGGCAGATGATGATCTTCCATCTCTTCAATTTGTCTC 2953  
 QY 2837 GCGTGTGTGTGGGAGTGTATGAGACCATGTTGGGACTGTATGAGAGTGTGTGTCAG 2896  
 Db 2954 GAGTGTGTGTGGGAGTGTATGAGACCATGTTGGGACTGTATGAGAGTGTGTGTCAG 3013  
 QY 2897 CCATGTGCTTACTGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATG 2956  
 Db 3014 CCATGTGCTTACTGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATG 3073  
 QY 2957 TCTTGTGCGCTTGTGTTGAGTGTATGATGATGATGATGATGATGATGATGATGATG 3016  
 Db 3074 TATTCCTGCGCTTGTGTTGAGTGTATGATGATGATGATGATGATGATGATGATGATG 3133  
 QY 3017 ATATATGAATGAATATCTTCAATTTGCTGTGATGATGATGATGATGATGATGATGATG 3076  
 Db 3134 ACAGGGAATGAATATCTTCAATTTGCTGTGATGATGATGATGATGATGATGATGATGATG 3193  
 QY 3077 TGAAGAAATATATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3136  
 Db 3194 CCAAGGAAATATATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3247  
 QY 3137 ATGAATATGAATATCTTCAATTTGCTGTGATGATGATGATGATGATGATGATGATGATG 3196  
 Db 3248 ATGAATATGAATATCTTCAATTTGCTGTGATGATGATGATGATGATGATGATGATGATG 3307  
 QY 3197 C---ARAGAAATTTGGAAAGATCTTGAATGATGATGATGATGATGATGATGATGATG 3253  
 Db 3308 CGGGCGGTGATATCCACCGGAGCGGCTTCCAGAAAGAGGAGGAGGAGGAGGAGGAGG 3367  
 QY 3254 GTATAGAACTGGCAGAGTGTGAAATATATGATGATGATGATGATGATGATGATGATGATG 3313  
 Db 3368 GCAT-----CGGAGAGAGGTGAGAGATGATGATGATGATGATGATGATGATGATGATG 3418  
 QY 3314 TCATTAACAAACCCAGTCTTACTGATGATGATGATGATGATGATGATGATGATGATGATG 3373  
 Db 3419 TCATTAACAAACCCAGTCTTACTGATGATGATGATGATGATGATGATGATGATGATGATG 3478  
 QY 3374 AAATTTAAACAGGAGATCTTATGATGATGATGATGATGATGATGATGATGATGATGATG 3433  
 Db 3479 AGAAGCTCAACAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3538  
 QY 3434 TGAATGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3493

Db 3539 TGAAGATATCC---AGTCTCTCAGAAAGAAATGATGATGATGATGATGATGATGATG 3595  
 QY 3494 AACAGCCGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3553  
 Db 3596 AAGTCCCGTGGAGACCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 3655  
 QY 3554 GTTACAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3613  
 Db 3656 GGTTCACAGGTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3715  
 QY 3614 GGAACCTGAGAAGAGAGTGTTCGAAATGATGATGATGATGATGATGATGATGATGATGATG 3673  
 Db 3716 GATG 3775  
 QY 3674 TTTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3733  
 Db 3776 TCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3835  
 QY 3734 GAAAGAGATTAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3793  
 Db 3836 GGAAGAGATTAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3895  
 QY 3794 TGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3853  
 Db 3896 TGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3955  
 QY 3854 GTTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3913  
 Db 3956 GCTGTTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4015  
 QY 3914 GTTACTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3973  
 Db 4016 GCTACTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4075  
 QY 3974 GAGCCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4033  
 Db 4076 GAGCCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4135  
 QY 4034 CATCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4093  
 Db 4136 COTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4195  
 QY 4094 GGTAAATTTGTTGCTGCGCAATTTCTACAGTGTATTAACACCAACCTGATGATGATGATG 4153  
 Db 4196 GAGTAACTGTTTGGGGAATTAACCTGATGATGATGATGATGATGATGATGATGATGATGATG 4255  
 QY 4154 TTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4213  
 Db 4256 TCGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4315  
 QY 4214 CTG---CTGATGCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4270  
 Db 4316 CGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4375  
 QY 4271 CTGTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4330  
 Db 4376 CCGTTCTTCAAGTGAACCTTCAAGGCTGATGATGATGATGATGATGATGATGATGATGATG 4435  
 QY 4331 CCAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4390  
 Db 4436 CCGGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4495  
 QY 4331 TTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4450  
 Db 4496 TCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4555  
 QY 4451 ATAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4510  
 Db 4556 ACAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4615  
 QY 4511 AGAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4570  
 Db 4616 AGAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4675



Db 242 TCGAGAGGGTATTCGCCGAGACGACGTCAGAAAACCAACCAAGGCGGATGCGACGCCACC 301  
Qy 122 AAAAGATGAGACGACAAAATGGCCCAAAATAGTACTTGGAGCTGGAAAAGACC 181  
Db 302 GGGAGAGAGATGAAGACGACCAAGCCCAAGACGACGACGCTGGGAAAGAGTT 361  
Qy 182 TTCCATTTATTTATGAGACATTTCTCCAGAGATGCTGACAGAGCCCTGGAGAGCTGG 241  
Db 362 TCCCTTATCTACGCGGAGACATCCCGCAAGGCTGCTGGGCTTCCCTGGAGAGCTTGG 421  
Qy 242 ACCCTTATATATCAATAGAAAACCTTTATATGATGATTAAGAGGAGGAGGACCTTCC 301  
Db 422 ACCCTTATATGAGGAGAAAACCTTTGATATTAACAGAGGAGGAGGAGGAGGAGGAGG 481  
Qy 302 GGTAGAGGCCACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 361  
Db 482 GATTAGAGGCCACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 541  
Qy 362 CTATTAAGATTTTGGTATTCATTCATTCAGCATGCTATTTATGACATATTTTGACA 421  
Db 542 CTATTAAGATTTTGGTATTCATTCATTCAGCATGCTATTCATGACATTCCTGACCA 601  
Qy 422 ACTGTGTATTAAGCAATGAGTAAACCTCTGATTTGACAAAGATGATGATACACT 481  
Db 602 ACTGTGTATTAAGCAATGAGTAAACCTCTGATTTGACAAAGATGATGATGATGATGAT 661  
Qy 482 TCACAGGAATATATCTTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 541  
Db 662 TCACAGGAATATATCTTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 721  
Qy 542 AAGATTTTACTTCTGCTGGGAGTATCATGATGATGATGATGATGATGATGATGATGAT 601  
Db 722 ACGGCTTACCTCTGCTGGGAGTATCATGATGATGATGATGATGATGATGATGATGAT 781  
Qy 602 CGTACGACAGAGTTTGTGACCTGCGGCAATGCTGCGCATTTGAGAACATTCAGAGTTC 661  
Db 782 CATATGACAGAGTTTGTGACCTGCGGCAATGCTGCGCATTTGAGAACATTCAGAGTTC 841  
Qy 662 TCCGAGCATTAAGACATTCATGATTCAGAGGCTGAAACCATTTGTTGGAGCCCTGCA 721  
Db 842 TCCGAGCATTAAGACATTCATGATTCAGAGGCTGAAACCATTTGTTGGAGCCCTGCA 901  
Qy 722 TCCAGTGTGAGAAAGGCTGCAAGTATGATGATGATGATGATGATGATGATGATGAT 781  
Db 902 TCCAGTGTGAGAAAGGCTGCAAGTATGATGATGATGATGATGATGATGATGATGAT 961  
Qy 782 TTGCTCTAATTTGGGCTGACGCTTTCATGAGGCAACCTGAGAAATTAATGATATACATG 841  
Db 962 TCGGCTGATTTGGGCTGACGCTTTCATGAGGCAACCTGAGAAATTAATGATATACATG 1021  
Qy 842 CTCGCCACCAATGCTTCTTGGAGAACATGATAGAAAAGAAATTAATGATGATATATA 901  
Db 1022 CCA-----TAAACTTCA 1033  
Qy 902 ATGTGACACTTATTAATGAACCTGCTTGAATTTGACGAGCAAGCATATATTAAGAT 961  
Db 1034 ACGAGAGCTACCTGGAGAACGCGACACAGGCTTGAACCTGGAGGAGAAATATATCAACATA 1093  
Qy 962 CAAGATATCATTTATTTCTGAGGCTTTTATGATGATGATGATGATGATGATGATGATG 1021  
Db 1094 AAACAACTTTTATATGATTTCTGAGGCTTTTATGATGATGATGATGATGATGATGATG 1153  
Qy 1022 ATGACAGGCAATGTCAGAGGAGATATATGATGATGATGATGATGATGATGATGATG 1081  
Db 1154 ATGCTGGGCAATGCGCAAGAGGATTCAGATGATGATGATGATGATGATGATGATG 1213  
Qy 1082 GCTAACAGAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1141  
Db 1214 GTTACACAGCTTTGACAGCTTACCTGAGGCTTCTGAGCATTTATTCGCTTATAGACC 1273  
Qy 1142 AGGACTTTCGGGAAATCTTTATCAAGTACATTAAGTCTGCTGGGAAACGATACATGA 1201  
Db 1274 AGGACTTTCGGGAAATCTTTATCAAGTACATTAAGTCTGCTGGGAAACGATACATGA 1333

Qy 1202 TATTTTGTGTTGTCATTTCTTGGGCTATTCACCAATTAATTTGATTCGCTG 1261  
Db 1334 TCTTCTTCTTGTGTCATTTCTTGGGCTATTCACCAATTAATTTGATTCGCTG 1393  
Qy 1262 TGTGGCCATGAGCTTCAGAGAACACAAATCAGGCTTGTGAAGAGCAAGCAACAAG 1321  
Db 1394 TGTGGCCATGAGCTTCAGAGAACACAAATCAGGCTTGTGAAGAGCAAGCAACAAG 1453  
Qy 1322 AGCCGAAATTCAGCAGATGATTAAGAACAGCTTAAAGCAAGAGGAGCTCAGCAG 1381  
Db 1454 AGCCGAAATTCAGCAGATGATTAAGAACAGCTTAAAGCAAGAGGAGCTCAGCAG 1513  
Qy 1382 CAGCAAGGCACTGCTC-----AGAACATTCAGAGAGCCCACTG 1424  
Db 1514 CTGCAATGAGCACTGAGGCACTGCTGAGAGAGCCCACTGAGAGAGGAGGAG 1573  
Qy 1425 ACGAGGAGGCTCTCAGACAGCTATGAGAGCTTAAAGTGAATTCAGAGAGCTT 1483  
Db 1574 ATGGGCTAGGCTCTCAGAGAGCTTCTGAACTGCTTAACATTCAGAGAGGAG 1633  
Qy 1484 AGGAAAGAAATTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1543  
Db 1634 AGGAGGAGGAG 1693  
Qy 1544 AAGATGA-----GATGATTCGAAATTCGATGATGATGATGATGATGATGATGAT 1600  
Db 1694 AAGGAGAGGAG 1753  
Qy 1601 TTCGCTTCCATTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1660  
Db 1754 TCCGCTTCCATTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1801  
Qy 1661 AGCTTTGTTGAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1720  
Db 1802 AGCTGCTGCTGAGCATTCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1861  
Qy 1721 TTTTACGCTTTAG-----AGGCGAGCAAGAGATGATGATGATGATGATGATGAT 1774  
Db 1862 TCTTACGCTTTAG-----AGGCGAGCAAGAGATGATGATGATGATGATGATGAT 1921  
Qy 1775 ATGATGAGACAGACACTTGTGAGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAG 1834  
Db 1922 ACGATGAGACAGACACTTGTGAGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAG 1981  
Qy 1835 GAGCAG 1879  
Db 1982 TCCGCGCCCGGAG 2041  
Qy 1880 GGTGATCCCGGAG 1939  
Db 2042 GGTGATCCCGGAG 2101  
Qy 1940 GCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1999  
Db 2102 GCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2149  
Qy 2000 TTCTGCGAGAGGATTAATGATTAAGCAGCTACTGATGATGATGATGATGATGATG 2059  
Db 2150 TCTGCGCTAGG-----CAAGCAGAGAG 2173  
Qy 2060 CTGAATGAG 2119  
Db 2174 TGAAGATTAAG 2233  
Qy 2120 CTTCGCAAG 2176  
Db 2234 ACGAG 2293  
Qy 2177 AACTGGAATTCAG 2236  
Db 2294 ACGTGAAG 2353

|    |       |   |      |
|----|-------|---|------|
| Qy | 2237  | TATCTGGAGCGTCTCCATTTGGTAAAGTGAACATGTCACACTGGTGTG                  | 2296 |
| Db | 22354 | TCATCTGGGAGTGCACCCCTCTGATATAACTGAAGAGATCGGAACCTTAATGCTCA          | 2413 |
| Qy | 2297  | TGGACCAATTTGTGACCTGGGCATCAACATCGTATTTGTCTTAATAATCTTTCATGG         | 2356 |
| Db | 2414  | TGGACCCCTTTTATAGCTTAAGCATACATCTGCATCGTCTCGAATATAGCCTATTATAG       | 2473 |
| Qy | 2357  | CCATGGAGACATATCCAAATGACGGACCATTTCAATATATGCTTACATGAGAACTTGG        | 2416 |
| Db | 2474  | CAATGGAGACCAATCCCAATGAGAACACACAGTTGCAACACGCTTGGCGGTAGAGAACTGG     | 2533 |
| Qy | 2417  | TTTTCACTGGGATCTTTACAGCAAAATGTTCTGAATAATATATGGCATATGATCTTACT       | 2476 |
| Db | 2534  | TGTTCAACCGGATCTTCAAGCGGGGAATTTCTGAAGCTCAATAGCAATGAGACCCCTACT      | 2593 |
| Qy | 2477  | ATTATTTCCAGAAAGGCTGGAATATCTTTGACGGTTTTATTTGACGCTTAAGCTGGTAG       | 2536 |
| Db | 2594  | ATTATTTCCAGAAAGGCTGGAACATTTTATGACGATTTATTTGCTCCCTCAAGTTAATGG      | 2553 |
| Qy | 2537  | AACTTGGACCTGCGCATATGTAAGATTAATCTTCTCCGTTTCATTTGATTCGTGAG          | 2596 |
| Db | 2654  | AACTGATGCTCGAGATGTGAGAGGGGCTCTCAATGCTGGCGGTCTTTCGACCTGCTCGAG      | 2713 |
| Qy | 2597  | TTTTCAAGTTGGCAAAATCTTGGCCACAGTTAAATATGCTAAATAAAGATCATGGCAATT      | 2656 |
| Db | 2714  | TCTTCACAGCTGGGCAAGTCTTGCGCCACCTGGAACATGTGATCAACAGATCATGGGAACCT    | 2773 |
| Qy | 2657  | CGTGGGGGCTCTGGGAAATTAACCTGCTCTTGGCATCATCGTCTCATTTTGGCG            | 2716 |
| Db | 2774  | CGTGGGTCCTCGGGCAACCTACCTGCTGCGCATCATCGTCTTATCTTGGCG               | 2833 |
| Qy | 2717  | TGGTCGGACATGACGCTTTTGTGTAAAGATACACAAAGATTTGTCTGCAAGATGCGCAGT      | 2776 |
| Db | 2834  | TGGTGGGGAATGCAGCTGTTTGAAAGATTAACAAGAGTGCAGTCTGTGAATCAACAGG        | 2893 |
| Qy | 2777  | ATTGTCAACTCCAGCGTGGCACATGATGACTTCTTCACTCCTTCTGATTTGTCTC           | 2836 |
| Db | 2894  | AGTGCAGAGTCCCGCCTGCGACATGAAACAGACTTCTTCCACTCCTTCCATGCTCTTCC       | 2953 |
| Qy | 2837  | GGCTGCTGTTGGGAGATGATAGAGCAATGTTGGGACTATAGAGAGTTGCTGGTCAAG         | 2896 |
| Db | 2954  | GAGTGTGTTGTTGGGAGTGTGATGAGACCAATGTGGACTCATATGAGAGTGGCGGCCAGG      | 3013 |
| Qy | 2897  | CCATGTGCTTACTGTCCTTATGATGATGGTCTCATGTGATTTGGAACCTATAGTGTCTGATC    | 2956 |
| Db | 3014  | CCATGTGCTTACTGTCCTTATGATGATGGTATATGATGCAACCTGTGGTGTGATC           | 3073 |
| Qy | 2957  | TCTTTCTGCGCTTGTCTTTGAGCTCATTTATGTGACAGCAACCTTGACGCATGATATG        | 3016 |
| Db | 3074  | TATTTCTGCGCTTGTCTTTGAGCTCTTTCAGCGAGCAACCTGGCCGACACAGACAGC         | 3133 |
| Qy | 3017  | ATATATGAATGAATTAATCTCCAAATGCTGTGGATAGAGATGACAAAGAGGATCTTATG       | 3076 |
| Db | 3134  | ACGGGAAATGAACACTCTGAGATCTCACTGATCCGATATMAAAGGGGTGGCTTGA           | 3193 |
| Qy | 3077  | TGAAAAAGAAATATATGAATTTATTTAACAAGTCTTTCATTAGGAAACAAAGATTTTAA       | 3136 |
| Db | 3194  | CCAAATGAAAGTGACAGCGCTTCAATGAGGCTCACTTC-----AACAGCGGGAGGGCGG       | 3247 |
| Qy | 3137  | ATGAAATTTAAACACTTGATGATCTAAACACAAAGAAAGACGTTTATGTCCAAATATA        | 3196 |
| Db | 3248  | ATGAAATGAAGCCCTTCGAGAGCTGTATGAGAAGGCAACCTGATGCGCAACACACA          | 3307 |
| Qy | 3197  | C---AACAGAAATTTGGAAAGATCTTACATATCTTAAGATGTAAATGGAACATCAAGTG       | 3253 |
| Db | 3308  | CGGGCGTGGATTCACACCGAGCGGCACTTCCAGAAAGACGGGACGGAAACACACAGCG        | 3367 |
| Qy | 3254  | GATATGAAATCGACAGATGTTGAAAAAATACATATTTGATGAAAGATCAATCATGTCTAT      | 3313 |
| Db | 3368  | GCAT-----CGGACAGAGGCTGGAAGAAATACATCATGACGA---GGACACATATGTCT       | 3418 |
| Qy | 3314  | TCATTAACAACCCAGTCTTACTGTACTGTACATTCACCAATTTGCTGTAGAGAAATCTCACTTTG | 3373 |

|    |      |  |      |
|----|------|--|------|
| Db | 3419 | TCATTAAACAAACCAACCTGACCGCTCCGGGGTCCCATTTGCTGTGGGGACAGTCTGACTTCGG | 3478 |
| Db | 3419 | TCATTAAACAAACCAACCTGACCGCTCCGGGGTCCCATTTGCTGTGGGGACAGTCTGACTTCGG | 3478 |
| Qy | 3374 | AAAATTTAAACAGGAGACTTTAGTAGTAATTCGATCTGGAGAAACCAAGAAAC            | 3433 |
| Db | 3479 | AGAACCTCAACACAGAGAGATTTACGACGAAATACAGCCCTGAAAGGACGAAAGTAAAC      | 3538 |
| Qy | 3434 | TGAATGAACACAGTAGTATATCAAGAGTAGACAGTGGACATCGGGCACCTGTAGAG         | 3493 |
| Db | 3539 | TGGACGATAC - - - AGCTCCTCGAAGGAAGTACATCCACATCCATCAAGCTGAGGTGGAG  | 3595 |
| Qy | 3494 | AACAGCCCGTAGTAGAAGCTGAGAAACCTTGAACACGAAACCTTGTTCACCTGAAGCT       | 3553 |
| Db | 3536 | AAGTCCCGGTGGACCAACCTGAGGAATTAAGTGGATCCGAGCCCTGTTACAGAGGTT        | 3655 |
| Qy | 3554 | GTTGACAAAGATTCACACTGTTGTCAAATCAATGTGAGAAAGGACAGGAAACATAGT        | 3613 |
| Db | 3656 | GCCTCAGCGGTTCAAGTGTGCGACAGGTCAACATCGAAGAAAGCACTGAGCAAGTGTGT      | 3715 |
| Qy | 3614 | GGAACCTGAGAAAGAGCTGTTTCCGAATAGTGAACATTAACCTGGTTTGAAGCTTCATG      | 3673 |
| Db | 3716 | GGATCTTGGCGGAAACCTGCTCTCTCATTTGTGGAGCACAAATGGTTTGAACCTTCAACA     | 3775 |
| Qy | 3674 | TTTTCATGATTCCTCTAAGTAGAGTGGTCTGGCATTTGAATPATAATATGATAGC          | 3723 |
| Db | 3776 | TCTTCATGATTCCTCTAAGTAGAGTGGTCTGGCATTTGAATPATAATATGATAGC          | 3855 |
| Qy | 3734 | GAAAGACATTTAAAGCAGATTTGGAATATGCTGACAGGTTTTCACCTACATTTTCATTC      | 3793 |
| Db | 3836 | GGAAGACATTCGACACATCTGGAATATGCTGACAGGTTTTCACCTACATTTTCATTC        | 3895 |
| Qy | 3794 | TGGAATGCTTTAAATGGGTGGCATATGCTATCAAAACATATTTACCAATGCTCTGT         | 3833 |
| Db | 3836 | TGGAGATTTGCTCAAGTAGACAGCCACGCTTCCTCAAGTTCCTACCAATGCTCTGT         | 3955 |
| Qy | 3854 | GTTGGCTGAGCTTTCTAATTTGATGATTTTCATTTGTCAGTTTAAAGCAAAATGCTCTGG     | 3913 |
| Db | 3956 | GCTGGTGGACTTCTCATATTTGTGCTGTCTCTTTAGTACCTTATAGCTATAGTCCCTGG      | 4015 |
| Qy | 3914 | GTTACTCGAAGCTTGGAGCCATCAAACTCTCGACAGACATAAGAGCTGAGACCTCA         | 3973 |
| Db | 4016 | GCTACTCGAAGCTTGGAGCCATCAAAAGTCCCTTGAAGACCTTAAGAGCTTGAAGACCTTAA   | 4075 |
| Qy | 3974 | GAGCTTATCTCGATTTGAAGGATGAGGTTGTGTAATGCCCTTTTGAAGCAATTC           | 4033 |
| Db | 4076 | GAGCTTATCTCGATTTGAAGGATGAGGTTGTGTAATGCCCTTTTGAAGCAATTC           | 4135 |
| Qy | 4034 | CATCATCATGAATGCTGCTGTGTTGCTTATTTGCGCAATTTACACATCAGG              | 4093 |
| Db | 4136 | CCTCATCATGAATGCTGCTGTGTTGCTTATTTGCGCAATTTACACATCAGG              | 4195 |
| Qy | 4094 | GCGTAAATTTTGTGCGCAAAATTCACACATGATTAACACACAACTGCTGAACGT           | 4153 |
| Db | 4196 | GAGTTAACTGTTTGGCGGGAAATACACATACGCTTTATAGACTTCTGAAATCCGGT         | 4255 |
| Qy | 4154 | TTGACATCGAAGAGCTGGAATATCATATCTGATTCCTAAAACTATAGAAAGAAATGAGA      | 4213 |
| Db | 4256 | TGCAATATGGAATTTGTCAACAATTAACGAGCATGTGAGAAGCTCAGAGGGCAACACA       | 4315 |
| Qy | 4214 | CTG - - - CTGAGTGGAAAAATGTGAATACTGATATGAGGATTTGGGTATCTCT         | 4270 |
| Db | 4316 | CGGAGATCCGATGGAAGAAATGTCAAGTCAACTTTGACATGTGCGAGCAGGGTACCTGG      | 4375 |
| Qy | 4271 | CTTGTGCTCAAGTTGGCCACATTTCAAGAGATGATGATTAATATGACAGCAGTTGAT        | 4330 |
| Db | 4376 | CCCTTCTTCAAGTGGCAACCTTCAAAAGCTGATGAGCATCATGTAATGGCGCTGATAGAT     | 4435 |
| Qy | 4331 | CCGAAATGATGGAACTCCAGCTTAAGTATGAAGAAAGTCTGATCATATCTTTACTTGG       | 4390 |
| Db | 4436 | CCCGAAACCCAGAGAGAGGCTGACACAGAGGCAACATCTCATGATCATCTCTTGG          | 4495 |
| Qy | 4391 | TTAATTTCATCATCTTTGGGTCTCTTCAACCTTGAACCGTTTATGGTGCATCATAG         | 4450 |

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|----|------|--|------|
| Qy | 5531 | CAAAACAATCTCAGCTCATTTGCATTTGGCCATGGTGAAGTGTGACCGATCCACT        | 5590 |
|    |      |  |      |
| Db | 5633 | CCAAACACCATCGAGCTCATTCGCGCATGGACTCGCCCATGGTAGCGGAAATTCGATCCACT | 5692 |
| Qy | 5591 | GCTCTTGCAATCTATTTCCTTTTACAAAGCGGGTCTCTAGAGAGAGTGGAGAGATGATG    | 5650 |
|    |      |  |      |
| Db | 5693 | GCTTGGAACATCCCTTTTCGCTTCACCAACGAGTCTCGGAAACAGTGGGGAGTTGGACA    | 5755 |
| Qy | 5651 | CTCTACGAATACAGATGGAAGAGACGAAATGCATTCGAATCTTCCAAAGTCTCTCTAC     | 5710 |
| Db | 5753 | TCTCTGGCGGACAGAGATGAGAGAGCGGTTCGTGCGATCCATCTCTTCCAAAGTGTCTACG  | 5812 |
|    |      |  |      |
| Qy | 5711 | AGCCCAATCACTACTACTTTAAACGAAAACAAGAGAGATATCTGCTCATTTATTCAGC     | 5770 |
|    |      |  |      |
| Db | 5813 | AGCCTATCAACAACACTCTCGCGCGGAAGACAGAGAGAGGTGTCTGACGTGGTCTCGAGC   | 5872 |
| Qy | 5771 | GTCGCTTACAGAGCGCAACTTTTAAACG                                   | 5798 |
|    |      |  |      |
| Db | 5873 | GTCGCTTACAGAGGACACTTGTGCTAGGCG                                 | 5900 |

RESULT 12  
 US-09-024-020B-8  
 ; Sequence 8, Application US/09024020B  
 ; Patent No. 6030810  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DELGADO, STEPHEN G.  
 ; APPLICANT: DIETRICH, PAUL S.  
 ; APPLICANT: FISH, LINDA M.  
 ; APPLICANT: HERMAN, RONALD C.  
 ; APPLICANT: SANGAMESWARAN, LAKSHMI  
 ; TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE  
 ; TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF  
 ; NUMBER OF SEQUENCES: 43  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: JANET PAULINE CLARK  
 ; STREET: 3401 HILLVIEW AVENUE, MS A2-250  
 ; CITY: PALO ALTO  
 ; STATE: CA  
 ; COUNTRY: U.S.A.  
 ; ZIP: 94304-1397  
 ;  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/024,020B  
 ; FILING DATE: 16-FEB-1998  
 ; CLASSIFICATION: 536  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 60/039,447  
 ; FILING DATE: 26-FEB-1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: CLARK, JANET P.  
 ; REGISTRATION NUMBER: 34,799  
 ; REFERENCE/DOCKET NUMBER: R0020B-BEG  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (650) 852-3097  
 ; TELEFAX: (650) 855-5322  
 ; INFORMATION FOR SEQ ID NO: 8:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 6826 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: linear DNA (genomic)  
 ; US-09-024-020B-8  
 ;  
 Query Match 44.3%; Score 2674.2; DB 3; Length 6826;  
 Best Local Similarity 68.8%; Pred. No. 0;  
 Matches 4009; Conservative 3; Mismatches 161; Indels 166; Gaps 18;





|    |      |  |      |
|----|------|--|------|
| Db | 2079 | TCAACAGCATTAAGAGAGGTGGTGCACAAACACCGTAGTGAAAGCTGGAAGTCTCAGAG    | 2138 |
| OY | 2196 | GAAATGCCACACCGTGTGGTAATAAATTTCACACATATCTTAATCTGGAGCTGTCTCC     | 2255 |
| Db | 2139 | AAATCGCCACCGCGCTGGTAAAGTTATGGCAACACTTTCACATCTGGAGGTGCACCC      | 2198 |
| OY | 2256 | ATATGGTTAAAGTGAACATCTTCGCAACCGTGGTGGATGAGGACCCATTTGGTGAACCT    | 2315 |
| Db | 2199 | CTACGTGATTAAGATGAAGAGATGCGAATTAATGCTACGACACCCCTTTGTAGACTT      | 2258 |
| OY | 2316 | GGCCATCACCATCTGTATTTCTTAATATACCTTTTTCATAGGCCAGAGACACTATCCAAAT  | 2375 |
| Db | 2259 | AGCCATCACCATCTGCATCTCTTGATTAATGCGATTTATGGAATGAGACACACATCCAT    | 2318 |
| OY | 2376 | GACGACCATTTCAATAATGTGCTTACAGTAGAACAATTGTTTTACTGGGATCTTTAC      | 2435 |
| Db | 2319 | GACACACAGTGTGAACACGCTTTGGCCGAGGAATACTGGTTACACCGGATCTTAC        | 2378 |
| OY | 2436 | AGCAGAAATGTTTCTGAATAATTATGCCATGATCTTACTATTTATTCACAAAGGCTG      | 2495 |
| Db | 2379 | GGCGGAATGTCTGTGAAGCTCATACCACTGACCCCTTCTTTATTTTCCAAAGAGCTG      | 2438 |
| OY | 2496 | GAATATCTTGAAGCTTTATTTGAGCGCTTACGCGTGAAGAACTTGGACATCGCAACT      | 2555 |
| Db | 2439 | GAACATTTTTCAGGATTTATATGTCTCCGACATTTAAATGAGCTGAGCTGTGCGAGATGT   | 2498 |
| OY | 2556 | GGAAGATTAATCTTCTCCGTCATTTGATTTGATTTGCGACAGTTTTCAAGTTGGCAAAATC  | 2615 |
| Db | 2499 | GGAGGGGCTCTCACTGCTGGGCTTTCCGACGCTCGAGCTTCAAGCTGCGCAACTC        | 2558 |
| OY | 2616 | TTTGCCCAACGTTAAATATGCTAATTAAGATCATGCGCAATTCGCTGGGGCTGTGGAAA    | 2675 |
| Db | 2559 | CTGGCCACACCTGAAACATGCTGATCAAGATCAATCGGGAACCTCGTGGGTGCGCTGGGCAA | 2618 |
| OY | 2676 | TTTAACCTGTCTGGCCATTCATGCTTCATTTTGGCGGTGCGGATGACACACTT          | 2735 |
| Db | 2619 | CTGACCCCTGTGCTGGCACTATCGTCTTCATCTTTCGCGGTGGTGGGATGACACTT       | 2678 |
| OY | 2736 | TGCTAAAGACTCAAAAGATTGTGTCTGCAAGATGCGCAGTGTATGTCAACTCCACAGCTG   | 2795 |
| Db | 2679 | TGGAAGAGTTACAAAGAGTGGCGTGTAGATCAACAGAGAGTGAACACTCCGCGCTG       | 2738 |
| OY | 2796 | GCACATGATGACTTCTTCCACTCTCTGATTTGTTCCGCGTCTGTGTGGGAGTG          | 2855 |
| Db | 2739 | GCACATGATGATCTTCTCCACTCTCTCCATCTGCTTCCGAGTCTGTGTGGGAGTG        | 2798 |
| OY | 2856 | GATAGAGACCATGTGGGACTGTATGAGAGTGTGTGTGCAAGCCATGTGCTTACGTCT      | 2915 |
| Db | 2799 | GATGAGACCATGTGGGACTGTATGAGAGTGTGTGTGCAAGCCATGTGCTTACGTCT       | 2858 |
| OY | 2916 | CATGATGCTGTGATGTGAAGAACTGATGAGTCTGATATCTTCTTGGCTTCTT           | 2975 |
| Db | 2859 | CATGATGCTTATGTTCATGTGGCAACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT       | 2918 |
| OY | 2976 | GAGCTCATTTAGTGCAGACAACTTGCAGCCACTGATGATGATTAATAATGAATTAATCT    | 3035 |
| Db | 2919 | GAGCTCTTTCAGCGCAGACAACTTGGCGGCACAGACGAGACGGGGAATTAATGAACACT    | 2978 |
| OY | 3036 | CCAAATTCCTGTGATAGATGCACAAAGAGTATGCTTATGTGAAAAAATATATGA         | 3095 |
| Db | 2979 | GCAAGTCTCATGTATCGGATCAAGAAAGGCGTGGCTGGACCAAAAGTGAAGGTGCACGC    | 3038 |
| OY | 3096 | ATTTATTCACAGCTCTTCATTTAGAGCAAAAGATTTTAAAGTAATTAACACTTGA        | 3155 |
| Db | 3039 | CTTCAATGACGCTCACTT-----AAGCACGGGAGCGAGATGAAGTAAACCCCTCGA       | 3092 |
| OY | 3156 | TGATCTTAAACAACAAGAAAGACATTTATGTCAATCATATAC---ARCAAAATTTGGAA    | 3212 |
| Db | 3093 | CGAGCTGTATGAAGAAAGGCAACCTCATCTGCGCAACACAGCGGTGATATCACGC        | 3155 |
| OY | 3213 | AGATCTTGACTATCTTAAGATGTAATGAACTCAAGATGTGTATGGAATCTGGACAGAG     | 3272 |

|   |      |   |      |
|---|------|---|------|
| D | 3153 | GAACGGGACCTTCCACAAAGACGGGAACGAAACCAACAGCCGCAT-----CGGCACGAG   | 3206 |
| Q | 3273 | TGTTGAAAATPACATPATTGTAGAAAGATATTACATGTGATCATCAATAAACCCACTCT   | 3332 |
| D | 3207 | CGTGGAAATACATACATACAGACA---GGACCAACATGTCTCTCATTAACAAACCAAACT  | 3263 |
| Q | 3333 | TACTGTACCTGTACCAATGTCTGTAGGAATCTACCTTTGAAAATTTTAAACAGGAGA     | 3392 |
| D | 3264 | GACCGTCCGGGTCCCATTTGCTGTGGGCGAGTGTACTCTCGAAGAACCTCAACAGAGGA   | 3323 |
| Q | 3393 | CTTTTAGTAGTAATCGAATCTGGAGAAAGCAAAAGAAACTGAATGAAACGATAGCTC     | 3452 |
| D | 3324 | TGTTAGCAGGAAATCAGACCCCTGAAGCGAGCAAAAGATTAACGTGCAGATACC---AGTC | 3380 |
| Q | 3453 | ATCAGAAAGTAGACACTGTGACATCGGCCACTGTAGAAACAGCCCGTAGTGGAAAC      | 3512 |
| D | 3381 | CTCAGGAAGGAGTACCATGACATGCATCAAGCCTGAGGTGGAAAGTTCCCGGTGAGCAAC  | 3440 |
| Q | 3513 | TGAAGAAACCTTGAACCAAGAGCCTGTTCACTGAGGCGTGTACAAAGATTCAAGTG      | 3572 |
| D | 3441 | TGAGGAATACCTTGATCCGAGCCCTGCTTACAGAGGTTGCGTCCAGCGGTCAAGTG      | 3500 |
| Q | 3573 | TTTGCATATCAATGTGGAGAAAGGACAGAAAACAATGTTGGAACTCGAGAAGGACGTG    | 3632 |
| D | 3501 | CTCGACAGCTAACATCGAGGAAGACACTAGGCAAGCTGTGTGATCTTCCGAAAACCTG    | 3560 |
| Q | 3633 | TTTCCGAAATAGTTGAACATACTGTTTGAGACCTTCATTTGTTTCATGATTTCTCTT     | 3692 |
| D | 3561 | CTTCTCATTTGTGAGAGCAAAATTTGTTAGACCTTCATCTTCATGATTTCTCTCAG      | 3620 |
| Q | 3693 | TACGTGTCTGTGGCACTTTGAAGATATATATATATGATCAAGCAAGACAGATTAGACAT   | 3752 |
| D | 3621 | CAGTGGGCGCCCTGGCTTGAGAGCACTTCACATGTGACAGAGGAAGACCACTCCGACAT   | 3680 |
| Q | 3753 | GTTGGAATATGCTGACAGAGTTTCTACTTACATTTCTCATTTCTGGAATGCTCTTAAATG  | 3812 |
| D | 3681 | CTGTGATATGCGGACAAAGTCTTCAACCTACATCTTCATCCTCGAGATGTGTCTAATG    | 3740 |
| Q | 3813 | GGTGGCATGTGCTATCAAAACATATTTCAACCAATGCTGTGTGGCTGGACTCTTAT      | 3872 |
| D | 3741 | GACCACTAGCGGCTTCGTCAAAAGTTCTTCAACATAGCTGTGTGGTGGAACTTCTCAT    | 3800 |
| Q | 3873 | TGTTGATGTTTCANTGTGTCACTTTAACACCAATGCTTGGGTTACTAGAACTTGAGAC    | 3932 |
| D | 3801 | TGTGGCTGTCTTTATCTATCGCCTTATACCTAATGCTTGGGCTACTCGGAATGAGTGC    | 3860 |
| Q | 3933 | CATCAAAATCTCTGAGCACTATAGACCTCGAGACCTTAAAGCCTTATCTGCATTTGA     | 3992 |
| D | 3861 | CATTAAGTCCCTTAGACCTTAAGACCTTAGACCTTAAAGCCTTATACAGATTGA        | 3920 |
| Q | 3993 | AGGATAGAGGTGTGTGTGATGCCCTTTTAGAGCAATTTCCATCCATCATGAATGTCT     | 4052 |
| D | 3921 | AGGATAGAGGTGTGTGTGATGCCCTTTTAGAGGTGCATCCCTCATCATGAATGTCT      | 3980 |
| Q | 4053 | TCTGTTTGTCTTATATTTGCGCTAAATTTACAGATCATGGCGTAAATTTGTTGCTGG     | 4112 |
| D | 3981 | GCTGTGTCTCATCTTCTGCGCTGATTTTCAACATCAATGGAAGTAACTGTTTGGCGG     | 4040 |
| Q | 4113 | CAAAATTCACACGTATTTAAACCAACAACTGTGTGACAGTTTGATCATGAAGAGTAA     | 4172 |
| D | 4041 | GAATTAACCACTACTCTTTTATATAGACTTCTGAATCCGTTTGAATCATGATATTTGTCA  | 4100 |
| Q | 4173 | TAAATCATACGATGCTCTAAACATTAATAGAAACAAATGAGACTG---CTCGATGGAAAA  | 4228 |
| D | 4101 | CAATTAACGGAAGTGAAGAGCTCATGAGGAGCAACACAGGAGATCCATGTGAAGA       | 4160 |
| Q | 4230 | TGTGAAGTAACTTTGATATGTATAGAGTTGGGTATCTCTTCTCTCAAGTTCCAC        | 4288 |
| D | 4161 | TGTCAAAATCAATTTTACATATGTGAGAGAGGTACTCGGCCCTCTTCAAGTGGCAAC     | 4220 |
| Q | 4280 | ATTCAAAGATGATGATATATATATGATGACAGATGTAAATCCAGAAATGTGCAATCTCA   | 4348 |
| D | 4221 | CTTCAAAAGGTGTGAGACATATATATGTGGGTGTAGATCTCCGAAACCAAGACAGACA    | 4280 |





QY 2018 TAGATTAAGCAGCTACTGATGACATGGAACAACACCTGAACTGAAATGAGAAAGAA 2077  
DB 1985 -----TGAGGCAACGACTGAGTGAAATTAAGAAAGAA-AA 2018  
QY 2078 GGTCAAGTTCTTCCACGTTTCCATGAGACTTGTAGAAAGTCTTCCCAAGGCAACGAG 2137  
DB 2019 GGGCTGAGACTCTTATGATGAGACCACTGCTCCCTACGAGCGGAGGAGACGAA 2078  
QY 2138 CATGAGTATAGCCAGCATTTCTACAAATACAGTA--GAAGAATTGAAGATCCAGGCA 2195  
DB 2079 TCAGACGATTAATAGCGTGTGTACAAACGCTAGTAGAGACTGGAAGAGTCTGAG 2138  
QY 2196 GAAATGCCACCTGTGTGTATTAATTTTCCAAATATCTTAATCTGGAGCTGTCTCC 2255  
DB 2139 AAAGTCCCAACCGTGTGTATTAATTTTCCAACTTCTCCATCTGGAGAGTGCACCC 2198  
QY 2256 ATATGTGTTAAAGTGAACATGTTTCAACCGGTGTGTATGAGAGCCATTTGTACCT 2315  
DB 2199 CTATGATTAATACTGAAGAGATGCTGAACCTTAATGCTATGAGCCCTTTGTAGACT 2258  
QY 2316 GGCATACCATCTGATGATGCTTAATATCTTTTCAATGGCCATGAGACATCCAT 2375  
DB 2259 AGCATACCATCTGATGATGCTTAATATCTTTTCAATGGCCATGAGACATCCAT 2318  
QY 2376 GACGACCATTTCAATATGCTTACAGTGAAGAACTGTGTGTGTGTGTGTGTGTGTGT 2435  
DB 2319 GACACGACATTTCAATATGCTTACAGTGAAGAACTGTGTGTGTGTGTGTGTGTGTGT 2378  
QY 2436 AGCAGAAATGTTCTGAATAATTTTCCATGATGATGATGATGATGATGATGATGATG 2495  
DB 2379 GGGGGAATGTTCTGAATAATTTTCCATGATGATGATGATGATGATGATGATGATGATG 2438  
QY 2496 GAATATCTTTGAGGTTTATGATGATGATGATGATGATGATGATGATGATGATGATG 2555  
DB 2439 GAATATCTTTGAGGTTTATGATGATGATGATGATGATGATGATGATGATGATGATG 2498  
QY 2556 GGAAGATTAATCTGTTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 2615  
DB 2499 GGGGGAATGTTCTGAATAATTTTCCATGATGATGATGATGATGATGATGATGATGATG 2558  
QY 2616 TTGGCCAAAGTTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2675  
DB 2559 GTGGCCAAAGTTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2618  
QY 2676 TTAAACCTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2735  
DB 2619 CCGACCTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2678  
QY 2736 TTGTTAAAGCTACAAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2795  
DB 2679 TGGTAAAGCTACAAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2738  
QY 2796 GCAATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2855  
DB 2739 GCAATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2798  
QY 2856 GATAGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2915  
DB 2799 GATAGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2858  
QY 2916 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2975  
DB 2859 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2918  
QY 2976 GAGCTCATTTAGGAGAGAACTGAGCACTGATGATGATGATGATGATGATGATGATG 3035  
DB 2919 GAGCTCATTTAGGAGAGAACTGAGCACTGATGATGATGATGATGATGATGATGATG 2978  
QY 3036 CCAATATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3095  
DB 2979 GAGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3038  
QY 3096 ATTATATCAACGCTCTTCAATTAAGAAACAAAGATTTTATGATGAAATTAACCACTG 3155  
DB 3039 CTTCATCAGGCT 3092  
QY 3156 TGATCTAATAACAG 3212  
DB 3093 CGAGCTATGAG 3152  
QY 3213 AGATCTTACATCTTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 3272  
DB 3153 GAAGGAG 3206  
QY 3273 TGTGAAATATCAATTTATGATGATGATGATGATGATGATGATGATGATGATGATG 3332  
DB 3207 CGTGAG 3263  
QY 3333 TACTGTATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3392  
DB 3264 GAGCTGCGGAG 3323  
QY 3393 CTTTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3452  
DB 3324 TGTGAG 3380  
QY 3453 ATGAG 3512  
DB 3381 CTGAG 3440  
QY 3513 TGAAG 3572  
DB 3441 TGAAG 3500  
QY 3573 TTGCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3632  
DB 3501 CTGCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3560  
QY 3633 TTTCGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3692  
DB 3561 CTTCGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3620  
QY 3693 TATGAG 3752  
DB 3621 TATGAG 3680  
QY 3753 GTTGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3812  
DB 3681 CTGCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3740  
QY 3813 GTTGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3872  
DB 3741 GATGAG 3800  
QY 3873 TGTGAG 3932  
DB 3801 TGTGAG 3860  
QY 3933 CATCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3992  
DB 3861 CATCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3920  
QY 3993 AGGAG 4052  
DB 3921 AGGAG 3980  
QY 4053 TGTGAG 4112  
DB 3981 GATGAG 4040  
QY 4113 CAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4172  
DB 4041 GAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4100  
QY 4173 TAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4229

|   |   |      |  |      |
|---|---|------|--|------|
| D | b | 4101 | CATAAAGCGACTGAGAGAGCTCATGAGGGCCAAACACGAGNATCCGATGGAAGA           | 4160 |
| O | y | 4230 | TGTGAAGTAACCTTGGTAATGTAGAAATTTGGGTATCTCTTTGCTTCAAGTTGCCAC        | 4289 |
| D | b | 4161 | TGTCAAGATCAACTTTGACATATGTGGACAGAGGTACGTGGCCCTTCTTCAAGTGGCAAC     | 4220 |
| O | y | 4290 | ATTCAAGATGSGATGATATATATGTATGACAGAGTTGATTCAGAAATGTGSACTCCA        | 4349 |
| D | b | 4221 | CTTCAAGGCTGGATGAGACATCATGTATCGGGCTGTAGATTCGCCAAGGCACAGACGA       | 4280 |
| O | y | 4350 | GGCTAGTATGAGAAAGCTGACATGATCTTATCTTATTTGATTCATCTTTGG              | 4409 |
| D | b | 4281 | GGCTGACTGAGGGGCACACATCTACATGTACATCTTCTTCGTATCTTCACTTTCCG         | 4340 |
| O | y | 4410 | GTCCTCTCTACCTTGAAACCTGTTTATTTGATCATATAGATAATTTCAACGACGAA         | 4469 |
| D | b | 4341 | CTCTCTCTTCACTTCACCTTCACCTGTTATCGGTGTATCATGACACACTTCAACGACGAA     | 4400 |
| O | y | 4470 | AAAGAATTGGAGGTCAAGACATCTTTATGACAGAAAGACAGAAATACTATATGC           | 4529 |
| D | b | 4401 | GAAAAAGTTGGAGGTGACAGACATCTTCAATGACAGAGAAACAGAAAGTACTATATGC       | 4460 |
| O | y | 4530 | AATGAAAAAATTAGATTCGAAAAAACCGAAAAACCTATACCGTCGACACGAGAAACAAAT     | 4589 |
| D | b | 4461 | CATGAAAAAGCTGGGCTCCAGAGGCCACAGAAAGCCATCCCCGACCTTGACCAAAAT        | 4520 |
| O | y | 4590 | TCAAGAAAGTCTTTTGACTTCTGTAACACAGACAAAGTTTTGACATATGATCATGTTCT      | 4649 |
| D | b | 4521 | CCAAGGATATGCTTTGATTTGTGTACTCAACAAAGCCTTTGACATTTGATCATGATGCT      | 4580 |
| O | y | 4650 | CATCTGTCTTAAACATGTCACAAATGATGTTGGAAACAGATGACACAGATGATATGTGAC     | 4709 |
| D | b | 4581 | CATCTGCTTAAACATGTCACAAATGATGTTGGAGAACAGACACACAGACAGACAGATGGA     | 4640 |
| O | y | 4710 | TACATTTGTACGATCATATGATGTTGTCATTTGTCATTTACTGAGAGATGTAAT           | 4769 |
| D | b | 4641 | GAACTATCTTAACTGATTAATATGATGATCTTTGATCTTCTTCACTCTTCACTCGGAGTGTGCT | 4700 |
| O | y | 4770 | GAACTCATCTCTCTAGCCCATTAATTTTACCATGATGATGAAATATTTTGATTTTGT        | 4829 |
| D | b | 4701 | CAAAATGTTTGCCTTAGACACACACACACACATTCACCATTTGGTGGAACATCTTGACTTGT   | 4760 |
| O | y | 4830 | GGTGTCAATCTCTCCATGTGTAGTATGTTTCTTGCCGAGCTGATAGAAAATTTTGT         | 4889 |
| D | b | 4761 | GGGTGCATCTCTCCATGTGTAGTATGTTTCTTGCCGATATCATGAGAAAGTACTTGT        | 4820 |
| O | y | 4890 | GTCCTTACCTCTTCCGAGTATGTCGTGTGTAGATTTGGCGAATCCTAGTCTGAT           | 4949 |
| D | b | 4821 | CTCCCCAACCCCTAATTCGAGTATTCGAGTATGCGATGGCCGATTTGGCGCATCTTGCTGAT   | 4880 |
| O | y | 4950 | CAAGAGACAAAGGGGATCCGACAGCTGCTTGTGTTGATGATGCTTCCTCGGTT            | 5009 |
| D | b | 4881 | CAAGGCGCCAAAGGATCCGACACTGTGCTTTGCTGTATGATGTGCTGGCCCGCT           | 4940 |
| O | y | 5010 | GTTTAACTGCGGCTCTACTCTTCTCTAGTCAATGTTCACTACGCAATCTTTGGGATGTC      | 5069 |
| D | b | 4941 | GTTCAACATCGGCTCTGCTCTCTCTCTCGCATGTTCAATCTTCCATTTTGGCATGTC        | 5000 |
| O | y | 5070 | CAACTTGGCCTATGTTAAAGGAAATTTGGATCGATGACATATTCAACTTAGACCTT         | 5129 |
| D | b | 5001 | CAACTTGGATACGTAAAGACAGAGCCCGCATTTGAGACATATTCAACTTCGAGACATT       | 5060 |
| O | y | 5130 | TGGCAGACAGATGATGCTGCTATTCGAAATTTACAACTGCTGGCTGGGATGGATGCT        | 5189 |
| D | b | 5061 | TGGCAGACAGATGATGCTGCTATTCGAAATTCGAAATGCTGGCTGGGATGGCTGCT         | 5120 |
| O | y | 5190 | AGCACCATCTTCCACAGTAAAGCCACCCGACTGTGACCCCTAATAAAGTTAAACCTGGAG     | 5249 |
| D | b | 5121 | GGTGCACATCTGTAACCG --- CCCCCGTGACTGAGGATTTGACAAAGACCAAGGAG       | 5177 |
| O | y | 5250 | CTCAGTTAAAGGAGACTGTGTGGAAACCATATGTTGCAATTTTCTTTTGTCAATTCAAT      | 5309 |
| D | b | 5178 | TGGCTTCAAAAGGGGAGACTGTGTGGAAACCCCTCGGTGGGCAATCTTCTTGTGTAGCTACAT  | 5237 |





|   |      |   |      |
|---|------|---|------|
| D | 2061 | GAACCGCTCGCCCAAGCGCTACCTGATCTGAGGATGCTGCTCCCGCTGCTGGATGTCATCA   | 2120 |
| Q | 2274 | ACATGTTGTCAACCTGGTGTGTGATGGACCCATTTGTTGACCTGGCCATCACACTGTAT     | 2333 |
| D | 2121 | GCAGGAGATGAAGTTGGTGTGTCATVGAACCCGTTTACTGACCTCACACATCATGTGCAT    | 2180 |
| Q | 2334 | TGCTTAATATCTTTTTCATGGCCATGGACATCTATCATATGACGAGCACTTCAATA        | 2393 |
| D | 2181 | CGTACTCAACACACTCTTCTCATGGCCGTGGAGCATCAACATGACAACTGTATCGAGGA     | 2240 |
| Q | 2394 | TGTGCTACAGTAGAAGAACTTGGTTTCTACCTGGGATCTTTACAGCAAAATGTTCTGAA     | 2453 |
| D | 2241 | GATGCTGAGAGTGGGAAACCTGGTCTTTCACAGGGAATTTTCAACAGAGATGACCTTAA     | 2300 |
| Q | 2454 | AATTAATGCCATVGAATCTTACTATTAATTTCCAAAGAGCGTGAATATCTTTGACGTTT     | 2513 |
| D | 2301 | GATCATTTGCCCTGACACCCCTACTACTATCTTCCAAAGAGCGTGAATATCTTTGACGTTT   | 2360 |
| Q | 2514 | TATTTGACGTTTGGCTGGTAAACTTGGACCTGGCATGTGGAAAGATTATCTGTTCT        | 2573 |
| D | 2361 | CATGCTCAATCTTTGACCTCTATGAGAGCTGGGCCCTGTCCGCATGACCAACTTGTCCGCTCT | 2420 |
| Q | 2574 | CGGTTCATTTTGGATTTGGCTGGAGATTTTCAAATTTGGCAAAATCTTGGCCAACTTAAATAT | 2633 |
| D | 2421 | GCGCTCTTTCGGCTGCTGCGGGGTCTTCAAGCTGGCCAAATATGAGCCACCTTCACAC      | 2480 |
| Q | 2634 | GCTAATAAAGATCATCCGCAATTCCTGCGGGCTCGGGAATTTAAACCTGCTTGGC         | 2693 |
| D | 2481 | ACTATCAAGATCATCTGGGAACCTAGTGGGGGACATGGGGAACCTGACCTGTCTAGC       | 2540 |
| Q | 2684 | CATCATGCTCTTCAATTTTGGCTGGTGGCATGACGCTCTTGGTAAAGCTACAAAGA        | 2733 |
| D | 2541 | CATCATGCTCTTCAATTTTGGCTGGTGGCATGACGCTCTTGGTAAAGCTACAAAGA        | 2600 |
| Q | 2754 | TTTGCTCGCAAGATGCGCAAGTATGTTCAACCTCCAGCGCTGGCAATGAATGACTCT       | 2813 |
| D | 2601 | GCTGAGGAGCAGCACTGAGC-----CTGCTGCTGCTGCTGGCAATGATGACTTCTT        | 2654 |
| Q | 2814 | CCACTCTTCTCTGAATTTGTTCGCGCTGCTGTGGGAGTGCATAGACCATGTGGGA         | 2873 |
| D | 2655 | TCAATCCCTTCTTATTCATCTTCCGCAATCCCTGTGAGAGTGAATGAGAACCATGTGGGA    | 2714 |
| Q | 2874 | CTGTATGGAAGTCTCTGATCAAGCATGTGCTTACTGTCTTCATGATGATGATGAT         | 2933 |
| D | 2715 | CTGCAATGAGGTGTGCGGGGAGTCAATATCCGTGCTGCTTCTTCTGTTAATGATAT        | 2774 |
| Q | 2934 | TGGAACTACTGGTCCGTAATCTCTTTCGGCGCTTGTGTGAGCTCAATTAAGTCGA         | 2993 |
| D | 2775 | TGGCACTTGTGTGCTCGAATCTCTTCTCTGCGCTTGTGTGAGCTCAATTAAGTCGA        | 2833 |
| Q | 2994 | CAACCTTCACACCATGATGATGATTAATGAATGAATATCTCAAAATGCTGTGATAG        | 3053 |
| D | 2835 | CAACTTCACACCATGATGATGATTAATGAATGAATGAATGAATGAATGAATGAATGAAT     | 2894 |
| Q | 3054 | GATGCTCAAAAGAGTACGTTATGTGAAAGAAATATATGATTTATTAACACTCTT          | 3113 |
| D | 2895 | CATTCAGAGGGGCTCTGGCTTTTTCACAGCGACACCTGGGATTTCTGCTGTGCTCT        | 2954 |
| Q | 3114 | CATTGAGAAAGAAATTTAGTGTGAATTAACACATGATGATCTTAAACAAAGAA           | 3173 |
| D | 2955 | GCGGCAAGGCTCTCAAGAACCCCGAGCCTTGGCCGACAGGCGCACTCCCACTGCTAT       | 3014 |
| Q | 3174 | AGACAGTTGATATGTCATATCAATCAACAGAAATTTGGGAAAGATCTGATCTTAAAGA      | 3233 |
| D | 3015 | TGCCACCCCTCACTCTCCCGCACCCCGAGAGAGAGAGTGTCTCCACCCGGAAGA          | 3074 |
| Q | 3234 | -----TGT  | 3233 |
| D | 3075 | AACACAGTTGAGAAAGCGCAGCAACACAGCGCACCGCCCGGAGATCCAGAACCCGT        | 3134 |
| Q | 3237 | AAATGGAATCAATAGTGTATATAGAACTGGCAGACAGTGTGAAATATATATATATGATGA    | 3296 |
| D | 3135 | GTGTGTGCCATCTGCTGTGGCGAGTCAAGACACAGATGACCAAGAAAGATGAGAGAGA      | 3194 |

|    |      |  |      |
|----|------|--|------|
| 0Y | 3297 | AAGGATTAATCAATG-----TCAATTATATAACAAACCCAGCTTACTGTGACTG           | 3343 |
| Db | 3195 | CAGCCTGGGACCGGAGGAGGAGTCCAGACAGACAGAGAAATCCAGCCTGTGTCCGGCTG      | 3254 |
| 0Y | 3344 | TACCAATTCGCTGTGGAGAACTGTGACTTTGAA-----                           | 3375 |
| Db | 3255 | GCCCAAGAGCCCTCCGGATTCCAGAACCTGTGAGCCAGGTGTACAGCACTGCCCTCTCGA     | 3314 |
| 0Y | 3376 | -----AATTTAAACACGGAAAGACTTTAGTAGTG--AATCGATCTGGAGA               | 3419 |
| Db | 3315 | GCCCGAGGCCAGTGCATCTCAGGCCGACGTGGGGGCGAGCATGTGAAAGCGGAACCCACGAC   | 3374 |
| 0Y | 3420 | AAGCAAAAGAAACTGATATATAAAGACAGTACGTCTATCAGAAAGGTACACTGTGTGACAT--- | 3476 |
| Db | 3375 | CCCAAGGTGCGGTGAGACCCCAAGAGACAGATGTCTCCGAGGCGACACAGCAGACAGCATAC   | 3434 |
| 0Y | 3477 | ---GGGGCAGACTGTATACAAACAGGCCGAGTAGGAACTGGAAGAACTCTTGAAACCGA      | 3533 |
| Db | 3435 | CACACACCGCTAGCTCCTGGAGACAGATCCCTGACTCGGGCCAGGATGTCAAGGACCCAGA    | 3494 |
| 0Y | 3534 | AGCTTGTTCACCTAGAACGCTGTGTACAAAGATTCAGATGTGTCAATCAATGTGGAGA       | 3593 |
| Db | 3495 | GGAATCGTCTACCTGAAGCGTGTGTCCGGGGCTGTCCCTCTGTGGGGGTGAACACACACA     | 3554 |
| 0Y | 3594 | AGGCAGAGAAACATAGTGTGAACCTGAGAGAGACGTGTTCGCAATATGTTGAACATPA       | 3653 |
| Db | 3555 | GGCCCCAGGGAAGGTGTGCGGGGGGTGGCGCAAGACCTCTACCAACATCTGTGAGACAG      | 3614 |
| 0Y | 3654 | CTGTGTGAGACCTTCAATTTTTCATGATTCCTCTATAGTGCTCTGGCATTTGA            | 3713 |
| Db | 3615 | CTGGTTCAGACATTCATCACTTCATGATTCCTACACACAGCTGAGCGCTGGCTTGA         | 3674 |
| 0Y | 3714 | AGATATATATATATATATACGAAAGAGATTAAGACAGTGTGGAATATCTGACAGAGT        | 3773 |
| Db | 3675 | GGACATCTACTTAAGAGAGCGGGAAGACATCAAGGTCTTCTGTGAGTATGCGGACAAAGT     | 3734 |
| 0Y | 3774 | TTTCACATTCATTTTCATTTCTGTGAAATGCTTCTMAAATGGGTGGCATATAGCTATCAAC    | 3833 |
| Db | 3735 | GTTCACATATGTCCTGCGTGGAGATGCTGTCAAGTGGGTGGCCCTACGGCTTCAAGA        | 3794 |
| 0Y | 3834 | ATATTTTACCAATGCTCGTGGTGTGGCTGGACCTCTTAATGTGTGATGTTTCAATTTGTG     | 3893 |
| Db | 3795 | GTACTTTCACAAATGCTGCGTGGTGTGGCTGGACCTTCCATCTGAGAGCTCTCTGTGTAG     | 3854 |
| 0Y | 3894 | TTTAAACACAAATGCTTGGGTTACTGAGAACTTGGAGCATCAAAATCTCTCAGAGACT       | 3953 |
| Db | 3855 | CCTGGTGGCCAAACCTCGGGCTTTGCCGAGATGGGCCCATCAATGACTCTCGGACGCT       | 3914 |
| 0Y | 3954 | AAGACCTCTGAGACCTCTAAGAGCCTTATCTGATTTGAAGGAGTAGGGGTGTGNA          | 4013 |
| Db | 3915 | GGGTCACTCGTCCTCTGAGAGCTGTGCACATTTGAAGGCAATGAGGAGTGGTGTCAA        | 3974 |
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| Db | 3975 | TGCCCTGTGGCGCATCCCGTCAATCAAGAAAGCTCTCTGCTGTCTCATATTTCTG          | 4034 |
| 0Y | 4074 | GCTAATTTTTCAGATCAATGGGCGTAAATTTGTTGTGGCAATTTCTACACTGTATTAA       | 4133 |
| Db | 4035 | GCTCATCTTCACATCATGGGCGTGAACCTCTTTCGGGGGAAGTTTGGGAGGTGCATCAA      | 4094 |
| 0Y | 4134 | CACCAACAATGCTGTGACAGGTTTGCATCGAAGACGTGAATTAATCATATGATTGCTTAA     | 4193 |
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| 0Y | 4194 | ACTAATFACAAAGAAATGAGACTGCTGCATGGAATAATGTGAAGTAACTTTGATATGT       | 4253 |
| Db | 4155 | GTCTTGTGAATCTTGACCGGAGAAATGTACTGACCAAGGTGAAGATCACTTTGACAAAGT     | 4214 |
| 0Y | 4254 | AGGATTTGGGATATGCTCTTTGCTGTAAGTTGGCAATTCAAAGATGAGATGATATAT        | 4313 |
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 DB 5772 GATGAGTGTATCCAGAAATGTGAAGTCCAGCTTGAAGTATGAGAAAGTCTGTA 5831

RESULT 15  
 US-08-836-325-1  
 ; Sequence 1, Application US/08836325  
 ; Patent No. 6110672  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mandel, Gail  
 ; APPLICANT: Halepoua, Simon  
 ; APPLICANT: Borden, Laurence A.  
 ; TITLE OF INVENTION: Peripheral Nervous System Specific  
 ; TITLE OF INVENTION: Sodium Channels, DNA Encoding Thereof, Crystallization,  
 ; TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational  
 ; TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Use  
 ; NUMBER OF SEQUENCES: 19  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
 ; STREET: 1100 New York Ave., N. W., Suite 600  
 ; CITY: Washington  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20005-3934  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; OPERATING SYSTEM: IBM PC compatible  
 ; SOFTWARE: Patent Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/836,325  
 ; FILING DATE: 2-MAY-1997  
 ; CLASSIFICATION: 514  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US95/14251  
 ; FILING DATE: 02-NOV-1995  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/482,401  
 ; FILING DATE: 07-JUN-1995  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/334,029  
 ; FILING DATE: 02-NOV-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Ludwig, Steven R.



Db 1853 ACTTCCTGGGGTGGGAACATTTTGTATTTTGTGGAGATCTCTCCATGTTGGAA 1912  
 Oy 4856 TGTTCCTGGCGAGTGAATGAAGAATTTGTCGCCCTTACCTGTTCCGATGTC 4915  
 Db 1913 TGTTCCTGGCGAGTGAATGAAGAATTTGTCGCCCTTACCTGTTCCGATGTC 1972  
 Oy 4916 GTTCCTGAAGATGGCCGAATCTTACGTCGTATCAAGAGCAAGAGGATCCGACGC 4975  
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 Job time : 215 secs

GenCore version 5.1.4.P5.4578  
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OM nucleic - nucleic search, using sw model

Run on: April 22, 2003, 09:58:53 : Search time 379 Seconds

(without alignments)  
17312.444 Million cell updates/sec

Title: US-09-930-871-11

Perfect score: 6030  
Sequence: 1 atggagcaaacagctgtgtt.....aaaaagcaaacaggaataa 6030

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 709820 seqs, 544064369 residues

Total number of hits satisfying chosen parameters: 1419640

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database :

Listing first 45 summaries

Published Applications NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/ECT\_NEM\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEM\_PUB.seq:\*
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- 13: /cgn2\_6/ptodata/1/pubpna/US60\_NEM\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score  | Query Match | Length | ID                  | Description       |
|------------|--------|-------------|--------|---------------------|-------------------|
| 1          | 6028.8 | 100.0       | 6030   | US-09-930-871-11    | Sequence 11, Appl |
| 2          | 5952.8 | 98.7        | 5997   | US-09-930-871-1     | Sequence 1, Appl  |
| 3          | 5915.8 | 98.1        | 5922   | US-09-930-871-13    | Sequence 13, Appl |
| 4          | 5839.8 | 96.8        | 5889   | US-09-930-871-3     | Sequence 3, Appl  |
| 5          | 4336.8 | 71.9        | 4362   | US-09-930-871-15    | Sequence 15, Appl |
| 6          | 4260.8 | 70.7        | 4329   | US-09-930-871-5     | Sequence 5, Appl  |
| 7          | 4150.8 | 68.8        | 4179   | US-09-930-871-17    | Sequence 17, Appl |
| 8          | 4074.8 | 67.6        | 4146   | US-09-930-871-7     | Sequence 7, Appl  |
| 9          | 4057.8 | 67.3        | 4197   | US-09-930-871-9     | Sequence 9, Appl  |
| 10         | 3981.8 | 66.0        | 4164   | US-09-930-871-19    | Sequence 19, Appl |
| 11         | 3563.8 | 59.1        | 6822   | US-09-917-800A-1604 | Sequence 1604, Ap |
| 12         | 1907.2 | 31.6        | 6048   | US-09-896-994-1     | Sequence 1, Appl  |
| 13         | 1907.2 | 31.6        | 6048   | US-09-840-125-3     | Sequence 3, Appl  |
| 14         | 1181   | 19.6        | 1992   | US-09-864-761-10189 | Sequence 10189, A |
| 15         | 1157   | 19.2        | 1194   | US-09-864-761-18334 | Sequence 18334, A |
| 16         | 1141   | 18.9        | 1178   | US-09-864-761-26829 | Sequence 26829, A |
| 17         | 969    | 15.1        | 969    | US-09-864-761-1576  | Sequence 1576, Ap |
| 18         | 346.2  | 5.7         | 347    | US-09-864-761-31970 | Sequence 31970, A |
| 19         | 333.2  | 5.5         | 467    | US-09-864-761-15456 | Sequence 15456, A |

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|----|-------|-----|------|----|---------------------|--------------------|
| 20 | 318.8 | 5.3 | 343  | 10 | US-09-030-4828-17   | Sequence 17, Appl  |
| 21 | 264   | 4.4 | 480  | 10 | US-09-864-761-10615 | Sequence 10615, A  |
| 22 | 262   | 4.3 | 487  | 10 | US-09-864-761-15573 | Sequence 15573, A  |
| 23 | 250.4 | 4.2 | 264  | 10 | US-09-864-761-27235 | Sequence 27235, A  |
| 24 | 249   | 4.1 | 249  | 10 | US-09-864-761-32083 | Sequence 32083, A  |
| 25 | 243   | 4.0 | 249  | 10 | US-09-864-761-32083 | Sequence 32083, A  |
| 26 | 232   | 3.8 | 465  | 10 | US-09-864-761-10437 | Sequence 10437, A  |
| 27 | 172.6 | 2.9 | 304  | 9  | US-10-040-739-10472 | Sequence 10472, Ap |
| 28 | 142   | 2.4 | 5565 | 9  | US-10-029-413A-1    | Sequence 1, Appl   |
| 29 | 139.2 | 2.3 | 473  | 10 | US-09-864-761-1944  | Sequence 1944, Ap  |
| 30 | 139.2 | 2.3 | 473  | 10 | US-09-864-761-13959 | Sequence 13959, A  |
| 31 | 138   | 2.3 | 297  | 10 | US-10-029-413A-3    | Sequence 22921, A  |
| 32 | 136.4 | 2.3 | 6501 | 9  | US-10-029-413A-3    | Sequence 3, Appl   |
| 33 | 117.6 | 2.0 | 472  | 10 | US-09-864-761-6181  | Sequence 6181, Ap  |
| 34 | 115   | 1.9 | 6639 | 10 | US-09-917-800A-1586 | Sequence 1586, Ap  |
| 35 | 114.8 | 1.9 | 142  | 10 | US-09-864-761-20706 | Sequence 20706, A  |
| 36 | 105.2 | 1.7 | 1177 | 12 | US-10-033-026-7     | Sequence 7, Appl   |
| 37 | 105.2 | 1.7 | 7364 | 10 | US-09-954-456-1179  | Sequence 1179, Ap  |
| 38 | 105.2 | 1.7 | 7364 | 12 | US-10-029-413A-11   | Sequence 5, Appl   |
| 39 | 101.8 | 1.7 | 6160 | 9  | US-10-029-413A-11   | Sequence 11, Appl  |
| 40 | 101.8 | 1.7 | 6160 | 9  | US-10-029-413A-13   | Sequence 13, Appl  |
| 41 | 101.8 | 1.7 | 7376 | 12 | US-10-033-026-3     | Sequence 3, Appl   |
| 42 | 98.8  | 1.6 | 142  | 10 | US-09-864-761-30523 | Sequence 30523, A  |
| 43 | 96.6  | 1.6 | 6503 | 10 | US-09-935-541-12    | Sequence 12, Appl  |
| 44 | 94.4  | 1.6 | 6816 | 10 | US-09-935-541-1     | Sequence 1, Appl   |
| 45 | 94.4  | 1.6 | 6855 | 10 | US-09-935-541-3     | Sequence 3, Appl   |

## ALIGNMENTS

Result 1  
US-09-930-871-11  
Sequence 11, Application US/09930871  
Patent No. US20020076780A1  
GENERAL INFORMATION:  
APPLICANT: Turner, C. Alexander Jr.  
APPLICANT: Mathur, Daniel  
TITLE OF INVENTION: No. US20020076780A1 Human Ion Channel Proteins and Polym  
FILE REFERENCE: Same  
CURRENT APPLICATION NUMBER: US/09/930,871  
CURRENT FILING DATE: 2001-08-14  
PRIOR APPLICATION NUMBER: US 60/225,989  
PRIOR FILING DATE: 2000-08-16  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 11  
LENGTH: 6030  
TYPE: DNA  
ORGANISM: homo sapiens  
US-09-930-871-11

Query Match 100.0% Score 6028.8; DB 10; Length 6030;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 6030; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|    |     |   |     |
|----|-----|---|-----|
| QY | 1   | ATGAGCAACAAGTGTGTACACGACGCTGACAGCTTCAACTTCTACACAGAA   | 60  |
| DB | 1   | ATGAGCAACAAGTGTGTGTACACGACGCTGACAGCTTCAACTTCTACACAGAA | 60  |
| QY | 61  | TCTCTGGCGCTATTGAAGAGCGATTCGAGAGAAAGCAAGATCCCAACGAC    | 120 |
| DB | 61  | TCTCTGGCGCTATTGAAGAGCGATTCGAGAGAAAGCAAGATCCCAACGAC    | 120 |
| QY | 121 | AAAAAGATGACGACGAAATGCGCAAGCCAAATAGTACTGGAGCTGGAAGAAC  | 180 |
| DB | 121 | AAAAAGATGACGACGAAATGCGCAAGCCAAATAGTACTGGAGCTGGAAGAAC  | 180 |
| QY | 181 | CTTCAATTTATTTATGAGACATCTCCAGAGATGTTCAAGCCCTGAGAGACTG  | 240 |
| DB | 181 | CTTCAATTTATTTATGAGACATCTCCAGAGATGTTCAAGCCCTGAGAGACTG  | 240 |



|    |      |   |      |
|----|------|---|------|
| OY | 241  | GACCCCTACTATATCAATAAGAAAACCTTTTATATGTAATTGAATAAAGCGAAGGCCACATCTTC   | 300  |
| Db | 241  | GACCCCTACTATATATCAATAAGAAAACCTTTTATATGTAATTGAATAAAGCGAAGGCCACATCTTC | 300  |
| OY | 301  | CGGTTCAGTGCAACCTGTGCCTGCPACATTTTTTAACCTCCTTCAATCCTTTAGGAAAAATA      | 360  |
| Db | 301  | CGGTTCAGTGCAACCTGTGCCTGCTGACATTTTAACTCCCTTCAATCCTTTAGGAAAAATA       | 360  |
| OY | 361  | GCTATTAAGAATTTTGGTACATTCATTATTTACAGCATGCTAATATNTGCACTAATTTTGACA     | 420  |
| Db | 361  | GCTATTAAGAATTTTGGTACATTCATTATTTACAGCATGCTAATATNTGCACTAATTTTGACA     | 420  |
| OY | 421  | AACGTGTGTTTATAGAACAAATGATTAACCTCCCTGATGTGGACAAAAATGTAGATACACC       | 480  |
| Db | 421  | AACGTGTGTTTATAGAACAAAGATTAACCTCCCTGATGTGGACAAAAATGTAGATACACC        | 480  |
| OY | 481  | TTCACAGGAATATATACCTTTTGAATACCTATATATAATATATGCAAGGGGATTCGTGTTA       | 540  |
| Db | 481  | TTCACAGGAATATATACCTTTTGAATACCTATATATAATATATGCAAGGGGATTCGTGTTA       | 540  |
| OY | 541  | GAAGATTTTACTTTCTTGGGGATCCATGAGAACCTGGCTCGATTCACGTGCATTAACATTT       | 600  |
| Db | 541  | GAAGATTTTACTTTCTTGGGGATCCATGAGAACCTGGCTCGATTCACGTGCATTAACATTT       | 600  |
| OY | 601  | GCGTAGCTCACAGAGTTTGTGGACCTGGGGCAATGTCTGGGCATPTGAGAAACATACAGATTT     | 660  |
| Db | 601  | GCGTAGCTCACAGAGTTTGTGGACCTGGGGCAANGTCTGGGCATPTGAGAAACATTCAGATTT     | 660  |
| OY | 661  | CTCCGACGATTTGAAGACGATTTTCAGTCAATTCACAGGCGTGAACCAATGTGGAGCCCTG       | 720  |
| Db | 661  | CTCCGACGATTTGAAGACGATTTTCAGTCAATTCACAGGCGTGAACCAATGTGGAGCCCTG       | 720  |
| OY | 721  | ATPCAGAGCTGTGGAAGAGCTCTCAGATGTAAATGTAAATCTGTCTGTCTGTAGCGTA          | 780  |
| Db | 721  | ATPCAGAGCTGTGGAAGAGCTCTCAGATGTAAATGTAAATCTGTCTGTCTGTAGCGSTA         | 780  |
| OY | 781  | TTTGTCTTAATTTGGGCGCAGCTGTTCATGTGAGGCAACCTGAGAAATAATGTATACAAAGG      | 840  |
| Db | 781  | TTTGTCTTAATTTGGGCGCAGCTGTTCATGTGAGGCAACCTGAGAAATAATGTATACAAAGG      | 840  |
| OY | 841  | CCTCCCACACAAATGCTTCTCTTGAGGAAGCAATGATATAGAAAAGAAATATACTGTGATTAAT    | 900  |
| Db | 841  | CCTCCCACACAAATGCTTCTCTTGAGGAAGCAATGATATAGAAAAGAAATAATCTGTGATTAAT    | 900  |
| OY | 901  | AATGSGTACCTTATTAATTAAGAACTGTCTTGAATTTGACTGAGACATATATTCACAAAT        | 960  |
| Db | 901  | AATGSGTACCTTATTAATTAAGAACTGTCTTGAATTTGACTGAGAAATCATATATTCACAAAT     | 960  |
| OY | 961  | TCAAAGTATATCAATTAATTTCTGGAAGGGTTTTTATAGATGCACTATATGTGGAATAGCTCT     | 1020 |
| Db | 961  | TCAAAGTATATCAATTAATTTCTGGAAGGGTTTTTATAGATGCACTATATGTGGAATAGCTCT     | 1020 |
| OY | 1021 | GATGACAGGCCAAATGTCCACAGAGGATATATGTGTGTGGAAGCGGTGAGAAATCCCAATAT      | 1080 |
| Db | 1021 | GATGACAGGCCAAATGTCCACAGAGGATATATGTGTGTGGAAGCGGTGAGAAATCCCAATAT      | 1080 |
| OY | 1081 | GCGTACACAAAGCTTGTATACCTTCAGTTGGGCTTTTGTCTCTTGTTCGACTATGACT          | 1140 |
| Db | 1081 | GCGTACACAAAGCTTGTATACCTTCAGTTGGGCTTTTGTCTCTTGTTCGACTATGACT          | 1140 |
| OY | 1141 | CAGAGACTTTCGGGAAAAATCTTTATATCAATGACATTAATGCTGTCTGGGAAAAACGTACATG    | 1200 |
| Db | 1141 | CAGAGACTTTCGGGAAAAATCTTTATATCAATGACATTAATGCTGTCTGGGAAAAACGTACATG    | 1200 |
| OY | 1201 | AATATTTTGTGTGGTGCATTTCTTGGGCTCATCTTCACATTAATTAATTTGATCTCGCT         | 1260 |
| Db | 1201 | AATATTTTGTGTGGTGCATTTCTTGGGCTCATCTTCACATTAATTAATTTGATCTCGCT         | 1260 |
| OY | 1261 | GTGTGGCATGGCTCTACGAGGAACAGAAATCAGGCCACCTTGGAAAGAACAGAACAGAA         | 1320 |
| Db | 1261 | GTGTGGCATATGGCTCTACGAGGAACAGAAATCAGGCCACCTTGGAAAGAACAGAACAGAA       | 1320 |

|    |      |  |      |
|----|------|--|------|
| QY | 1321 | GAGGCCGAATTTTCAGCAGATGATTTGAACACGCTTTAAAAGCACAGAGGACGACTCAGCAG | 1380 |
| DB | 1321 | GAGGCCGAATTTTCAGCAGATGATTTGAACACGCTTTAAAAGCACAGAGGACGACTCAGCAG | 1380 |
| QY | 1381 | GCAGCAACGGCAACGCGCTCCAGAACATTTCCAGAGAGCCAGTGCACACGAGGACGCGTCGA | 1440 |
| DB | 1381 | GCAGCAACGGCAACGCGCTCCAGAACATTTCCAGAGAGCCAGTGCACACGAGGACGCGTCGA | 1440 |
| QY | 1441 | GACAGCTCATCTGGAAGCCTCTAAGTTGATTTCCAAAGTGTCTTAAGGAAGAAAGAAATGCG | 1500 |
| DB | 1441 | GACAGCTCATCTGGAAGCCTCTAAGTTGATTTCCAAAGTGTCTTAAGGAAGAAAGAAATGCG | 1500 |
| QY | 1501 | AGGAAGAAAAGAAAAACAGAAAAGACAGCTGTGTGGGGAGAGAAAGATGAGATGAATTC    | 1560 |
| DB | 1501 | AGGAAGAAAAGAAAAACAGAAAAGACAGCTGTGTGGGGAGAGAAAGATGAGATGAATTC    | 1560 |
| QY | 1561 | CAAAAATCTGAATCTGAGAGACAGATCAGAGAGAAAGGTTTTCGCTTCCCAATTAAGGG    | 1620 |
| DB | 1561 | CAAAAATCTGAATCTGAGAGACAGATCAGAGAGAAAGGTTTTCGCTTCCCAATTAAGGG    | 1620 |
| QY | 1621 | AACCAATTCAGATATATGAAAAAGAGTACTCTCCGCCACACAGCTTTGTGTGACATCCGT   | 1680 |
| DB | 1621 | AACCAATTCAGATATATGAAAAAGAGTACTCTCCGCCACACAGCTTTGTGTGACATCCGT   | 1680 |
| QY | 1681 | GCGTCCCTAATTTTCACCAAGCGCCAAATAGCAGAAACAAGCCTTTTCAGCTTTAGAGGGCA | 1740 |
| DB | 1681 | GCGTCCCTAATTTTCACCAAGCGCCAAATAGCAGAAACAAGCCTTTTCAGCTTTAGAGGGCA | 1740 |
| QY | 1741 | GCAAAAGATGTGGATCTGAGAACGACTTCCAGATGATGACACAGCACCTTTGAGAT       | 1800 |
| DB | 1741 | GCAAAAGATGTGGATCTGAGAACGACTTCCAGATGATGACACAGCACCTTTGAGAT       | 1800 |
| QY | 1801 | AACGAGACCGCTAAGATATCTCTGTGTTGTGTCGCCCGACGACAGGAGAGAGACGAAACGC  | 1860 |
| DB | 1801 | AACGAGACCGCTAAGATATCTCTGTGTTGTGTCGCCCGACGACAGGAGAGAGACGAAACGC  | 1860 |
| QY | 1861 | AACCTGAGTCAGACACGATAGTGCATCCCGAGTCTGTGGAGTGTTCACAGCAATGGCAG    | 1920 |
| DB | 1861 | AACCTGAGTCAGACACGATAGTGCATCCCGAGTCTGTGGAGTGTTCACAGCAATGGCAG    | 1920 |
| QY | 1921 | ATGCACAGCACTGTGGATTCGATAGTGTGTGTTTCTTGTTGTGTGACCTTCAGTTCCT     | 1980 |
| DB | 1921 | ATGCACAGCACTGTGGATTCGATAGTGTGTGTTTCTTGTTGTGTGACCTTCAGTTCCT     | 1980 |
| QY | 1981 | ACATGCGCTGTGGACAGCTCTGCGCAGAGGTATATATGATTAAGCCACTCTGATATAC     | 2040 |
| DB | 1981 | ACATGCGCTGTGGACAGCTCTGCGCAGAGGTATATATGATTAAGCCACTCTGATATAC     | 2040 |
| QY | 2041 | AATGGAACACACACTGAAATCTGAATATGAGAAAGAGAAGTCAAGTCTTTCACAGTTTCC   | 2100 |
| DB | 2041 | AATGGAACACACACTGAAATCTGAATATGAGAAAGAGAAGTCAAGTCTTTCACAGTTTCC   | 2100 |
| QY | 2101 | ATGGACTTCTAGAAAGATCCTTCCCAAGGCAACGACATGAGTATACCGACGACTCTCA     | 2160 |
| DB | 2101 | ATGGACTTCTAGAAAGATCCTTCCCAAGGCAACGACATGAGTATACCGACGACTCTCA     | 2160 |
| QY | 2161 | ACAAATACAGAGAAAGAACTTGAAGATTCAGGACAGAAATGCCACCCCTGTGGATATAA    | 2220 |
| DB | 2161 | ACAAATACAGAGAAAGAACTTGAAGATTCAGGACAGAAATGCCACCCCTGTGGATATAA    | 2220 |
| QY | 2221 | TTTTTCCACATATCTTAATCTGGGACTGTCTTCCATATATTTGGTTAAAAGTGAACATGTT  | 2280 |
| DB | 2221 | TTTTTCCACATATCTTAATCTGGGACTGTCTTCCATATATTTGGTTAAAAGTGAACATGTT  | 2280 |
| QY | 2281 | GTCACACTGGTGTGATGAGACCAATTTGTTGACCTGACCACATCTGATTTGTCTTA       | 2340 |
| DB | 2281 | GTCACACTGGTGTGATGAGACCAATTTGTTGACCTGACCACATCTGATTTGTCTTA       | 2340 |
| QY | 2341 | AATATCTTTTCAAGGGCAGAGAGCACTAACCAATAGAGGACATTTCAATTAATGTCGT     | 2400 |
| DB | 2341 | AATATCTTTTCAAGGGCAGAGAGCACTAACCAATAGAGGACATTTCAATTAATGTCGT     | 2400 |
| QY | 2401 | ACAGTAGGAACATCTGTTTTCACTGGGATCTTTACAGCAAGATGTTTCTGAAATTAATTT   | 2460 |

|||||  
Db 2401 ACAGTAGAAGAACTGGTTTACCTGGGATCTTTACACAGAAATGTTTCGAAATATTT 2460  
OY 2461 GCACATGATCCCTACTTATTTTCCAGAAAGCTGGAAATCTTTGACGGTTTATATGTG 2520  
Db 2461 GCACATGATCCCTACTTATTTTCCAGAAAGCTGGAAATCTTTGACGGTTTATATGTG 2520  
OY 2521 ACCCTTACCTGGTAGAAGCTTGACCTGCAATGTGAGAGATTAATCTGTTCCCTTCA 2580  
Db 2521 ACCCTTACCTGGTAGAAGCTTGACCTGCAATGTGAGAGATTAATCTGTTCCCTTCA 2580  
OY 2581 TTTTCATGCTGGAGAGTTTCAAGTTGGCAAAATCTTGGCCAAAGTTAAATATCTATA 2640  
Db 2581 TTTTCATGCTGGAGAGTTTCAAGTTGGCAAAATCTTGGCCAAAGTTAAATATCTATA 2640  
OY 2641 AAGATCATGGCAATTCCTGGGGGCTCTGAGAAATTTAACTCTGCTTGGCCATATC 2700  
Db 2641 AAGATCATGGCAATTCCTGGGGGCTCTGAGAAATTTAACTCTGCTTGGCCATATC 2700  
OY 2701 GTCTCATTTTGGCCGGTCCGGATGAGCTCTTGTGTAAAGCTTCAAAAGATTTGTC 2760  
Db 2701 GTCTCATTTTGGCCGGTCCGGATGAGCTCTTGTGTAAAGCTTCAAAAGATTTGTC 2760  
OY 2761 TGCAGATTCGCAAGTGAATTTCAACTCCACGCTGGCAATGATGACTTCTTCCACTCC 2820  
Db 2761 TGCAGATTCGCAAGTGAATTTCAACTCCACGCTGGCAATGATGACTTCTTCCACTCC 2820  
OY 2821 TTCCATGATTTGTTCCGGCTGCTGTGGAGATGATAGAGACATGTGGAGCTGTATG 2880  
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OY 2881 GAGGTCTGTGTAAGCATGCTTACTGTCTTCAATGATGATGATGATGATGATGATG 2940  
Db 2881 GAGGTCTGTGTAAGCATGCTTACTGTCTTCAATGATGATGATGATGATGATGATG 2940  
OY 2941 CTAGTGTCTGTAATCTCTTGTGGCTTGTGTGATGATGATGATGATGATGATGATG 3000  
Db 2941 CTAGTGTCTGTAATCTCTTGTGGCTTGTGTGATGATGATGATGATGATGATGATG 3000  
OY 3001 GCAGCCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3060  
Db 3001 GCAGCCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3060  
OY 3061 AAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3120  
Db 3061 AAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3120  
OY 3121 AAGCAAAAGATTTAGATGATGATGATGATGATGATGATGATGATGATGATGATG 3180  
Db 3121 AAGCAAAAGATTTAGATGATGATGATGATGATGATGATGATGATGATGATGATG 3180  
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Db 3181 TGTATGTCCATTCATACACAGAAATTTGGAAAGATCTTGTACTATCTTAAAGATTA 3240  
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Db 3241 GGAAGTCAAGTGTATAGAGAACTGGCAAGCTTTGAAAAATACATTAATGATGAAGT 3300  
OY 3301 GATTATGTCATTCATTAACCAACCCAGCTTCTGTCGATGATGATGATGATGATGATG 3360  
Db 3301 GATTATGTCATTCATTAACCAACCCAGCTTCTGTCGATGATGATGATGATGATGATG 3360  
OY 3361 GAATCTGACTTTGAAAAATTTAAACAGAGAGACTTTAGTAGATGATGATGATGATG 3420  
Db 3361 GAATCTGACTTTGAAAAATTTAAACAGAGAGACTTTAGTAGATGATGATGATGATG 3420  
OY 3421 AGCAAAAGAGAACTGATGATGATGATGATGATGATGATGATGATGATGATGATG 3480  
Db 3421 AGCAAAAGAGAACTGATGATGATGATGATGATGATGATGATGATGATGATGATG 3480  
OY 3481 GCACCTGTAGAAAGACCCGCTAGTGAACCTGAAGAACTCTTGAACCAAGACTTGT 3540  
Db 3481 GCACCTGTAGAAAGACCCGCTAGTGAACCTGAAGAACTCTTGAACCAAGACTTGT 3540

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Db 3481 GCACCTGTAGAAAGACCCGCTAGTGAACCTGAAGAACTCTTGAACCAAGACTTGT 3540  
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OY 3601 GAAAAACAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3660  
Db 3601 GAAAAACAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3660  
OY 3661 GAGACCTTCAATGTTTCAATGATGATGATGATGATGATGATGATGATGATGATGATG 3720  
Db 3661 GAGACCTTCAATGTTTCAATGATGATGATGATGATGATGATGATGATGATGATGATG 3720  
OY 3721 TATATGTAGCGGAAAGAGATTAAGAGATGTTGGAATGATGATGATGATGATGATG 3780  
Db 3721 TATATGTAGCGGAAAGAGATTAAGAGATGTTGGAATGATGATGATGATGATGATG 3780  
OY 3781 TACATTTTCATTCGGAATGCTTCTAAATGGGTGGCATATGCTATCAAAATATTC 3840  
Db 3781 TACATTTTCATTCGGAATGCTTCTAAATGGGTGGCATATGCTATCAAAATATTC 3840  
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Db 3841 ACCAATGCTGTGTGTGCTGACTTCTTAATGTTGATGTTTCAATGCTGATTAACA 3900  
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Db 3901 GCAATGCTGT 3960  
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Db 4021 TTAGAGCAATTCATCATCATGATGATGATGATGATGATGATGATGATGATGATG 4080  
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OY 4141 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4200  
Db 4141 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4200  
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Db 4201 GAAAGAAATGAGACTGCTGATGAAATATGAAAGTAACTTGAATATGATGATGATG 4260  
OY 4261 GGGTATCTCTTCTTCTTCAAGTGTCCACATTTCAAGAGATGATGATGATGATGATG 4320  
Db 4261 GGGTATCTCTTCTTCTTCAAGTGTCCACATTTCAAGAGATGATGATGATGATGATG 4320  
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Db 4321 GCAGTGTATTCAGAAATGATGATGATGATGATGATGATGATGATGATGATGATG 4380  
OY 4381 CTTTACTTGTATTTTCAATCATCTTGTGGTCTTCTTCACTTGAACCTGTTATG 4440  
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OY 4441 GTCATCATGATTAATTTCAACGAGAAAGAAAGTTGAGAGTCAAGACATCTTTATG 4500  
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OY 4501 ACAGAAAGAGAGAAATATGATGATGATGATGATGATGATGATGATGATGATGATG 4560  
Db 4501 ACAGAAAGAGAGAAATATGATGATGATGATGATGATGATGATGATGATGATGATG 4560  
OY 4561 AAGCTATACCTGACACAGAAACAAATTTCAAGAAATGCTTTGACTGTGAACGAG 4620  
Db 4561 AAGCTATACCTGACACAGAAACAAATTTCAAGAAATGCTTTGACTGTGAACGAG 4620

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OY 4621 CAAATTTTGCATAGCATATGCTCATCTGCTTAAACATGTCATCATATGATGCTG 4680
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OY 4741 ATTTGCTATTTACTGAGAGTGTCTACTGAAACATCTCTCTACGCCATATATTTT 4800
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DB 4741 ATTTGCTATTTACTGAGAGTGTCTACTGAAACATCTCTCTACGCCATATATTTT 4800
OY 4801 ACCATTTGATGGAATATTTTGTATTTGTGTTGCTCATCTCTCATTTAGTATGTTT 4860
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DB 4801 ACCATTTGATGGAATATTTTGTATTTGTGTTGCTCATCTCTCATTTAGTATGTTT 4860
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DB 4861 CTTCGCCAGCTGATGAAAGATTTTGTGTCCTTACCTCTGTTCCGAGTATCCGCTTT 4920
OY 4921 GCTAGAGTGGCCGAAATCTACGCTGTATCAAGAGGAAAGGGGATCCGACGCTGTC 4980
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DB 4981 TTTCCTTTGATGATGTCCTCTCTGCTGCTTGTATTAATGCGCTCTCTCTCTAGTC 5040
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DB 5101 ATTCATGACATGTTCAATTTGAGACCTTTGGGCAACAGATGATGCTGCTATCCAAAT 5160
OY 5161 ACAACCTCTGCTGCTGGGATGATGATGCTAGACACCATTTCTCAAGATGACACCCGAC 5220
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DB 5161 ACAACCTCTGCTGCTGGGATGATGATGCTAGACACCATTTCTCAAGATGACACCCGAC 5220
OY 5221 TGTGACCTTAATAAGTTAACCTGGAAGCTCAGTTAAGGAGACTGTGGAAACCATCT 5280
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DB 5221 TGTGACCTTAATAAGTTAACCTGGAAGCTCAGTTAAGGAGACTGTGGAAACCATCT 5280
OY 5281 GTTGGAAATTTCTTTTGTGATGATGATGATGATGATGATGATGATGATGATGATG 5340
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DB 5281 GTTGGAAATTTCTTTTGTGATGATGATGATGATGATGATGATGATGATGATGATG 5340
OY 5341 TACATCGGCTCATCTGAGAACTTCAAGTGTGCTACTGAAAGAAAGTGCAGAGCTCTG 5400
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DB 5341 TACATCGGCTCATCTGAGAACTTCAAGTGTGCTACTGAAAGAAAGTGCAGAGCTCTG 5400
OY 5401 AGTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5460
    |||||||
DB 5401 AGTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5460
OY 5461 CAGTTCAATGAAATTTGAAATTAATCTAGTTTGAAGTGTGCTGAAACCGCTCTCAT 5520
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DB 5461 CAGTTCAATGAAATTTGAAATTAATCTAGTTTGAAGTGTGCTGAAACCGCTCTCAT 5520
OY 5521 CTGCAACAAACAAACAACTCCAGCTCATGCTCATGATTTGCCATGAGTGTGATGCTG 5580
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DB 5521 CTGCAACAAACAAACAACTCCAGCTCATGCTCATGATTTGCCATGAGTGTGATGCTG 5580
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DB 5581 CGGATCCACTGCTGATATCTTATTTGCTTTTACAAAGCGGCTCTAGAGAGAGTGG 5640
OY 5641 GAGATGATGCTCTACGAAATACAGATGGAAGAGGATTCATGCTTCCAAATCTTCAAG 5700
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DB 5761 ATTATTCAGCGTGTATCAGAGCCACCTTTTAAAGCGATGTAAACAGCTTCTT 5820
OY 5821 ACCTACATTTAAACAAATCAAGTGGGCTAATCTTATTAAGAAAGACATGTA 5880
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DB 5821 ACCTACATTTAAACAAATCAAGTGGGCTAATCTTATTAAGAAAGACATGTA 5880
OY 5881 ATTGACAGATTTAAAGAAACCTTATTCAGAAAAAATGATCTGACCATGCACTGCA 5940
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DB 5881 ATTGACAGATTTAAAGAAACCTTATTCAGAAAAAATGATCTGACCATGCACTGCA 5940
OY 5941 GCTTCCACCTCTTATGACCGGGTGACAAAGCCAAATTTGGAAGAAACATGAGCAAGA 6000
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DB 5941 GCTTCCACCTCTTATGACCGGGTGACAAAGCCAAATTTGGAAGAAACATGAGCAAGA 6000
OY 6001 GGCAAGATGAAAGAAAGCCAAAGGAAATPA 6030
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DB 6001 GGCAAGATGAAAGAAAGCCAAAGGAAATPA 6030

RESULT 2
US-09-930-871-1
; Sequence 1, Application US/09930871
; Patent No. US20020076780A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Daniel
; APPLICANT: Mathur, Brian
; TITLE OF INVENTION: No. US20020076780A1el Human Ion Channel Proteins and Polynuci
; FILE REFERENCE: LEX-0216-US
; CURRENT APPLICATION NUMBER: US/09/930,871
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225,989
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 5997
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-930-871-1

Query Match          98.7%; Score 5952.8; DB 10; Length 5997;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 5997; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

OY 1 ATGAGCAAAACAGTCTGTACACACGAGCTGACAGCTTCACTTCTACAGAGAA 60
    |||||||
DB 1 ATGAGCAAAACAGTCTGTACACACGAGCTGACAGCTTCACTTCTACAGAGAA 60
OY 61 TCTCTTGGCGCTATTTGAAAGAGCATTTGCAAGAAAGGCAAAAGATTCACCAAGAC 120
    |||||||
DB 61 TCTCTTGGCGCTATTTGAAAGAGCATTTGCAAGAAAGGCAAAAGATTCACCAAGAC 120
OY 121 AAAAAGATGACAGCAAAATGAGCCAAAGCCAAATATGTAAGTGAAGTGAAGAAAC 180
    |||||||
DB 121 AAAAAGATGACAGCAAAATGAGCCAAAGCCAAATATGTAAGTGAAGTGAAGAAAC 180
OY 181 CTTCATTTATTTATGAGACATTTCTCCAGAGATGATGAGTGTGAGACCTCGTAGAGACTG 240
    |||||||
DB 181 CTTCATTTATTTATGAGACATTTCTCCAGAGATGATGAGTGTGAGACCTCGTAGAGACTG 240
OY 241 GACCCCTACTATATCAATTAAGAAACCTTTTATAGTATGATTAAGGAGGACCATCTTC 300
    |||||||
DB 241 GACCCCTACTATATCAATTAAGAAACCTTTTATAGTATGATTAAGGAGGACCATCTTC 300
OY 301 CGTTCACTGACCACTGCTGCTGTACATTTTAACTCCCTCAATCTCTTAGAGAAATA 360
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Db 301 GGGTTCAGTGGCCACCTGCTCCCTGTACATTTTAACTCCCTTCACTCCCTTGGAAAAA 360  
 Oy 361 GCTATTAAGATTGGTACATTCATTTATTCACATCTCAATTAATGTCACATATTTGACA 420  
 Db 361 GCTATTAAGATTGGTACATTCATTTATTCACATCTCAATTAATGTCACATATTTGACA 420  
 Oy 421 AACTGTGATTATGACATAGTAAACCTCTGATGTCACAAAGAAATGATACATTCACAC 480  
 Db 421 AACTGTGATTATGACATAGTAAACCTCTGATGTCACAAAGAAATGATACATTCACAC 480  
 Oy 481 TTCACAGAAATATATCTTTTGAATCACTTATTAATAAATATGCAAGGGATTCCTTTA 540  
 Db 481 TTCACAGAAATATATCTTTTGAATCACTTATTAATAAATATGCAAGGGATTCCTTTA 540  
 Oy 541 GAAGATTTTACTTCTCTCGGGATCCATGGAAGTGGCTGATTCACATCTCAATTCATTT 600  
 Db 541 GAAGATTTTACTTCTCTCGGGATCCATGGAAGTGGCTGATTCACATCTCAATTCATTT 600  
 Oy 601 GGTGTGTCACAGATTTGTGTGACCTGTGCGCAATGTCTGGCATTTGAGAACATTCAGAGT 660  
 Db 601 GGTGTGTCACAGATTTGTGTGACCTGTGCGCAATGTCTGGCATTTGAGAACATTCAGAGT 660  
 Oy 661 CTCGAGCATTTGAGAACATTTCACTTCATTCAGAGCTGAAACCATTTGGGAGGCTTG 720  
 Db 661 CTCGAGCATTTGAGAACATTTCACTTCATTCAGAGCTGAAACCATTTGGGAGGCTTG 720  
 Oy 721 ATCCAGTCTGTGAGAACATCTCAATGATGATGATCTGATCTGTCTGTCTGAGCCGTA 780  
 Db 721 ATCCAGTCTGTGAGAACATCTCAATGATGATGATCTGATCTGTCTGTCTGAGCCGTA 780  
 Oy 781 TTTGCTCTAATTTGGGCTGAGCTGTTCATGGGCAACCTGAGAAATATATGATATACATG 840  
 Db 781 TTTGCTCTAATTTGGGCTGAGCTGTTCATGGGCAACCTGAGAAATATATGATATACATG 840  
 Oy 841 CCTCCACCAATGCTCTCTCTGAGGAGACATATATAGAAATATATATATCTGATTAAT 900  
 Db 841 CCTCCACCAATGCTCTCTCTGAGGAGACATATATAGAAATATATATATCTGATTAAT 900  
 Oy 901 AATGCTACATTTAATGAAATCTCTGTTGAGTTGACTGAGAGTCAATATATCAAGAT 960  
 Db 901 AATGCTACATTTAATGAAATCTCTGTTGAGTTGACTGAGAGTCAATATATCAAGAT 960  
 Oy 961 TCAATATATCAATTTCTCTGAGGCTTTTATGATGACATCTATGTTGAAATATGCTCT 1020  
 Db 961 TCAATATATCAATTTCTCTGAGGCTTTTATGATGACATCTATGTTGAAATATGCTCT 1020  
 Oy 1021 GATGAGGCAATGTCAGAGGATATATATGTTGAAAGGCTGAGAAATCCCAATTAAT 1080  
 Db 1021 GATGAGGCAATGTCAGAGGATATATATGTTGAAAGGCTGAGAAATCCCAATTAAT 1080  
 Oy 1081 GGTCTACACAAAGCTTGTATACCTTCAGTTGGGCTTTTGTCTCTGTTTCGATTAATGACT 1140  
 Db 1081 GGTCTACACAAAGCTTGTATACCTTCAGTTGGGCTTTTGTCTCTGTTTCGATTAATGACT 1140  
 Oy 1141 CAGGACTCTGAGGAAATCTTATATCACTGACATTCAGTGTCTGAGGAAACGTAATG 1200  
 Db 1141 CAGGACTCTGAGGAAATCTTATATCACTGACATTCAGTGTCTGAGGAAACGTAATG 1200  
 Oy 1201 AATATTTTGTGTTGCTATTTCTTGGGCTCATTTCTACCTAATTAATTTGATCTGGCT 1260  
 Db 1201 AATATTTTGTGTTGCTATTTCTTGGGCTCATTTCTACCTAATTAATTTGATCTGGCT 1260  
 Oy 1261 GTGTGTCATGCTGCTACAGAGAACATACAGTCCAGCTTGGAGAGACAGAACAGAA 1320  
 Db 1261 GTGTGTCATGCTGCTACAGAGAACATACAGTCCAGCTTGGAGAGACAGAACAGAA 1320  
 Oy 1321 GAGGCGCAATTTGACAGATGATTTGACAGCTTAAAGAAACAGAGGAGGAGCTACAG 1380  
 Db 1321 GAGGCGCAATTTGACAGATGATTTGACAGCTTAAAGAAACAGAGGAGGAGCTACAG 1380  
 Oy 1381 GCAGCAAGGCAATGCTGCTGAGAACATTCAGAGAGGAGGAGGAGGAGGCTGCTCA 1440  
 Db 1381 GCAGCAAGGCAATGCTGCTGAGAACATTCAGAGAGGAGGAGGAGGAGGCTGCTCA 1440

Db 1381 GCAGCAAGGCAATGCTGCTGAGAACATTCAGAGAGGAGGAGGAGGAGGCTGCTCA 1440  
 Oy 1441 GACAGCTCATCTGAGAGCTCTTAAGTTGAGTTCCAGAGAGTCTTAAGAGAAAGAAATCGG 1500  
 Db 1441 GACAGCTCATCTGAGAGCTCTTAAGTTGAGTTCCAGAGAGTCTTAAGAGAAAGAAATCGG 1500  
 Oy 1501 AGGAG 1560  
 Db 1501 AGGAG 1560  
 Oy 1561 CAATAATCTGAATCTGAG 1620  
 Db 1561 CAATAATCTGAATCTGAG 1620  
 Oy 1621 AACCGATTGACATATGAAAAAGAGTCTCTCCACACAGCTTTGTTGAGCATTCG 1680  
 Db 1621 AACCGATTGACATATGAAAAAGAGTCTCTCCACACAGCTTTGTTGAGCATTCG 1680  
 Oy 1681 GGTCTCCATTTTTCACCAAGGCGAATATGACAGAACAGAGCTTTTACAGAGGCGA 1740  
 Db 1681 GGTCTCCATTTTTCACCAAGGCGAATATGACAGAACAGAGCTTTTACAGAGGCGA 1740  
 Oy 1741 GCAAGAGATGAGGATCTGAGAACAGAGCTTCGAGATGATGAGACAGACCTTTGAGAT 1800  
 Db 1741 GCAAGAGATGAGGATCTGAGAACAGAGCTTCGAGATGATGAGACAGACCTTTGAGAT 1800  
 Oy 1801 AACGAGAGCGGTAGAGATTCCTGTTGTTGTCGCCGAGACAGAGAGAGAGAGAGAGAG 1860  
 Db 1801 AACGAGAGCGGTAGAGATTCCTGTTGTTGTCGCCGAGACAGAGAGAGAGAGAGAGAG 1860  
 Oy 1861 AACCTGATGACAGACAG 1920  
 Db 1861 AACCTGATGACAGACAG 1920  
 Oy 1921 ATGCAAG 1980  
 Db 1921 ATGCAAG 1980  
 Oy 1981 ACATGCGCTGTTGAGACAGCTTCTGCGAGAGGTGATATAGATTAAGCAAGCTACTGATGAC 2040  
 Db 1981 ACATGCGCTGTTGAGACAGCTTCTGCGAGAGGTGATATAGATTAAGCAAGCTACTGATGAC 2040  
 Oy 2041 AATGAGAACACACAGTGAATCTGAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2100  
 Db 2041 AATGAGAACACACAGTGAATCTGAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2100  
 Oy 2101 ATGAGACTTCTGAG 2160  
 Db 2101 ATGAGACTTCTGAG 2160  
 Oy 2161 ACAATATACAGTAG 2220  
 Db 2161 ACAATATACAGTAG 2220  
 Oy 2221 TTTTCCACATATCTTATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2280  
 Db 2221 TTTTCCACATATCTTATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2280  
 Oy 2281 GTCAACCTGTGTGATGAG 2340  
 Db 2281 GTCAACCTGTGTGATGAG 2340  
 Oy 2341 AATACTCTTTTTCATGAG 2400  
 Db 2341 AATACTCTTTTTCATGAG 2400  
 Oy 2401 ACAGTAG 2460  
 Db 2401 ACAGTAG 2460  
 Oy 2461 GGCATGAGATCTTACATATATTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2520  
 Db 2461 GGCATGAGATCTTACATATATTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2520  
 Oy 2487 GGCATGAGATCTTACATATATTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2540  
 Db 2487 GGCATGAGATCTTACATATATTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2540

|    |      |  |      |
|----|------|--|------|
| QY | 2521 | ACGTTTACGCGGTGAGAAACCTGGACACTCGCGCAATGTCGGAAGATTATCTGCTCCGCTTCA      | 2580 |
| Db | 2488 | ACGGTTTACGCGGTGAGAAACCTGGACACTCGCGCAATGTCGGAAGATTATCTGCTCCGCTTCA     | 2547 |
| QY | 2581 | TTTTCGATTTGGCTGGAGATTTCATCAAGTTTGGCAAAATCTTTGGCCAAACCTTTAAATATGCTATA | 2640 |
| Db | 2548 | TTTTCGATTTGGCTGGAGATTTCATCAAGTTTGGCAAAATCTTTGGCCAAACCTTTAAATATGCTATA | 2607 |
| QY | 2641 | AAGATCATTCGGCAATTCGCTGGGGGCTCTGGGAAATTTAACCTTCGCTTGGCCATATC          | 2700 |
| Db | 2608 | AAGATCATTCGGCAATTCGCTGGGGGCTCTGGGAAATTTAACCTTCGCTTGGCCATATC          | 2667 |
| QY | 2701 | GCTCTCAATTTTTGGCGGCGGTGCGGACATGACAGCTTTTGGTAAAAAGCTAACAAAAGATTGGTC   | 2760 |
| Db | 2668 | GCTCTCAATTTTTGGCGGCGGTGCGGACATGACAGCTTTTGGTAAAAAGCTAACAAAAGATTGGTC   | 2727 |
| QY | 2761 | TGCAGAATTCGGCAATTCGCTGGGGGCTCTGGGAAATTTAACCTTCGCTTGGCCATATC          | 2820 |
| Db | 2728 | TGCAGAATTCGGCAATTCGCTGGGGGCTCTGGGAAATTTAACCTTCGCTTGGCCATATC          | 2787 |
| QY | 2821 | TTTCTGATTTGTTCCGCGTCTGTGTGGGAGTGGATPAGAACATGTGGGACTGTATG             | 2880 |
| Db | 2788 | TTTCTGATTTGTTCCGCGTCTGTGTGGGAGTGGATPAGAACATGTGGGACTGTATG             | 2847 |
| QY | 2881 | GAGTTTCATGCTGGTCAAGCATGTCGCTTACATGCTTTCATGATGTCATGTCATGTCGATTTGGAAC  | 2940 |
| Db | 2848 | GAGTTTCATGCTGGTCAAGCATGTCGCTTACATGCTTTCATGATGTCATGTCATGTCGATTTGGAAC  | 2907 |
| QY | 2941 | CTATGCTGCTCTGAATCTCTTTTGGCGCTGCTTMTAGCTCAATTAATAGTCAGACACCTT         | 3000 |
| Db | 2908 | CTATGCTGCTCTGAATCTCTTTTGGCGCTGCTTMTAGCTCAATTAATAGTCAGACACCTT         | 2967 |
| QY | 3001 | GCACCCACTGATGATGATTAATGAAATTAATCTCCAAATTCGCTGGTGGATAGGATGCAC         | 3060 |
| Db | 2968 | GCACCCACTGATGATGATTAATGAAATTAATCTCCAAATTCGCTGGTGGATAGGATGCAC         | 3027 |
| QY | 3061 | AAAGAGTAGCTTATGTAAGAAAGAAAATATATGATTTATTTCAACAGTCCCTCATTTAGG         | 3120 |
| Db | 3028 | AAAGAGTAGCTTATGTAAGAAAGAAAATATATGATTTATTTCAACAGTCCCTCATTTAGG         | 3087 |
| QY | 3121 | AAACAAAAGATTTTATGATGAAATTTAAACCCACTGATGATCTTAAACAAAGAAAGACGT         | 3180 |
| Db | 3088 | AAACAAAAGATTTTATGATGAAATTTAAACCCACTGATGATCTTAAACAAAGAAAGACGT         | 3147 |
| QY | 3181 | TGTATGTCATCTATACARAGAAATTTGGGAAAGATCTTGATCTTAAAGATTAAT               | 3240 |
| Db | 3148 | TGTATGTCATCTATACARAGAAATTTGGGAAAGATCTTGATCTTAAAGATTAAT               | 3207 |
| QY | 3241 | GGAACTACAGTGGTATPAGAGACTGGCAGCAGTGTGAAAATTAATTTATGAGAAAGT            | 3300 |
| Db | 3208 | GGAACTACAGTGGTATPAGAGACTGGCAGCAGTGTGAAAATTAATTTATGAGAAAGT            | 3267 |
| QY | 3301 | GATTATCATGTATCTATPAAACAAACCCAGCTTACGTGACGTACACAAATTCGCTAGGA          | 3360 |
| Db | 3268 | GATTATCATGTATCTATPAAACAAACCCAGCTTACGTGACGTACACAAATTCGCTAGGA          | 3327 |
| QY | 3361 | GAATCTGACTTTGAAAAATTTAAACAGGGAAGACTTTAGTAGTAATCGGATCTGGAGAA          | 3420 |
| Db | 3328 | GAATCTGACTTTGAAAAATTTAAACAGGGAAGACTTTAGTAGTAATCGGATCTGGAGAA          | 3387 |
| QY | 3421 | AGCAAAAGAAACGATPAGAAACAGTAGTCTATCGAAGGTAGAGACTGTGGACATCGGC           | 3480 |
| Db | 3388 | AGCAAAAGAAACGATPAGAAACAGTAGTCTATCGAAGGTAGAGACTGTGGACATCGGC           | 3447 |
| QY | 3481 | GCACCTGTAGAAAGACGCCGTAGTGGAACTCGAAGAAACCTTTGAACCAAGAACTTGT           | 3540 |
| Db | 3448 | GCACCTGTAGAAAGACGCCGTAGTGGAACTCGAAGAAACCTTTGAACCAAGAACTTGT           | 3507 |
| QY | 3541 | TTTCACTGAAGGCTGTGTACAAAGTTTCAATGTGTTCCTCAATCAATGTGGAAAGAGCAGA        | 3600 |
| Db | 3508 | TTTCACTGAAGGCTGTGTACAAAGTTTCAATGTGTTCCTCAATCAATGTGGAAAGAGCAGA        | 3567 |

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|----|------|---|------|
| OY | 3601 | GGAAACAAGSTGGAACTCGAAGAGAGCTGGTTCGGAATGGTGAACATPACTGGTTT      | 3660 |
| Db | 3568 | GGAAACAAGSTGGAACTCGAAGAGAGCTGGTTCGGAATGGTGAACATPACTGGTTT      | 3627 |
| OY | 3661 | GAGACCTTCATGGTTTCATGATTCCTCTAGTAGAGGGCTCTGGCAATTTGAAATATA     | 3720 |
| Db | 3628 | GAGACCTTCATGGTTTCATGATTCCTCTAGTAGAGGGCTCTGGCAATTTGAAATATA     | 3687 |
| OY | 3721 | TATATTGATCAGCAGAAAGAGATTAAAGAGATGGTGGAAATATGCTGACAGGTTTCACT   | 3780 |
| Db | 3688 | TATATTGATCAGCAGAAAGAGATTAAAGAGATGGTGGAAATATGCTGACAGGTTTCACT   | 3747 |
| OY | 3781 | TACATTTTCATTCGGAATAGCTTCTTAAATGGGTGGCATATGGCTATCAACATATTTC    | 3840 |
| Db | 3748 | TACATTTTCATTCGGAATAGCTTCTTAAATGGGTGGCATATGGCTATCAACATATTTC    | 3807 |
| OY | 3841 | ACCAATGCTGGTGTGGCTGGAACTTCCTTAATGGTTGATGGTTCTCAATGGCTAGTTTACA | 3900 |
| Db | 3808 | ACCAATGCTGGTGTGGCTGGAACTTCCTTAATGGTTGATGGTTCTCAATGGCTAGTTTACA | 3867 |
| OY | 3901 | GCAATGCTGGTGGTGTACTAGAACTTGGAGCCATCAATCTCTAGACACTAAGAGCT      | 3960 |
| Db | 3868 | GCAATGCTGGTGGTGTACTAGAACTTGGAGCCATCAATCTCTAGACACTAAGAGCT      | 3927 |
| OY | 3961 | CTGAGACCTCTAAGAGCCTTAATCTCGATTTGAAGGAGTGGGTGTTGTGATGCCCTT     | 4020 |
| Db | 3928 | CTGAGACCTCTAAGAGCCTTAATCTCGATTTGAAGGAGTGGGTGTTGTGATGCCCTT     | 3987 |
| OY | 4021 | TTAGAGCAATTCATCCATCATAGATGTGTCTGTGGTTGTCTATATTCGGCTAATT       | 4080 |
| Db | 3988 | TTAGAGCAATTCATCCATCATAGATGTGTCTGTGGTTGTCTATATTCGGCTAATT       | 4047 |
| OY | 4081 | TTGACGATCATGGGCGTAAATTTGGTTGGCGAAATTTGACACGTATTAACACACA       | 4140 |
| Db | 4048 | TTGACGATCATGGGCGTAAATTTGGTTGGCGAAATTTGACACGTATTAACACACA       | 4107 |
| OY | 4141 | ACTGGTGCAGGTTTGCATCGAAGACGTGAATATCATATCATATGCTTAAACTAATA      | 4200 |
| Db | 4108 | ACTGGTGCAGGTTTGCATCGAAGACGTGAATATCATATCATATGCTTAAACTAATA      | 4167 |
| OY | 4201 | GAAAGAAATGAGACTGCTCGATGGAAAAATGTAAAGTAAACTTTGATATGTAGAGATT    | 4260 |
| Db | 4168 | GAAAGAAATGAGACTGCTCGATGGAAAAATGTAAAGTAAACTTTGATATGTAGAGATT    | 4227 |
| OY | 4261 | GGGATATCTCTTGTGCTTCAAGTTGCCACATTCAAGATGGATGGATATATATGATACA    | 4320 |
| Db | 4228 | GGGATATCTCTTGTGCTTCAAGTTGCCACATTCAAGATGGATGGATATATATGATACA    | 4287 |
| OY | 4321 | GCAGTTGATTCAGAAATGTGGAACTCCAGCCCTAAGTATGAAGAAAGCTGTGACATGTAT  | 4380 |
| Db | 4288 | GCAGTTGATTCAGAAATGTGGAACTCCAGCCCTAAGTATGAAGAAAGCTGTGACATGTAT  | 4347 |
| OY | 4381 | CTTATCTTGTATTTTCATCATCTTTGGGTCTTCTTACCTTGAACCTGTTATTTGGT      | 4440 |
| Db | 4348 | CTTATCTTGTATTTTCATCATCTTTGGGTCTTCTTACCTTGAACCTGTTATTTGGT      | 4407 |
| OY | 4441 | GTCAATCATAGTAAATTTTCAACACAGCAAAAAAAGTTTGGAGGTCAAGACATCTTATG   | 4500 |
| Db | 4408 | GTCAATCATAGTAAATTTTCAACACAGCAAAAAAAGTTTGGAGGTCAAGACATCTTATG   | 4467 |
| OY | 4501 | ACAGAGAACAAGAAATACTATATATGCAATAAAAAATTAGGATCGAAAAACCCGCA      | 4560 |
| Db | 4468 | ACAGAGAACAAGAAATACTATATATGCAATAAAAAATTAGGATCGAAAAACCCGCA      | 4527 |
| OY | 4561 | AAGCTTATCTCGACACAGAAACAATTTCAAGGAATGGTCTTTGACTTGTAAACAGA      | 4620 |
| Db | 4528 | AAGCTTATCTCGACACAGAAACAATTTCAAGGAATGGTCTTTGACTTGTAAACAGA      | 4587 |
| OY | 4621 | CAAGTTTTTGACATTAAGCATATGATTCATCTATGCTTAAATGGTCAACATATGATGTG   | 4680 |
| Db | 4588 | CAAGTTTTTGACATTAAGCATATGATTCATCTATGCTTAAATGGTCAACATATGATGTG   | 4647 |
| OY | 4681 | GAAACAGTATGCAGAGCTGAATGTGACTATCCATTTTCTACGCATCAATTCGTGTTC     | 4740 |



|   |      |  |      |
|---|------|--|------|
| D | 4648 | GAACAGATGACCGAGAGTGAATGTGACATACCATTTTGTCAACGATCAATGTGTTTC      | 4707 |
| Q | 4741 | ATTGTGCTATTTACTGGAGAGTGTGATCGAAATCTCATCTCTACGCCATTATATATTTT    | 4800 |
| D | 4708 | ATTGTGCTATTTACTGGAGAGTGTGATCGAAATCTCATCTCTACGCCATTATATATTTT    | 4767 |
| Q | 4801 | ACCATTCGATGSAATATTTTGTATTTTGTGGTGTGCATCTCTCCATTTGTAGTATGTTT    | 4866 |
| D | 4768 | ACCATTCGATGSAATATTTTGTATTTTGTGGTGTGCATCTCTCCATTTGTAGTATGTTT    | 4827 |
| Q | 4861 | CTTCCGAGCTGATAGAAAAGTATTTTCGTGTCGCCACCTGTCCGAGTATCCGCTTT       | 4920 |
| D | 4828 | CTTCCGAGCTGATAGAAAAGTATTTTCGTGTCGCCACCTGTCCGAGTATCCGCTTT       | 4887 |
| Q | 4921 | GCTAGATTTGGCCGAATCTCACTACGTCTGATCAAAAGAGCAAAAGGAGTCGCAAGCTGCTC | 4980 |
| D | 4888 | GCTAGATTTGGCCGAATCTCACTACGTCTGATCAAAAGAGCAAAAGGAGTCGCAAGCTGCTC | 4944 |
| Q | 4981 | TTTTCCTTTGATGATGTGTCCTCTCGGTGTTTAATATGGGCTCTACTCTCTATCTC       | 5044 |
| D | 4948 | TTTTCCTTTGATGATGTGTCCTCTCGGTGTTTAATATGGGCTCTACTCTCTATCTC       | 5007 |
| Q | 5041 | ATGTTCATCTACGCGCATCTTGGGATGTCCAACTTGGCTATGTTAAAGGGGAACTGTGG    | 5100 |
| D | 5008 | ATGTTCATCTACGCGCATCTTGGGATGTCCAACTTGGCTATGTTAAAGGGGAACTGTGG    | 5066 |
| Q | 5101 | ATCGATGACATGTTCACATTTTGGACCTTTGGCAACAGCATGATGTGCTATTCCAAAT     | 5160 |
| D | 5068 | ATCGATGACATGTTCACATTTTGGACCTTTGGCAACAGCATGATGTGCTATTCCAAAT     | 5127 |
| Q | 5161 | ACAACCTCTGCTGCTGGATGGAATGTCTAGACACCATTTCTCAACAGTAAAGCACCCGAC   | 5220 |
| D | 5128 | ACAACCTCTGCTGCTGGATGGAATGTCTAGACACCATTTCTCAACAGTAAAGCACCCGAC   | 5187 |
| Q | 5221 | TGTACCCCTATAAAGTTAACCTCGGAAGTCAGTAAAGGAGACGTGGGAAACCATCT       | 5280 |
| D | 5188 | TGTACCCCTATAAAGTTAACCTCGGAAGTCAGTAAAGGAGACGTGGGAAACCATCT       | 5247 |
| Q | 5281 | GTGTGGAATTTTCTTTTGTCACTATCAATCATATATCCCTGCTGGTGTGGTGAACATG     | 5340 |
| D | 5248 | GTGTGGAATTTTCTTTTGTCACTATCAATCATATATCCCTGCTGGTGTGGTGAACATG     | 5307 |
| Q | 5341 | TACATCGCGGTCACTCTGGAACTTCAGTGTGTCTACTGAAGAAAGTGCAGAGCCTCTG     | 5400 |
| D | 5308 | TACATCGCGGTCACTCTGGAACTTCAGTGTGTCTACTGAAGAAAGTGCAGAGCCTCTG     | 5367 |
| Q | 5401 | AGTAGAGATGACTTTGAGATGTTCTATGAGGTTTGGGAAATTTGATCCGATGCACT       | 5466 |
| D | 5368 | AGTAGAGATGACTTTGAGATGTTCTATGAGGTTTGGGAAATTTGATCCGATGCACT       | 5427 |
| Q | 5461 | CAGTTTCATGGAATTTGAAAAATATATCAATTTGGACGTGCGCTTGAACCGGCTCTCAAT   | 5520 |
| D | 5428 | CAGTTTCATGGAATTTGAAAAATATATCTCAATTTGGACGTGCGCTTGAACCGGCTCTCAAT | 5487 |
| Q | 5521 | CTCGCACCAACCAAAACAACTCCAGCTCATTTGCCATGGATTTGCCATGGTAGTGGTAGC   | 5580 |
| D | 5488 | CTCGCACCAACCAAAACAACTCCAGCTCATTTGCCATGGATTTGCCATGGTAGTGGTAGC   | 5547 |
| Q | 5581 | CGGATCCAGCTGTCTGATATCTTATTTGCTTTTACAAACGGGGTCTAGAGAGAGTGA      | 5640 |
| D | 5548 | CGGATCCAGCTGTCTGATATCTTATTTGCTTTTACAAACGGGGTCTAGAGAGAGTGA      | 5607 |
| Q | 5641 | GAGATGATGCTCTACGAATACAGATGGAAGAGACGATTCATGGCTTCCAAATCCCTTCAAG  | 5700 |
| D | 5608 | GAGATGATGCTCTACGAATACAGATGGAAGAGACGATTCATGGCTTCCAAATCCCTTCAAG  | 5667 |
| Q | 5701 | GTCCTCATACGCCAATCACTACTACTTTTAAACGAAAAACAAGAGATATCTCTGTCTC     | 5766 |
| D | 5668 | GTCCTCATACGCCAATCACTACTACTTTTAAACGAAAAACAAGAGATATCTCTGTCTC     | 5727 |
| Q | 5761 | ATTATTCAGCGTGTCTTACAGAGCCACCTTTTAAAGCAACTGTAAACAGCTTCCTTT      | 5820 |

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Db 5728 ATTATTCAGCGCTGCTTACAGACGCCACCTTTTAAAGGACGACTGTAAAAACAAGCTTCCTT 5787
OY 5821 ACGTCACTATAAAACAAATCAAAAGGTGGCGCTAATCTTTTATATAAAAAGAACATGATA 5880
Db 5788 ACGTCACTATAAAACAAATCAAAAGGTGGCGCTAATCTTTTATATAAAAAGAACATGATA 5847
OY 5881 ATTGACACATATAATGAAGAAACCTATTTACAGAAAAAACTGATCTGCACATGCA 5940
Db 5848 ATTGACACATATAATGAAGAAACCTATTTACAGAAAAAACTGATCTGCACATGCA 5907
OY 5941 GCTGTGCCACCTCTCTATAGACCGGGTGCAAAAGCCAAATTTGTGAAAAACATGACCAAGAA 6000
Db 5908 GCTGTGCCACCTCTCTATAGACCGGGTGCAAAAGCCAAATTTGTGAAAAACATGACCAAGAA 5967
OY 6001 GGCAAAAGATGAAAAAGCCAAAGGGAATATA 6030
Db 5968 GGCAAAAGATGAAAAAGCCAAAGGGAATATA 5997

RESULT 3
US-09-930-871-13
; Sequence 13, Application US/09930871
; Patent No. US20020076780A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Machut, Daniel
; APPLICANT: Machut, Brian
; TITLE OF INVENTION: No. US20020076780A1el Human Ion Channel Proteins and Polynu
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0216-USA
; CURRENT APPLICATION NUMBER: US/09/930,871
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: US 60/225,989
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 5922
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-930-871-13

Query Match 98.1%; Score 5915.8; DB 10; Length 5922;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5917; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGGAGCAAAAGAGTCTGTACACACGAGACGCTGACCTCACTTCTTACCCAGAGAA 60
Db 1 ATGGAGCAAAAGAGTCTGTGTACACACGAGACGCTGACCTTCACTTCTTACCCAGAGAA 60
OY 61 TCTCTGGCGGTATTTGAAGAAGCAGCTTGCAGAGAAAAAGGCAAGAAATCCCAACACAGAC 120
Db 61 TCTCTGGCGGTATTTGAAGAAGCAGCTTGCAGAGAAAAAGGCAAGAAATCCCAACACAGAC 120
OY 121 AAAAAAGATGACGAGAAAAATGCCCCAAAGCCAAATAGTACTTGGAAGCTGGAAGAAC 180
Db 121 AAAAAAGATGACGAGAAAAATGCCCCAAAGCCAAATAGTACTTGGAAGCTGGAAGAAC 180
OY 181 CTTCATTTATTTATGAGAGACATTCCTCCAGAGATGGTGTAGAGCCCCCTGAGAGACCTG 240
Db 181 CTTCATTTATTTATGAGAGACATTCCTCCAGAGATGGTGTAGAGCCCCCTGAGAGACCTG 240
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Db 241 GACCCCTACTATATCAATAAGAAACTTTTATAGATTTGAATTAAGGGAAGGCCATCTTC 300
OY 301 CGGTTCAGTGCACACTCTGCCCTGTACATTTTAACTCCCTCAATCTCTTAGGAAAAATA 360
Db 301 CGGTTCAGTGCACACTCTGCCCTGTACATTTTAACTCCCTCAATCTCTTAGGAAAAATA 360
OY 361 GCTATTAGATTTTGTGTACATTCATTTATTCAGCATGCTAATTAATGTGTGACATTTTGA 420
Db 361 GCTATTAGATTTTGTGTACATTCATTTATTCAGCATGCTAATTAATGTGTGACATTTTGA 420

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OY 421 AACTGTGTATTGACAAATGAGTAACCTCTGATTGACAAAGATGATGATACACC 480  
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Db 421 AACTGTGTATTGACAAATGAGTAACCTCTGATTGACAAAGATGATGATACACC 480  
OY 481 TTCACAGGAATATATCTTTTGAATCACTTATATAAATATATGCAAGGGATTCGTGTTA 540  
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Db 481 TTCACAGGAATATATCTTTTGAATCACTTATATAAATATATGCAAGGGATTCGTGTTA 540  
OY 541 GAAGATTTTACTTCTCTGCGGATTCAGGAACTGGCTGATTTCACTGTCATTACATTT 600  
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Db 541 GAAGATTTTACTTCTCTGCGGATTCAGGAACTGGCTGATTTCACTGTCATTACATTT 600  
OY 601 GGTACGTCACAGAGATTGTGACCTGGGCAATGTCCTGCAATGAGAACATTCAGAGTT 660  
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Db 601 GGTACGTCACAGAGATTGTGACCTGGGCAATGTCCTGCAATGAGAACATTCAGAGTT 660  
OY 661 CTCACGACATTGAAAGCATTTTCATCATTCACGGCTGAAAAACATTTGTGGAGCCCTG 720  
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OY 721 ATCCAGTCTGTGAAGAAGCTCTCAGATGATATGATCTGCTGCTGAGAGCTA 780  
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Db 721 ATCCAGTCTGTGAAGAAGCTCTCAGATGATATGATCTGCTGCTGAGAGCTA 780  
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OY 3721 TATATTGATGACGAAAGCATATGATGATGATGATGATGATGATGATGATGATGATG 3780  
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## RESULT 7

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US-09-930-871-17
; Sequence 17, Application US/0930871
; Patent No. US20020076780A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Daniel
; APPLICANT: Mathur, Brian
; TITLE OF INVENTION: No. US20020076780A1 Human Ion Channel Proteins and Polym
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0216-USA
; CURRENT APPLICATION NUMBER: US/09/930,871
; PRIOR APPLICATION NUMBER: 2001-08-14
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 4179
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-930-871-17

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Query Match 68.8%; Score 4150.8; DB 10; Length 4179;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 ; Patent No. US20020076780A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Turner, C. Alexander Jr.  
 ; APPLICANT: Mathur, Daniel  
 ; APPLICANT: Mathur, Brian  
 ; TITLE OF INVENTION: No. US20020076780A1el Human Ion Channel Proteins and Polym  
 ; TITLE OF INVENTION: Same



FILE REFERENCE: LEX-0216-USA  
CURRENT APPLICATION NUMBER: US/09/930,871  
CURRENT FILING DATE: 2001-08-14  
PRIOR APPLICATION NUMBER: US 60/225,989  
PRIOR FILING DATE: 2000-08-16  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7  
LENGTH: 4146  
TYPE: DNA  
ORGANISM: homo sapiens  
US-09-930-871-7

Query Match 67.6%; Score 4074.8; DB 10; Length 4146;  
Best Local Similarity 99.2%; Pred. No. 0;  
Matches 4149; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

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OY 4141 ACTGATGACAGG 4152  
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RESULT 9  
US-09-930-871-19

Sequence 19, Application us/09930871  
Patent No. US20020076780A1  
GENERAL INFORMATION:  
APPLICANT: Turner, C. Alexander Jr.  
APPLICANT: Mathur, Daniel  
APPLICANT: Mathur, Brian  
TITLE OF INVENTION: No. US20020076780A1 Human Ion Channel Proteins and Polynucleot  
TITLE OF INVENTION: Same  
FILE REFERENCE: LEX-0216-USA  
CURRENT APPLICATION NUMBER: US/09/930,871  
CURRENT FILING DATE: 2001-08-14  
PRIOR APPLICATION NUMBER: US 60/225,989  
PRIORITY FILING DATE: 2000-08-16  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 19  
LENGTH: 4197  
TYPE: DNA  
ORGANISM: homo sapiens  
US-09-930-871-19

Query Match 67.3%; Score 4057.8; DB 10; Length 4197;  
Best Local Similarity 98.5%; Pred. No. 0;  
Matches 4133; Conservative 0; Mismatches 0; Indels 64; Gaps 1;

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2341 AATATCTTTTATGAGGAGAGAGATCTCAATGAGAGGAGGAGGAGGAGGAGGAGGAG 2400  
2401 ACAGTAAAGAACTGTGTTTCACTGGAGCTTTTACAGCAGAAATGTTCTGAAATATAT 2460  
2401 ACAGTAAAGAACTGTGTTTCACTGGAGCTTTTACAGCAGAAATGTTCTGAAATATAT 2460  
2461 GCAATGAGATCTTATATATTTTCAAGAGGCTGGAATATCTTTGAGGAGTTTATGAG 2520  
2461 GCAATGAGATCTTATATATTTTCAAGAGGCTGGAATATCTTTGAGGAGTTTATGAG 2520  
2521 ACCTTAACTGTGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 2580  
2521 ACCTTAACTGTGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 2580

2488 ACCTTAACTGTGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 2547  
2581 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2640  
2581 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2640  
2581 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2640  
2641 AAGATCATGAGCAATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2700  
2641 AAGATCATGAGCAATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2700  
2608 AAGATCATGAGCAATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2667  
2608 AAGATCATGAGCAATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2667  
2701 GTCTTCAATTTTCCCGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2760  
2701 GTCTTCAATTTTCCCGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2760  
2668 GTCTTCAATTTTCCCGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2727  
2668 GTCTTCAATTTTCCCGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2727  
2761 TGCAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2820  
2761 TGCAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2820  
2728 TGCAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2787  
2728 TGCAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2787  
2821 TTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2880  
2821 TTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2880  
2788 TTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2847  
2788 TTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2847  
2881 GAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2940  
2881 GAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2940  
2848 GAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2907  
2848 GAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2907  
2941 CTAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3000  
2941 CTAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3000  
2908 CTAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2967  
2908 CTAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2967  
3001 GCAGCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3060  
3001 GCAGCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3060  
2968 GCAGCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3027  
2968 GCAGCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3027  
3061 AAAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3120  
3061 AAAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3120  
3028 AAAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3087  
3028 AAAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3087  
3121 AAAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3180  
3121 AAAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3180  
3088 AAAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3147  
3088 AAAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3147  
3181 TGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3240  
3181 TGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3240  
3148 TGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3207  
3148 TGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3207  
3241 GGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3300  
3241 GGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3300  
3208 GGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3267  
3208 GGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3267  
3301 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3360  
3301 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3360  
3268 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3327  
3268 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3327  
3361 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3420  
3361 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3420  
3328 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3387  
3328 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3387  
3421 ACAGTAAAGAACTGTGTTTCACTGGAGCTTTTACAGCAGAAATGTTCTGAAATATAT 3480  
3421 ACAGTAAAGAACTGTGTTTCACTGGAGCTTTTACAGCAGAAATGTTCTGAAATATAT 3480  
3388 ACAGTAAAGAACTGTGTTTCACTGGAGCTTTTACAGCAGAAATGTTCTGAAATATAT 3447  
3388 ACAGTAAAGAACTGTGTTTCACTGGAGCTTTTACAGCAGAAATGTTCTGAAATATAT 3447  
3481 GCACTGTGAGAAAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3540  
3481 GCACTGTGAGAAAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3540  
3448 GCACTGTGAGAAAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3507  
3448 GCACTGTGAGAAAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3507  
3541 TTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3600  
3541 TTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3600  
3508 TTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3567  
3508 TTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3567  
3601 GGAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3660  
3601 GGAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3660  
3568 GGAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3627  
3568 GGAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3627





1314 TCAATGGACATTTGTAATGTAACATGAGCACTTCACTGAGAGATATATCGCA 1373  
OY 958 GATTCAAGATATCATATATTTCTGGAGGTTTTTATGACACTCATGTGGAATATAC 1017  
Db 1374 GATACAGATCACTTTATGTGTGTATGAGACAAAATCCCTTACTCTGTGGAATATGAC 1433  
OY 1018 TGTATGAGGCAATGATCCAGAGGATATATGTGTGAAGCTGTGAATATCCCAAT 1077  
Db 1434 TCCATGAGGACATGTCCAGAGAGGTACATCTGTGTGAAGCTGTGAAGACCCCAAC 1493  
OY 1078 TATGCTACACAACTTTGATATCTTCACTTGTGGCTTTTGTCTTTTGTGATGATG 1137  
Db 1494 TACGCTACACAACTTTGATATCTTCACTTGTGGCTTTTGTCTTTTGTGATGATG 1553  
OY 1138 ACTGAGCACTTGTGGGAAATCTTTATGACACTGACATTAAGCTGTGGGAAAGCTAC 1197  
Db 1554 ACTGAGCACTTGTGGGAAATCTTTATGACACTTGTGGGAAAGCTGTGGGAAAGCTAC 1613  
OY 1198 ATGATATTTTGT 1257  
Db 1614 ATGATATTTTGT 1673  
OY 1258 GCTGT 1317  
Db 1674 GCTGT 1733  
OY 1318 AAGAGGCGGATTTTACAGAGATGTATGACACTTAAAGCAAGAGAGAGAGAGAGAG 1377  
Db 1734 AAGAGGCGGATTTTACAGAGATGTATGACACTTAAAGCAAGAGAGAGAGAGAGAG 1793  
OY 1378 ---GAGGAG 1434  
Db 1794 GCAATGCTGT 1853  
OY 1435 CTCTCAGACAGCTCATGTGAAGCCCTTAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1494  
Db 1854 CTCTCAGACAGCTCATGTGAAGCCCTTAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1913  
OY 1495 AATGAGGAG 1551  
Db 1914 AATGAGGAG 1973  
OY 1552 GATGAATTTCCAAATTCGAATTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1611  
Db 1974 GATGAATTTCCAAATTCGAATTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2033  
OY 1612 ATTTGAAGGAG 1671  
Db 2034 CTGATGTGCAACCCGCTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2093  
OY 1672 AGCATCGT 1731  
Db 2094 AGTATCGT 2153  
OY 1732 AGAGGCGAG 1791  
Db 2154 AGAGGCGAG 2213  
OY 1792 TTTTGAAGTAAAG 1851  
Db 2214 TTTTGAAGTAAAG 2273  
OY 1852 CGCAACAG 1911  
Db 2274 CGCAACAG 2285  
OY 1912 AATGGAAGATGACAG 1971  
Db 2286 --- 2285  
OY 1972 TCAGTTCTACATCCCTGT 2031

2286 --- 2285  
OY 2032 ACTGATGACAAATGSAAGAACACCTGTAAGTGAATAGAAAGAGAGAGAGAGAGAGAGAG 2091  
Db 2286 ---GTAACACACACCTGTAAGTGAATAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2333  
OY 2092 CAGCTTTCCAG 2151  
Db 2334 CAGATTTCAATGGAATATGCTGAGAGATTCCTGTGAAGAGAGAGAGAGAGAGAGAGAG 2393  
OY 2152 AGCATTTCAATGGAATATGCTGAGAGATTCCTGTGAAGAGAGAGAGAGAGAGAGAGAG 2211  
Db 2394 AGCATTTCAATGGAATATGCTGAGAGATTCCTGTGAAGAGAGAGAGAGAGAGAGAGAG 2453  
OY 2212 TGTATTAATTTTCCAAATATCTTAAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2271  
Db 2454 TGTATTAATTTTCCAAATATCTTAAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2513  
OY 2272 AATGATTTTCCAAATATCTTAAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2331  
Db 2514 AATGATTTTCCAAATATCTTAAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2573  
OY 2332 ATTTGCTTAAATATCTTAAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2391  
Db 2574 ATTTGCTTAAATATCTTAAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2633  
OY 2392 AATGCTTAAATATCTTAAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2451  
Db 2634 AATGCTTAAATATCTTAAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2693  
OY 2452 AATGCTTAAATATCTTAAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2511  
Db 2694 AATGCTTAAATATCTTAAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2753  
OY 2512 TTTATTTGAG 2571  
Db 2754 TTTATTTGAG 2813  
OY 2572 CTCCGCTTAAATATCTTAAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2631  
Db 2814 CTCCGCTTAAATATCTTAAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2873  
OY 2632 ATGCTTAAATATCTTAAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2691  
Db 2874 ATGCTTAAATATCTTAAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2933  
OY 2692 GGCATCATGCTTCAATTTTCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2751  
Db 2934 GGCATCATGCTTCAATTTTCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2993  
OY 2752 GATGT 2811  
Db 2994 GATGT 3053  
OY 2812 TTTCACTCTTCTGATTTGT 2871  
Db 3054 TTTCACTCTTCTGATTTGT 3113  
OY 2872 GACTGTATGAG 2931  
Db 3114 GACTGTATGAG 3173  
OY 2932 ATTTGAAG 2991  
Db 3174 ATTTGAAG 3233  
OY 2992 GACAACTTGCAG 3051  
Db 3234 GATTAACCTTGTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3293  
OY 3052 AGGATGCAAG 3111  
Db 3294 AGGATGCAAG 3353

OY 3112 TTTAGTAAAGAAAGATTTTATGATTAATTAACCACTGTGATGATTAACACAG 3171  
 Db 3354 TTTTTCAGAAAGCCGAGATGATGAATATCCAGAG-----GACACAAA 3398  
 OY 3172 AAAGACGTGTATGTCATATACARCA--GAAATGGAAAGATCTGTGATCTT 3228  
 Db 3399 ATGACAGCTGATGTCATTAACAGGGCATGAAATTAAGCAAGAGCTTACTACTT 3458  
 OY 3229 AAAGATTAATGAGACTACAGTGTATAGAACTGGCAGCTGTGAAATATCAT 3288  
 Db 3459 AAAGACGTATGAAACACAGCGGTGGAACCGGAGAGCTGTGAAATATGCTA 3518  
 OY 3289 ATTGATGAAGTATCATGTATCATTAACACCCAGCTGTACTGTGACTGACCA 3348  
 Db 3519 ATGATGAAGTATCATGTATCATTAACACCCAGCTGTACTGTGACTGACCA 3578  
 OY 3349 ATTGCTGTAGAGATCTGACTTTGAAATTAACACAGAGACTTATGATGAAATCG 3408  
 Db 3579 ATTGCTGTAGAGATCTGACTTTGAAATTAACACAGAGACTTATGATGAAATCG 3538  
 OY 3409 GATCTGAAAGAAAGCAAGCAAGATGAAAGCACTGATCATGAAAGTACACT 3468  
 Db 3639 GAATTTGAAAGAAAGTAAAGGAAATTAATGCAACAGCTCTTCTGAAAGAGCAAGTT 3698  
 OY 3469 GTGACATCGGCGACCTGTAGAAAGACCGGTAGTGAACCTGAAAGAACTCTGAA 3528  
 Db 3699 GATGTTCTCCACCCGAGAGAGTGAACAGCAAGAAATTAACCTGAGAGAGACTTAA 3758  
 OY 3529 CCAGAACTGTTTCACTGAAGCTGTGTACAAAGATTAAGTGTGATCAATCATGTG 3588  
 Db 3759 CCAGAACTGTTTCACTGAAGCTGTGTACAAAGATTAAGTGTGATCAATCATGTG 3638  
 OY 3589 GAAAGAGCAGAGAAAGCAAGTGTGAAACCTGAGAGAGCTGTGTTCCAAATGTTGAA 3648  
 Db 3819 GAAAGAGTAAAGAAAGTAAAGTGTGAAATTAAGTGTGAAAGTGTGAAAGTGTGAA 3678  
 OY 3649 CATATGCTGTAGACTGATCTGATGTTTATGATGTTTCTGATGATGTTGATGTTG 3708  
 Db 3879 CATATGCTGTAGACTGATCTGATGTTTATGATGTTTCTGATGATGTTGATGTTG 3738  
 OY 3709 TTTGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3768  
 Db 3939 TTTGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3818  
 OY 3769 AAGTGTTCATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTAT 3828  
 Db 3999 AAGTGTTCATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTAT 4058  
 OY 3829 CAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3888  
 Db 4059 CAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4118  
 OY 3889 GTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3948  
 Db 4119 GTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4178  
 OY 3949 ACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4008  
 Db 4179 ACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4238  
 OY 4009 GTGAATGCTTTTATGAGAAATTCATCATCATCATCATCATCATCATCATCATCAT 4068  
 Db 4239 GTGAATGCTTTTATGAGAAATTCATCATCATCATCATCATCATCATCATCATCATCAT 4298  
 OY 4069 TTTGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4128  
 Db 4299 TTTGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4358  
 OY 4129 ATTAACACCAAGCTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGT 4188  
 Db 4359 GTTAACACCAAGCTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGT 4418

OY 4189 CTAAACTAATTAAGAAATGAGACTGCTGATGAAATTAAGTGAATTAACCTTGTAT 4248  
 Db 4419 CAGGCTCTGCGCAAGCA-----GCGGCTGAGAAATGTAAGTCAACTTTGAC 4469  
 OY 4249 AATGATGATTTGGTATCT 4308  
 Db 4470 AATGATGATTTGGTATCT 4529  
 OY 4309 ATATGATGAGAGTGTGATTTCCAGAAATGTGAACTCCAGCTTAACTATGAAGAAAT 4368  
 Db 4530 ATATGATGAGAGTGTGATTTCCAGAAATGTGAACTCCAGCTTAACTATGAAGAAAT 4589  
 OY 4369 CTGATGATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTAT 4428  
 Db 4590 CTGATGATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTAT 4649  
 OY 4429 CTGATGATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTAT 4488  
 Db 4650 CTGATGATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTAT 4709  
 OY 4489 GACATCTTTATGAGAGAAAGCAAGAAATTAATTAATTAATTAATTAATTAATTAAT 4548  
 Db 4710 GACATCTTTATGAGAGAAAGCAAGAAATTAATTAATTAATTAATTAATTAATTAAT 4769  
 OY 4549 AAAAAGCCGAAAGCCATATCTGACCAAGAAAGAAATTAAGAAATGATGATGATGAC 4608  
 Db 4770 AAAAAGCCGAAAGCCATATCTGACCAAGAAAGAAATTAAGAAATGATGATGATGAC 4829  
 OY 4609 TTTGATTAACAGAAAGTGTGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4668  
 Db 4830 TTTGATTAACAGAAAGTGTGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4889  
 OY 4669 ACAATGATGATGAGAAAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4728  
 Db 4890 ACAATGATGATGAGAAAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4949  
 OY 4729 AATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4788  
 Db 4950 AATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5009  
 OY 4789 CATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4848  
 Db 5010 CATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 5069  
 OY 4849 GTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4908  
 Db 5070 GTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5129  
 OY 4909 GTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4968  
 Db 5130 GTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5189  
 OY 4969 GCGAGCTGCTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5028  
 Db 5190 GCGAGCTGCTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5249  
 OY 5029 CTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5088  
 Db 5250 CTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5309  
 OY 5089 AGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5148  
 Db 5310 AGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5369  
 OY 5149 CTATTCATAATTAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5208  
 Db 5370 CTATTCATAATTAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5429  
 OY 5209 AAGCCACCGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5268  
 Db 5430 AAGCCACCGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5489  
 OY 5269 GGAAGACCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5328



|    |      |   |      |
|----|------|---|------|
| Db | 666  | AGTCTCTCGGGCCCCCTGAAAACATATACACATCTATTCAGGGCTGGAAGACCATCGTGGGGC | 725  |
| Qy | 717  | CGTATCCAGCTCTGTGAMAGAGCTCTCAGATGTAAATGATTCCTGACTGTGTCTGTCTGAG   | 776  |
| Db | 726  | CGGTATCCAGTCTGTGAAGAGCTGCGTATGTATGTGTGCTCAACAGTCTCTCGCTCAG      | 785  |
| Qy | 777  | CGATTTTGCCTCTAATTTGGCTGCACTGTTCATGTGGCAACTGAGGAATTAATGTATACA    | 836  |
| Db | 786  | CGTCTTTGGCCCTCATGGCGCTGCAAGCTCTTCAATGGGCAACCTTAAGGCAAGATGTGTGC  | 844  |
| Qy | 837  | ATGSGCTCCCAACATGCTCTCTGTGAGGACATATGATATAGAAAAGATATATCTGTGA      | 896  |
| Db | 845  | -----GCAACTTTCACAGCGCTCAACGCAACAC-----                          | 873  |
| Qy | 897  | TTATATATGTACACTTATATAATTAACCTCTCTTGGATTGACTGGAAGCATATATATCA     | 956  |
| Db | 874  | -----GCTCCGTGTGAGGCCCAACGCGTTGGTCTGTGGAAATCCCTGACCTTTACCTCAG    | 926  |
| Qy | 957  | AGATTCAAGATATATCATTTATTTCTGTGAGGGCTTTTATGATGCATCATATGTGGAAATAG  | 1016 |
| Db | 927  | TGATCCAGAAAAATTAACCTGCTCAAGAAAGGCAACCTCTGTATGTATCTGTGTGGGAACAG  | 986  |
| Qy | 1017 | CTCTGATGCAAGGCCATATGCCAAGGGGATATATGTGTGTGAAGCTGTGTAGAAATCCCA    | 1076 |
| Db | 987  | CTCTGACGCTGGGACATGTCCGAGGGGCTACCGGTGCTTAAGAGCGAGCGAGAACCCCGA    | 1046 |
| Qy | 1077 | TTATGCTTACACAAAGCTTTATACCTTCATAGTTGGGCTTTTGTCTTTGTTCGACTAT      | 1136 |
| Db | 1047 | CCACGGCTACACACAGCTTCGATTCCTTTTGGCTTGGGCTTTCTTGTGACATCTTCCGCTGAT | 1106 |
| Qy | 1137 | GACTCAGAGACTTGTGGGAAAACTTTATACACTGCATTAAGTACGTGTGTGGGAAAAAGTA   | 1196 |
| Db | 1107 | GAGCCAGAGACTGCTGGGAGGGCCCTCATACAGACAGACCTCAGAGTCCGAGGGGAAGATCTA | 1166 |
| Qy | 1197 | CATATATTTTTTGTGTGTGCTCATTTTCTTGGGCTCATTTACCTAATTAATTTGATTCCT    | 1256 |
| Db | 1167 | CATATCTTCTTCATATGCTTCTCACTTCTTCCGTGGGCTCTTCTACGTGGAACCTGATCCT   | 1226 |
| Qy | 1257 | GGCTGTGTGGCCATGTGCTACGAGAGGACAGAAATCAGGCGCACTTGGAAAGAGCAACA     | 1316 |
| Db | 1227 | GCGCGTGTGCTGCATATGGCTCATATAGAGAGCAAAACAGCCACATTCGCTGAGACCGAGGA  | 1286 |
| Qy | 1317 | GAAAGAGGCGCAATTTTCAGCAGATGATGTGAACGCTTAAAAAGCAACAGAGGCACTCA     | 1376 |
| Db | 1287 | GAAAGAAAGGCGTTCACAGAGGCGCATGGAATATGCTCAAGAAAGAACACAGAG-----     | 1339 |
| Qy | 1377 | GCAAGGCAGCAACGGCAACTGCTCTCAGAAACTTTCAGAGAGCCCATGTGACAGCAGCGCT   | 1436 |
| Db | 1340 | -----CCCTCACCACTACAGGGGTGTGGATACGT                              | 1367 |
| Qy | 1437 | CTCAGACAGCTCATCTGAAAGCTCTTAAGTTGAATTCCAAGATGTGCTAAGAAAGAAAGAA   | 1496 |
| Db | 1368 | GTCCCCGTAGCTCTTGTGAAGATGTCCCTTTGGCCCCAGTAACAGCATGAGAGAAAGAG     | 1427 |
| Qy | 1437 | TGCGAGGAGAAAGAAAGAAACAGAAAGCAGTCTGTGGGGAGAGAAAGATGAGATGA        | 1556 |
| Db | 1428 | CAAGAGGAGAAAGAGGAG-----TGTCTTCAGAAATGAGAGATGTGGGAGAGAG          | 1478 |
| Qy | 1557 | ATTTCAAAAATCTGAATCTGAGGACAGCATCAGAGAGAAAGGTTTTTCGTTCTCATTTGA    | 1616 |
| Db | 1479 | GCTCCCAAGCTGACATCAAGAGTGTCCCAAGCAAGAAATCATCTCAGCTTACCCG         | 1538 |
| Qy | 1617 | AGGAGACGATTTGACATATGAAGAAAGATGCTCTCCACACACAGTCTTTGTGTGACAT      | 1676 |
| Db | 1539 | TGCGCTCAGCAGAGCACTCTATGAAGCCACGTTCC-----                        | 1572 |
| Qy | 1677 | CGGTGGCTCCCTATTTTACCAAGCGGAAATAGCAGAACAGCCTTTTACGCTTTAGAGG      | 1736 |
| Db | 1573 | -----ACCCCGGGAGATTTTACCTTTCCGAC                                 | 1601 |
| Qy | 1737 | CGAGCAAAAGATGTGGGATCTGAGAAAGCACTTCGAGATGATGAGACAGCACTTTGA       | 1786 |
|    |      | TTTTTTT   |      |

|    |      |  |      |
|----|------|--|------|
| Db | 1602 | GCGA-----GACCTGGGTCTTGAACCAATATTTGGACATGATGAAACACACACAGCGC     | 1655 |
| Oy | 1797 | GGATTAACGAAGCCGTAAGAGATTCCTTGTTGTGGCCCGACGACACGAGAGACGCA       | 1856 |
| Db | 1656 | GGAGAGCGAAGAGCCACACACATCACTGCTGGGTGCTTGCCCC-----TGCGCGGAC      | 1709 |
| Oy | 1857 | CAGCAACTGAGTCAAGCAGCTGAGGTCAATCCCGGATGCTGGGAGGTGTTCCAGCGAATG   | 1916 |
| Db | 1710 | CAGTCCCGAGGAGACGCGACGTCCCGGAACCTGGCTC---CTGGCCACAGCCCTTCATGG   | 1766 |
| Oy | 1917 | GAAGATGCACGACACTGTGGATGTGAATGGTGGTTCTTGTTGGTGGAGC---TTC        | 1973 |
| Db | 1767 | CAAAAGAAACAGCACTGTGACACCTGCAATGGGGGTGCTCATTACTGGGGGACGGGACCC   | 1826 |
| Oy | 1974 | AGTTCACATCGCTGTGGACAGCTTGTGCCAGAGGTGATTAATAGATTAAGCCAGCTAC     | 2033 |
| Db | 1827 | AGAGGCGCATCCCGCAGGAGAGCCACTCTCCGCCCCGTGATGTACAGACCCGCC--       | 1884 |
| Oy | 2034 | TGATGACAAATGGAACCAACCTTAACCTGAATGAGAAAGAAAGATCAAGTCTTTCCA      | 2093 |
| Db | 1885 | ---GACACGACCAACGCGCATCGGAGAGCGAGCGGCCGCCAGAGTCTACCTCCAGCG      | 1940 |
| Oy | 2094 | CGTTTCATGAGACTTCTTAAGATACCTTCCCAAAGGACAGAGAAATGATATAGAC        | 2153 |
| Db | 1941 | TCCGTGTGTAGATGGCTTCAGAGAGCCAGAGACAGCGACCGGCCCTCAGCGCAGTCAG     | 2000 |
| Oy | 2154 | CATTCTACAAATACAGTAGAAGAACTGAAAGATCCAGAGATCCAGGAATGCCACCTGTG    | 2213 |
| Db | 2001 | CGTCTCAACAAAGGCACTGGAAGAGTTAGAGAGTCTGCGCCAAAGTGTCCACATGCTG     | 2060 |
| Oy | 2214 | GTAATAATTTTCCACATATTTCTTAATCTGGGACCTTCTCCATATTGGTTAAAGTGA      | 2273 |
| Db | 2061 | GAACTGCTCGCCAGGCGTCACTGATCTGGGAGTGTCTCCGCTGTGATGTCCATCA        | 2120 |
| Oy | 2274 | ACATGTTGCAACCTGGTGTGATGAGAACCATTTGTTGACCTGGGCACTACCATCTGAT     | 2333 |
| Db | 2121 | CGAGGAGTGAAGTTGGTGGTCAATGAGACCGGTTACTGTACCTACACATACATATGTGAT   | 2180 |
| Oy | 2334 | TGCTTAAATACCTTTTTCATGGCCATGAGACACTATCCAAATGACGAGCACTTTCATTA    | 2393 |
| Db | 2181 | CGTACTCAACACTCTTCAATGGCGGTGGAGACCTCAACATGACAAAGTAAATTCGAGA     | 2240 |
| Oy | 2394 | TGTGCTTACAGTAGGAACCTTGGTTTCACTGGGATCTTTACAGCAGAAATGTTCTGA      | 2453 |
| Db | 2241 | GATGCTGAGGTGCGAAACCTGTGCTTCAAGGATTTTCAAGCAGAGATATACCTTAA       | 2300 |
| Oy | 2454 | AATATTGCAATGATTCCTACTAATATATTTCCAAAGAGCTGGAATATCTTGAAGGTT      | 2513 |
| Db | 2301 | GATCAATGGCCCTGACCCCTACTACTACTTCCAAAGGAGCTGGAACATCTTGCAGCAT     | 2360 |
| Oy | 2514 | TATGTGACGCTTGGCTGTGAGAACTGTGACACGCAATGTGGAAGTATATCTGTTCT       | 2573 |
| Db | 2361 | CATGCTACTCTTATGCTCTCAATGGAGGCTGGGCGTGTCCCGCATGAGAACATTTGTGCTCT | 2420 |
| Oy | 2574 | CCGTTCAATTTGATGCTGCGAGTTTTCAGAGTTGGCAAAATCTTGGCCAACTTAAATAT    | 2633 |
| Db | 2421 | GGCGTCTTCCGCTGCTGGGCGGTCTTCAAGCTGCGCAATATATGCCCCACCTCAACAC     | 2480 |
| Oy | 2634 | GCTAATAAAGATCAATGGGCAATTCGAGGGGGGCTGGGAAATTTAACTTCGCTTGGC      | 2693 |
| Db | 2481 | ACTCAATCAAGTATCAATGGGAATCAATAGGGGGGACATGGGGAACCTGCACCTGTGCTAGC | 2540 |
| Oy | 2694 | CATCATGCTTCTCAATTTTGTGCGGTGTGGCATGACAGCTTGTGGTAAAGGTACAAAGA    | 2753 |
| Db | 2541 | CATCATGCTTCTCAATTTTGTGCGGTGTGGCATGACAGCTTGTGGTAAAGGTACAAAGA    | 2600 |
| Oy | 2754 | TGTGTCTGCAAGATGCCAGTGTATGTCACTGCCACGCTGGCACATGATGACTTCTT       | 2813 |
| Db | 2601 | GCTGAGGACAGCACTCAAGGC-----CTGCTGCTCCTGCTGCACTATGATGACTTCTT     | 2654 |
| Oy | 2814 | CAACCTCTTCTGATTTGTGTTCCGCGTGTGTGGGAGTGGATGAGACCATTTGGGA        | 2873 |
| Db | 2655 | TGATGCTTCTCAATCACTTCCGCACTCTGTGGAGAGTGGATGAGACCATTTGGGA        | 2744 |

|    |      |   |      |
|----|------|---|------|
| OY | 2874 | CTGATGTAGAGTTCGTGCTCAACGCCATTGGCCCTTACTGTCTTCATGATGGCATAGTGAT | 2933 |
| Db | 2715 | CTCATGTAGAGTTCGGGGGAGCATTAACTGCCTGGCTGCTCTTGGCTTTAATGTCAT     | 2774 |
| OY | 2934 | TGGAACCTGTAGTGGTCTCGTAATCTCTTCTGGCCTTGGCTTMMGACCCTAATTAGTCAGA | 2993 |
| Db | 2775 | TGGCAACCTGTGTGCTCTGAATCTTCTTCTGGCCTTGTCTGTCACTCTTCATGTCAGA    | 2844 |
| OY | 2994 | CAACCTTGACGCCACTGATGATGATTAATAATGATAATCTCAAAATGGCTGTGATAG     | 3053 |
| Db | 2835 | CAACCTCACAGCCCTGATGAGAGCAGAGATGAACAACCTCCAGCTGGCCCTGGCCCG     | 2894 |
| OY | 3054 | GATGCACAAAAGGAGTAGCTTATGTGAAAAAATAATATGAAATTTATCAACAGTCTT     | 3113 |
| Db | 2895 | CATCCAGAGGGGCTGTGGCTTTCTTCAAGGGGACACCTGGGATTTCTGCTGGTCTCT     | 2954 |
| OY | 3114 | CATTAGAAACAAAAGTTTTTATGATAAATTAACCACTGATGTGATCTAAACAAGAA      | 3173 |
| Db | 2955 | GCGGCACCGGCTCTCAGAAGCCGACGCCCTTGGCCGCCAGGGCCAGCTGCCAGTGCAT    | 3014 |
| OY | 3174 | AGACAGTTGTATGTCCAATCATCAGACGAATAATGGGAAGATCTT-----            | 3219 |
| Db | 3015 | TGCCAACCCCTACTCTCCCCGCCACCCCCACAGAGGAGAAAGTGCTCCACCCGGAAGA    | 3074 |
| OY | 3220 | -----GACTATCTTAAAGATGT  | 3266 |
| Db | 3075 | AACACATTTTGAGGAAGGCGAGCAACACAGGCCACCCCGGGATTCACAGACGCGT       | 3134 |
| OY | 3227 | AAATGGAACTACAAAGTGTATAGAACTGGCAGCAGTGTGAAAAATCATTTATGTGA      | 3266 |
| Db | 3135 | GTGTGTCCCATGCTGTGTGGCCGAGTCAACACAGATGACCAAAGAGGATGAGAGAA      | 3194 |
| OY | 3297 | AAGGATTTACATG-----TCATATATAACACCCCACTGTACTGTGAGCTG            | 3343 |
| Db | 3195 | CAGCTGGGCAACGAGGAGAGATGCAGCAAGCAGCAGAAATCCAGCTGTGTGCGGCTG     | 3254 |
| OY | 3344 | TACCAATTTGCTGAGAGAACTGACTTTGAA-----                           | 3375 |
| Db | 3255 | GCCCAGAGGCCCTCCGGATCTCCAGAGACTGGAGCCAGGTGTCAAGGACTGCCTCTCTGA  | 3314 |
| OY | 3376 | -----AATTAAACGGGAAGACTTTAGTGTG--AATGGATCTGGAGAA               | 3419 |
| Db | 3315 | GCGCGAGGCCAGTGCATCTCAGGCCGACGTGGCGGACGCTGGAAGAGGGAACCCAGGC    | 3374 |
| OY | 3420 | AAGCAAGAGAACTGAATGAAGACAGTACGTCAATCAGAAAGGTATGACATGAGCAAT---  | 3476 |
| Db | 3375 | CCCAAGGTTGGGTGAGAACCCCAAGAGACATGTTCTCCAGGGCAGCAGACAGACATATAC  | 3424 |
| OY | 3477 | ---CGGCGCACTGTAGAAAMACAGCCGCTAGTGTGAACCTGAAAGAACTCTTGAACAGA   | 3533 |
| Db | 3435 | CAACACGGCTGAGGCTCTCTGAGAGATTCCTGACCTCGGCCAGANTGTCAAGAACCCAGA  | 3494 |
| OY | 3534 | AGCTTGTTCACGTGAAGGCTGTGTACAAAGATTCAAATGTGTCAAAATCATGTGGAAGA   | 3593 |
| Db | 3495 | GGACTGCTTCACTGAAGGCTGTGTCCGGGCGTGTCCCTGCTGTGGGTGAGACACACACA   | 3554 |
| OY | 3594 | AGGCAAGAGAAAACAATGTGTGAACCTGGAAGAGAGAGTCTTCCGAATAGTTGAACATA   | 3653 |
| Db | 3555 | GGCCCCCAGGGGAAGGTGTGGGTGGGTGGCCAGAGACTGTCAACATCTGTGGAGCACAG   | 3614 |
| OY | 3654 | CTGGTTTGAAGACCTCTATTTTTCATGATATCCCTTAGTATGTGGTGTGGCAATTTGA    | 3713 |
| Db | 3615 | CTGGTTGAGACATTCATCTTTCATGTATCTTACTCAGCAATGGAAGCGCTGGCTTCGA    | 3674 |
| OY | 3714 | AGATATATATATGTATCAGGAAAGACGATTAAGACGATTTGGAATATGCTGCACAGT     | 3773 |
| Db | 3675 | GGACATCTTACTAGAGGAGCGGAAGACATCAAGGTTCTGTTGATATGCCAGAACAT      | 3724 |
| OY | 3774 | TTTTCACCTTAATTTTCATTTTGGAATTCCTCTTAAATATGGGTGGCATATGCTATCAAC  | 3833 |
| Db | 3735 | GTTCACATATGTCTCTGTGTGAAGATGTGTCTCAAGTGTGGGTGTACGGCTGTTCACAA   | 3794 |

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|----|------|---|------|
| OY | 3834 | ATTTTACCAAAAGCCGGGTGGTGGGACCTCTTAATTTGGTAAAGTTTCAATTTGGCTAG     | 3893 |
| Db | 3795 | GTACTTACCAAAATCCCTGGTGGGTCTGCACTTCCATCTGAGACGTCTCTCTGGTAC       | 3854 |
| OY | 3894 | TTTTAAACGAAATACCTTTGGGTCTTACACAGAACTTGGAGCCATCAATCTCCAGACACT    | 3953 |
| Db | 3855 | CCTGGTGGCCAAACACCTGGGGCTTTGGCCAGATAGGGCCCCATCAAGTACTCCGACCT     | 3914 |
| OY | 3954 | AAGAGCTCTGAGACCTCTTAAGACCTTATCTCGATTTGAAAGGATAGAGGGTGTGTAA      | 4013 |
| Db | 3915 | GGGTGACACTCCGCTCTCTGAGACCTCTGTCACAGATTTGAGGCATAGAGGGTGTGTAA     | 3974 |
| OY | 4014 | TGCCCCTTTGGAGCAATTCACATCCCATCAATGATGCTCTGGGTTCCTATATCTCG        | 4073 |
| Db | 3975 | TGCCCCGTGGGGCCCAATCCCGTCCATCAATGAACGCTCTCTCGTCTGGCTCATCTCTGG    | 4034 |
| OY | 4074 | GCTAATTTTCAGACATCATATGGGCGCTAATTTGTTGGTGGCAATTTCAACATCTGATTA    | 4133 |
| Db | 4035 | GCTCATCTTCAGACATCATATGGGCGCTGAACCTCTTTGGGGGAAAGTTTGGAGTGCATCA   | 4094 |
| OY | 4134 | CACCACAACTGTGTGACAGGTTTGGACATCGAAGACGTGAATTAATCACTGATTTGCTAAA   | 4193 |
| Db | 4095 | CCAGACAGAGGAGACCTTGGCTTTGAAGTACACATCTGGAACAACAAGACGCACTGTGA     | 4154 |
| OY | 4194 | ACTAATTAAGAAATATAGCTCTCTGATGGAAAAATGTGAAGATTAACCTTGTATATGT      | 4253 |
| Db | 4155 | GTCCCTTAACCTTGACCGGAAATTTGATGTGGACCAAGGTGAATCACTTTTGACACAGT     | 4214 |
| OY | 4254 | AGGATTTGGGATATCTCTTTGGCTCAAGTGGCAATTCAAAGATGGATGATATAT          | 4313 |
| Db | 4215 | GGGGGCGGGTACTGGCCCTTTGCAAGGGGACATTTTAAAGGTGGATGACATAT           | 4274 |
| OY | 4314 | GTATGACAGAGTTGATTCACAGAAATGTGAACTCCAGCTAATGATTAAGAAAGTCTGA      | 4373 |
| Db | 4275 | GTATGACAGCTGTGACACTCCAGGGGGATTAAGAGACAGCCTCAGTGGGAATTAACACTCTA  | 4334 |
| OY | 4374 | CATGATATCTTACTTTGTATATTTTCAATCATCTTTGGGCTCTTCTTACCTGTGACCTGT    | 4433 |
| Db | 4335 | CATGATATCTAATTTGTGCATTTTTCATCATCTTTGGGCTCTTCTTACCTGTGACCTGT     | 4394 |
| OY | 4434 | TATTTGGTCACTCATATTAATTTTCAACGACGAAAAAGATTTGGAGGTCAAGACAT        | 4493 |
| Db | 4395 | TATTTGGTCACTCATTAATTTTCAACTTCAACAGAAAGAAAGTTTAGGGGCGCAGACAT     | 4454 |
| OY | 4494 | CTTTATGACAGAAAGACAGAAAGAAATACTATTAATGCAATGAAGAAAAATTTAGATCGAAAA | 4553 |
| Db | 4455 | CTTATGACAGAGGAGACAGAAAGAAATGATCAATGCCATGAAGAAAGCTGGCTCCAGAA     | 4514 |
| OY | 4554 | ACCGCAAAAGCTTATACCTCTGACCGAGGAAACAATTTCAAGAAATGCTTGTGACTGT      | 4613 |
| Db | 4515 | GCCCGAAGAGCCCATCCACAGGGCCCTTGAAAGATGACAGGGCTTCATATTTGACATTTGT   | 4574 |
| OY | 4614 | AACCAAGCAAGTTTATACATTAATGACATCAATGATGATCTCATCTGCTTAAGATGTGCACAT | 4673 |
| Db | 4575 | GACCAAGGAGGCTTTTATAGCTGCACATCAATGATTTGTGATCTCTCTGAATATGTGCACAT  | 4634 |
| OY | 4674 | GATGTGGAAACAGATGACAGAGTGAATTTGTGATTAACCTTTTCTACGATCAATCT        | 4733 |
| Db | 4635 | GATGTGGAGACAGATATACCAAAAGTCTCTGAGAAATCAACATCTTTGGCCAAATTAACCT   | 4694 |
| OY | 4734 | GGGTCTCATTTGTCTATTTACTGGAGAGTGTACTGAACATCATCTCTACAGGCATTA       | 4793 |
| Db | 4695 | GCTCTTTGTGGCCATCTTTCAACAGGCGAGTGTATTGTCAAGCTGGCGTGGCCGCGACATA   | 4754 |
| OY | 4794 | TTATTTTACATTTGATNGAATATTTTGTATTTTGGTGTGTGATTTCTCTCATTTGTAGG     | 4853 |
| Db | 4755 | CTACTTCAACCAAGCTGGGAATATCTTCGACTTCGTGGTGTGTATCTCTCATCTGTGGG     | 4814 |
| OY | 4854 | TATGTTTTCGCGAGCTGATTAAGAAAGTATTTTGTGTGCTCCGACCCCTGTGCGAGTAT     | 4913 |
| Db | 4815 | CACGTGTCTCTCGACATCATCAAGAGTATCTTCTCTCCCGACGCTCTTCCGAGTAT        | 4874 |
| OY | 4914 | CCGCTTGTCTAGATTTGGCCGAATCTTACGCTGATCAAGAGACAAAGGGATCCGAC        | 4973 |





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|----|------|---|------|
| QY | 777  | CGATTTGCTTAATTTGGGCTGAGCTGTCAATGGGCAACCTGGAGAAATAATGTATACA        | 836  |
| Db | 786  | CGCTTTTGCCCTATCGGGCTGAGCTGTCAATGGGCAACCTAAGGCAAGATGTGTGC-         | 844  |
| QY | 837  | ATGGCCCTCCACCAAATGCTCTCTGGAGAGCAATAGTATGAAAAAATAATAACTGTGAA       | 896  |
| Db | 845  | -----GCAACTTCACAGCGCTCAACGGCACCAAC-----                           | 873  |
| QY | 897  | TTATTAATGTATCACTTATAAATGAAACCTGCTCTTGAAGTTGACTGGAAGTCATATATCA     | 956  |
| Db | 874  | -----GGCTCGGTGAGAGCGAGCGAGCTTGTGTGGAAATCCCTGGACCTTTTACTCAG        | 926  |
| QY | 957  | AGATTCAGATATCATATTTTCTGTGAGGCTTTTTTAATGCACTACTAATGTGAATAG         | 1016 |
| Db | 927  | TGATTCAGAAAAATTTACCTGTGTCAAGAAAGGCAACCTGATGTTTACTGTGTGGAAACAG     | 986  |
| QY | 1017 | CTCTGATGACGGCAATATGTCACAGAGGATATATGTGTGGAAGCTGTGTAGAAATCCCA       | 1076 |
| Db | 987  | CTCTGACGCTGGGACATGTCCGAGGGCTACCGGTGCTCTAAAGGACGGCGGAACCCCGA       | 1046 |
| QY | 1077 | TTATGGCTACACAAGCTTGATACCTTCACGTTGGGCTTTTTTGTCCTTGTTCACATAAT       | 1136 |
| Db | 1047 | CCAGGGCTACACAGCTGTGATCTCTTTTCCCGGGCTTCTGTGACCTTCCGCGCTGAT         | 1106 |
| QY | 1137 | GACTCAGACCTTGTGGAAAAATCTTATATCACTGCATATAGCTGCTGTGGAAAAAGTA        | 1196 |
| Db | 1107 | GACCCAGACATGTGGGAGGCGCTCATACAGACACCTCAAGTGTCGCGAGGGAAGATCTA       | 1166 |
| QY | 1197 | CATATATTTTTTGTGTGTGTCATTTTTCTTGGGCTCATTTCACTTAATAATTTGATCCT       | 1256 |
| Db | 1167 | CATATCTTTCTTATGTGTTCTCATCTTCCTCGGGGTCTTTCACCTGTGGAACCTGATCCT      | 1226 |
| QY | 1257 | GGCTGTGTGGCCATGGCTCCACAGGAGACAGATACAGGCCCTTGGAAGAGACAGACA         | 1316 |
| Db | 1227 | GGCCGTGTGTGCAATGGCTCATATGAGAGCAAAAACCAAGCCACATCGCTGAGACCGAGA      | 1286 |
| QY | 1317 | GAAGAGCGCCGAATTCAGCAGCATGTATGATTAACGCTTAAAAACAACAGAGGCAAGCTCA     | 1376 |
| Db | 1287 | GAAGAAAAAGCGCTTCAGAGAGGCCATGGAATGCTTCAAGAAAGAACACAGAG-----        | 1339 |
| QY | 1377 | GCAGGCAGCAAGGCAACCTGCTCACAACATTCACAGAGGCCCATGTGACAGCAGCAGCT       | 1436 |
| Db | 1340 | -----CCTCACCATCAAGGGGTGTGTGATACCT                                 | 1367 |
| QY | 1437 | CTCAGACAGCTCATCTGAACCTCTTAAGTTGATTCCAAGATGCTTAAGAAAGACAAA         | 1496 |
| Db | 1368 | GTCCCGTATGCTCTTGTGAGATGTGCCCTTTGGCCCCAGTAAACACCCATGAGAGAAAG       | 1427 |
| QY | 1497 | TGCGAGGAAGAAAAAGAAACAGAAAGAGCAGTCTGTGTGGGGAAGAAAGATGAGATGA        | 1556 |
| Db | 1428 | CAGAGGGAGAAACGGA-----TGTCTTCAGAACTGAGAGGTGTGGGAGAGACAG            | 1478 |
| QY | 1557 | ATTCCAAAAATCTGAATCTGAGACAGCATCAGAGAGAAAGTTTTCGTTCTCATTTGA         | 1616 |
| Db | 1479 | GCTCCCCAAAGTCTACTCACAAGATGTGTCCACAGACGAATATCTCTCAGCCTCACCG        | 1538 |
| QY | 1617 | AGGGACCGATTGACATATGAAGAAAGAGTACTGCCACACAGCAGCTTTGTGTGAGCAT        | 1676 |
| Db | 1539 | TGGCTCTACAGCAGCACTTCTTGAAGCCAGCTTC-----                           | 1572 |
| QY | 1677 | CCGTGGCTCCTATTTTCAACCAAGGGCAATATGACAGACAAACCTTTTCAGCTTTAGAG       | 1736 |
| Db | 1573 | -----AGCGCGGGAGCATTTCACCTTTCCGAG                                  | 1601 |
| QY | 1737 | GGGAGCAAGAGATGGGATCTGAGAACGACTTCCGAGATGATGAGCAGACGACCTTTGA        | 1796 |
| Db | 1602 | GGCA-----GACCTGGGTTCTGAAGCAGATTTTTCGAGATGATGAAAAACAGCAGCGCG       | 1655 |
| QY | 1797 | GGATTAAGAGCGGTAGATATCTTGTGTTGGCCCCGAGACAGACGAGAGAGAGCGAA          | 1856 |
| Db | 1656 | GGAGAGCGAGAGCCACACACATCTACTGCTGTGTGGCTTGCCCTTGCCCC-----TGTGCCGGAG | 1709 |

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|----|------|---|------|
| QY | 1857 | CAGCAACCTGAGTCACAGCAAGTAGTCACTCCGAGNCGTGGGAGAGTTCACAGCAATGG         | 1916 |
| Db | 1710 | CAGTGCCTCAGGGACAGGCCAGTCCGGGAACCTCGGCTC---CTGGCCACGGCCCTCCAGTGG     | 1766 |
| QY | 1917 | GAAATCATCAGACAGCTGGATTGCTCAATAGTGTGGTTTCCTGTGTGGTGGAGC---TTC        | 1973 |
| Db | 1767 | CAAAAACAAACAGCACTGTGTGACCTGCAATGGGGTGGTCTCATTTACTAGCGGGGACAGGCCACC  | 1826 |
| QY | 1974 | AGTTCCTACATCGCCCTGTGTGGACAGCTTCGTGCGCAAGAGGTGATATAGATTAAGCAAGCTAC   | 2033 |
| Db | 1827 | AGAGGCCACATCCCGCCAGGAAGGACCACTCCTCCGCCCTGTGATGTAGTACAGCACCGGCCA--   | 1884 |
| QY | 2034 | TGATGCAAAATGTAAACAACCACTGTAAACCTGAATATGAGAAAGAAAGAGCTCAACTTCTTCCCA  | 2093 |
| Db | 1885 | ---GACAGACACACGGCATCTGGAGGAGGACCGAGCGGCCCCCGACATGCTGACCTCCAGGC      | 1940 |
| QY | 2094 | CGTTTCATGAGCTTTCTTAGAAGATCTCTTCCCAAAAGCAGACAGCAATAGATTAATAGCCAG     | 2153 |
| Db | 1941 | TCCGTGTGTAGATAGGCTTCGAGGAGGCCAGAGACAGCGACGCGGCCCTCAGCGCAGTACG       | 2000 |
| QY | 2154 | CATTCTAACAATAATACAGTAGAAGACCTTGAAAGATTCAGGCGAAGAAATGCCACCCCTGTG     | 2213 |
| Db | 2001 | CGTCTCACAAGGCGCACTGGAAAGATTAAGAGTGTGCGCCACAAAGTGTCCACCATGTGTG       | 2060 |
| QY | 2214 | GTAATAAATTTTCCAAATATTTCTTAATCTGCGACACTTCTCCATATTTGGTTAAAGTGA        | 2273 |
| Db | 2061 | GAAACCGTCTGCGCCAGGCGACTTACTGTATGTGGGAGTGTCTGCCCGCTGGATGTCCATCA      | 2120 |
| QY | 2274 | ACATGTTGTACACCTGGTGTGTATGTGAGACCATTTGTTGACCGGCACTCACATCTGTAT        | 2333 |
| Db | 2121 | GCAGGAGGTGAAGTTGGTGTGTCAAGGACCGCTTTACTGTACCTCACCACTCATATGTGCAT      | 2180 |
| QY | 2334 | TGTCTTAAATACTCTTTTCAAGGCGCATGTGAGAGCACTATCAATGACGAGCAATTTCAATA      | 2393 |
| Db | 2181 | CGTACTCAACACACTCTTCTATGGCGGTGGAGGACATCAACATGACAAGTGAATTGGAGGA       | 2240 |
| QY | 2394 | TGTGCTTACAGTAGAAGAACTGGTTTTCACATGGGATCTTTACAGCAAGAAATGTTTCTGA       | 2453 |
| Db | 2241 | GATGCTGAGGTGCGAAGAACTGTGCTTTCACAGGAGATTTCACAGCAGAGATGACCTTCAA       | 2300 |
| QY | 2454 | AATTAATGACATGGAATCCTTACATTAATTTCCAAAGAGGCTGGATATCTTGTGACGGTTT       | 2513 |
| Db | 2301 | GATCATGTGCGCTCGAACCCCTACTACTACTTCCAAACAGGCTTGGAAACATCTTCGACAGCAT    | 2360 |
| QY | 2514 | TATTTGTGACGCTTAGCCCTGTGTAGACACTGTGACTGCGCAATGTGGAAGATTAATCTGTTCT    | 2573 |
| Db | 2361 | CATGCTATCTTATGACCTCATATGAGAGGTGGGCGCTGTCCCGCATAGACAACTGTGCGTCT      | 2420 |
| QY | 2574 | CCGTTTCAATTTGATGCTGTGCGAGTTTTCAGAGTTTGGCAAAATCTTGGCCAAAGSTTAATAT    | 2633 |
| Db | 2421 | GGCGTCCCTTCCGCTGTGTGGGGCTTTCAAAGCTGGCGCAATATATGGCCACCCCTGMAAC       | 2480 |
| QY | 2634 | GCTAATAAAGATCATGTGGGCAATTCGCGGGGGGCTGGGAAATTAACCCCTGCTTGGC          | 2693 |
| Db | 2481 | ACTCATCAAGATCATCGGGAACCTGAGGGGGGACTGGGGAACCTGACACTGTGGTCTAGC        | 2540 |
| QY | 2694 | CATCATGCTCTTCAATTTTTCGCGTGTGCGGACTGCGCATGACACTTCTTGGTAAAGGCTCAACAGA | 2753 |
| Db | 2541 | CATATCGTGTATCTTTTGTGTGTGGTGGGCAATGACAGCTCTTTGGCAAGAACTACTGGA        | 2600 |
| QY | 2754 | TTGTGTCTGCAAGATGCGCAGATGATGTCAACTCCACGCGTGGCAATGATGACTTCTT          | 2813 |
| Db | 2601 | GCTGAGGAGACAGCACTCAGGC-----CTGCTGCGCTCCCTGGCAATGATGAACTGTCTT        | 2654 |
| QY | 2814 | CCACCTCTTCTCTGATTTGTGTTCCGCGTGTGTGGGGAGTGGATAGAGAACCATGTGGGA        | 2873 |
| Db | 2655 | TCAATGCTTCTTCAATCACTTTCGCGACTCTCTGTGAGAGTGTGATGAGAACCATGTGGGA       | 2714 |
| QY | 2874 | CTGTATGAGAGGTTCTGTGATCAAGCAATGTGCTTACTGTCTTCATGATGATGATGAT          | 2933 |
| Db | 2715 | CTGCAATGAGAGTGTGCGGGGACATGATTAATGCCCTGTGGTCTTCTTGTGTTATGTGAT        | 2774 |
| QY | 2934 | TGGAAACCTAATGATGCTGAATCTCTTTCTGCGCTTCTTMTGACATATTTAGTGACA           | 2993 |

Db 2775 TGGAACTTGTGCTGGAATCTTCTGCGCTTGTGCTGAGCTCTTCTGAGCGA 2834  
 Oy 2994 CACCTTGCACCACTGATGATGATGATGATGATGATGATGATGATGATGATGATG 3053  
 Db 2885 CACCTTGCACCACTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2894  
 Oy 3054 GATCACAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3113  
 Db 2895 CATCAGAGGGGCTGCGCTTGTGCAAGCGGACCACTGGGATTTCTGCTGTGCTCT 2954  
 Oy 3114 CATTAGCAACAAAGATTTAGTGAATTAATTAATTAATTAATTAATTAATTAATTA 3173  
 Db 2955 GCGGACCGGCTGAGAGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCAT 3014  
 Oy 3174 AGACAGTTGTATGTCATCTATGACAGAAATTTGGGAAATTTGCTGCTATTTAAGA 3233  
 Db 3015 TGCCACCCCTACTCCCGCCACCCCGAGAGCGAGAGAGGTGCTCCACCCCGAAGA 3074  
 Oy 3234 -----TGT 3236  
 Db 3075 AACACATTTGAGAGAGCGGACCAAGCGGAGCGACCCCGGGATCCAGAGCCCT 3134  
 Oy 3237 AATATGAACTACAAAGTGTATGAACTGCGAGAGTGTGAAAAATACATTATTTGATGA 3296  
 Db 3135 GTGTGTGCCCCATCGCTGTGCGCGAGTACAGACAGATGACCAAGAAGAGATGAGAGAA 3194  
 Oy 3297 AAGATATTACATG-----TCATTCATTAACAAACCCCAAGTTTACTGTGACTG 3343  
 Db 3195 CAGCTGTGGCGAGAGAGAGAGTCCAGACAGACAGAAATCCAGCTGTGTGCTGCTG 3254  
 Oy 3344 TACCAATTTGCTGTAGAGAACTGACTTTGAA----- 3375  
 Db 3255 GCCAGAGAGCGCTCGGATTTCCAGAGCTGAGCGGAGCTGACGAGCTGCTCTCTGA 3314  
 Oy 3376 -----AATTTAAACAGGAGAGCTTTAGTAGTG--AATCGATCTGGAAGA 3419  
 Db 3315 GCGCGAGGCGCATCTCTGCGCGAGCTGCGCGAGAGAGAGGAGAAAGCGGAAAGCCGAGGC 3374  
 Oy 3420 AAGCAAGAGAGAACTGAAATGAAAGCAAGTACTCATCAGAAAGTGCATGTGAGCAT--- 3476  
 Db 3375 CCCAGGCTGCGGAG 3434  
 Oy 3477 ---CGGCGCACTGTAG 3533  
 Db 3435 CAAACAGCGCTGAGCTCTGAGAGAGAGATCCCTGAGCTGCGGCGAGAGAGAGAGAGAGAG 3494  
 Oy 3534 AGCTTTGCTGCTGAG 3593  
 Db 3495 GAGCTGCTGCTGAG 3554  
 Oy 3594 AGGAG 3653  
 Db 3555 GGGCGCGAG 3614  
 Oy 3654 CTGGTTGAG 3713  
 Db 3615 CTGGTTGAG 3674  
 Oy 3714 AGAT 3773  
 Db 3675 GAGAT 3734  
 Oy 3774 TTTTACATTTTACATTTTACATTTTACATTTTACATTTTACATTTTACATTTTACATTT 3833  
 Db 3735 GTTACAT 3794  
 Oy 3834 ATATTTACCAATGCTGT 3893  
 Db 3795 GTACTTACCAATGCTGT 3854  
 Oy 3894 TTTTAAACGAAGTCTTGT 3953

Db 3855 CCTGTGGCCAAACCTTGGGCTTTTGGCCAGATGGGCGCCATCAAGTCACTGCGGAGCT 3914  
 Oy 3954 AAGAGCTGTGAG 4013  
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RESULT 15
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: Sequence 18334, Application US/09864761
: Patent No. US20020048763A1
: GENERAL INFORMATION:
: APPLICANT: Penn, Sharon G.
: APPLICANT: Rank, David R.
: APPLICANT: Hanzel, David K.
: APPLICANT: Chen, Wensheng
: TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
: FILE REFERENCE: Aemolca X-1
: CURRENT APPLICATION NUMBER: US/09/864,761
: CURRENT FILING DATE: 2001-05-23

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PRIORITY FILING DATE: 2000-02-04
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PRIORITY FILING DATE: 2000-05-26
PRIORITY APPLICATION NUMBER: US 09/632,366
PRIORITY FILING DATE: 2000-08-03
PRIORITY APPLICATION NUMBER: GB 24263,6
PRIORITY FILING DATE: 2000-10-04
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PRIORITY APPLICATION NUMBER: PCT/US01/00663
PRIORITY FILING DATE: 2001-01-30
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PRIORITY FILING DATE: 2001-01-30
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PRIORITY APPLICATION NUMBER: US 09/608,408
PRIORITY FILING DATE: 2000-06-30
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PRIORITY FILING DATE: 2001-01-29
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
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GenCore version 5.1.4.p5.4578  
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OM nucleic - nucleic search, using sw model

Run on: April 22, 2003, 11:26:44 ; Search time 987 Seconds

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Post-processing: Listing first 45 summaries

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32: em.htg.other:\*

33: em.htg.mus:\*

34: em.htg.pin:\*

35: em.htg.rod:\*

36: em.htg.mam:\*

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39: em.htgo.hum:\*

40: em.htgo.mus:\*

41: em.htgo.other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
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| 5          | 4338  | 71.9  | 4362   | 6  | AX3911144   | AX3911144 Sequence    |
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| 7          | 4003  | 66.4  | 4197   | 6  | AX3911148   | AX3911148 Sequence    |
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| 14         | 2011  | 33.3  | 4164   | 6  | AX3911138   | AX3911138 Sequence    |
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| 16         | 1109  | 19.6  | 191194 | 2  | AC021673    | AC021673 Homo sapi    |
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| 28         | 274   | 4.5   | 409    | 6  | AX164182    | AX164182 Sequence     |
| 29         | 274   | 4.5   | 539    | 6  | AX164201    | AX164201 Sequence     |
| 30         | 245   | 4.1   | 829    | 6  | AX164191    | AX164191 Sequence     |
| 31         | 245   | 3.6   | 845    | 6  | AX164186    | AX164186 Sequence     |
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| 34         | 192   | 3.2   | 818    | 6  | AX164189    | AX164189 Sequence     |
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| 37         | 170   | 2.8   | 892    | 9  | AX164234    | AX164234 Sequence     |
| 38         | 170   | 2.8   | 4337   | 9  | FE327224523 | FE327224523 Homo sapi |
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ALIGNMENTS

| RESULT 1   | AX3911140   | 6030 bp     | DNA | Linear | PAT 19-MAR-2002 |
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| LOCUS      | AX3911140   |             |     |        |                 |
| DEFINITION | Sequence 11 from Patent WO02144498.                               |             |     |        |                 |
| ACCESSION  | AX3911140   |             |     |        |                 |
| VERSION    | AX3911140.1   | GI:19584237 |     |        |                 |
| KEYWORDS   |   |             |     |        |                 |
| SOURCE     | human.  |             |     |        |                 |
| ORGANISM   | Homo sapiens  |             |     |        |                 |
| REFERENCE  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |             |     |        |                 |
| AUTHORS    | Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.         |             |     |        |                 |
| TITLE      | Turner,C.A., Mathur,B. and Mathur,D.                              |             |     |        |                 |
|            | Novel human ion channel proteins and polynucleotides encoding the |             |     |        |                 |
|            | same  |             |     |        |                 |

JOURNAL Patent: WO 0214498-A 11 21-FEB-2002;

Lexicon Genetics Incorporated (US)

Location/Qualifiers

FEATURES

SOURCE 1. 6030

/organism="Homo sapiens"

BASE COUNT 1786 a 1190 c 1345 g 1706 t 3 others

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;

Matches 6030; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
AX164171 8378 bp DNA linear PAT 22-JUN-2001
LOCUS AX164171
DEFINITION Sequence 1 from Patent W00138564.
ACCESSION AX164171
VERSION AX164171.1 GI:14545110
KEYWORDS
SOURCE
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Rouleau,G.A., Lafreniere,R.G., Rochefort,D., Cossette,P. and
Ragsdale,D.
TITLE Loci for idiopathic generalized epilepsy, mutations thereof and
method using same to assess, diagnose, prognosis or treat epilepsy
JOURNAL Patient: W0 0138564-2. 1 31-MAY-2001;
FEATURES
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/db_xref="taxon:9606"
BASE COUNT 2496 a 1575 c 1782 g 2525 t
ORIGIN
Query Match 94.6%; Score 5705; DB 6; Length 8378;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 6025; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
OY 1 ATGAGCAAAACAGTGTCTGTACACAGAGCTGACAGCTTCACTTTCTTACACAGAGAA 60
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DB 266 ATGAGCAAAACAGTGTCTGTACACAGAGAGCTGACAGCTTCACTTTCTTACACAGAGAA 325
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OY 61 TCTCTGCGGCTATTGAAAGACGATTCGAGAGAAAGGCAAGATCCCAACGAC 120
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Db 326 TCTCTGCGGCTATTGAAAGACGATTCGAGAGAAAGGCAAGATCCCAACGAC 385
OY 121 AAAAAAGATGACGAGAAAGTGGCCCAAGCCAAATAGTACTTGGAACTGGAAAGC 180
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Db 386 AAAAAAGATGACGAGAAAGTGGCCCAAGCCAAATAGTACTTGGAACTGGAAAGC 445
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OY 241 GACCCCTACTATATCAATATAGAAACCTTTATAGTATGAAATAGAGAGGCACTCTC 300
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Db 4645 CTTTACTTGTATTTTATCATCTTTTGGGCTCTTTCACCTTGAACCTGTTATTTGCT 4704

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| Oy | 444.1 | GTTCATCAGATTAATTTCAACGACGAGAAABAACATTGGAGGTCAACACATCTTTAG       | 4500 |
| Db | 4705  | GTCAATCAATGAATTAATTTTCAACGACGAGAAABAAGATTGGAGGTCAACACATCTTTAG   | 4764 |
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| Oy | 4551  | AAGCCTATACCTCGACGAGAAACAAATTTCAAGAAATGCTCTTGTACTTGTCAACAGA      | 4620 |
| Db | 4825  | AAGCCTATACCTCGACGAGAAACAAATTTCAAGAAATGCTCTTGTACTTGTCAACAGA      | 4884 |
| Oy | 4621  | CAATTTTGTACATTAACCATCATGATTCATCTATCTGTCTTAAACATGCTCAATGATGCTG   | 4680 |
| Db | 4885  | CAATTTTGTACATTAACCATCATGATTCATCTATCTGTCTTAAACATGCTCAATGATGCTG   | 4944 |
| Oy | 4681  | GAAACAGATGACGACGATGAAATATGATCAACATTTTGTACAGCTCAATGTGCTGTC       | 4740 |
| Db | 4945  | GAAACAGATGACGACGATGAAATATGATCAACATTTTGTACAGCTCAATGTGCTGTC       | 5004 |
| Oy | 4741  | ATTTGCTATTTTACTGAGAGATGTATACGAAACATCATCTCTACGCCATTAATTAATTT     | 4800 |
| Db | 5005  | ATTTGCTATTTTACTGAGAGATGTATACGAAACATCATCTCTACGCCATTAATTAATTT     | 5064 |
| Oy | 4801  | ACCATTTGATGGAATATTTTGAATTTTGTGCTGTCAATCTCTCCATTTGTAGATATGTT     | 4860 |
| Db | 5065  | ACCATTTGATGGAATATTTTGAATTTTGTGCTGTCAATCTCTCCATTTGTAGATATGTT     | 5124 |
| Oy | 4861  | CTTCCCGAGCTGATAGAAAAAGTAAATTTGTGTCTTCCCTTACCTGTTCGAGATGATCCGTCT | 4920 |
| Db | 5125  | CTTCCCGAGCTGATAGAAAAAGTAAATTTGTGTCTTCCCTTACCTGTTCGAGATGATCCGTCT | 5184 |
| Oy | 4921  | GCTAGAGATTGGCCGAATCCTACGCTGTGATCAAGAGACAAAGGGGATCCGACGCTGCTC    | 4980 |
| Db | 5185  | GCTAGAGATTGGCCGAATCCTACGCTGTGATCAAGAGACAAAGGGGATCCGACGCTGCTC    | 5244 |
| Oy | 4981  | TTTGTCTTATGATATGTCCTCTCTGCTGTGTTAAACATGAGGCTCTCTACTCTTCTAGTC    | 5040 |
| Db | 5245  | TTTGTCTTATGATATGTCCTCTCTGCTGTGTTAAACATGAGGCTCTCTACTCTTCTAGTC    | 5304 |
| Oy | 5041  | ATGTTCAATCAACGCAATCTTTGGGATGTCCAACTTTCGCAATGTTAAAGGGGAACATGTGG  | 5100 |
| Db | 5305  | ATGTTCAATCAACGCAATCTTTGGGATGTCCAACTTTCGCAATGTTAAAGGGGAACATGTGG  | 5364 |
| Oy | 5101  | ATTCATGACATGTTCAACTTTTGAAGACCTTTGGCAACAGACATGATCTGCTATTTCCAAAT  | 5160 |
| Db | 5365  | ATTCATGACATGTTCAACTTTTGAAGACCTTTGGCAACAGACATGATCTGCTATTTCCAAAT  | 5424 |
| Oy | 5161  | ACAACCTCTGCTGGCTGGGATGATGTTCTAGACCAATTCCTCAACAGTAAAGCACCCGAC    | 5220 |
| Db | 5425  | ACAACCTCTGCTGGCTGGGATGATGTTCTAGACCAATTCCTCAACAGTAAAGCACCCGAC    | 5484 |
| Oy | 5221  | TGTGACCTTAATTAAGTTAAACCCGGAAGCTCAGTTAAAGGAGACGTGGGAAACCATCT     | 5280 |
| Db | 5485  | TGTGACCTTAATTAAGTTAAACCCGGAAGCTCAGTTAAAGGAGACGTGGGAAACCATCT     | 5544 |
| Oy | 5281  | GTTGGAAATTTCTTTTGTGTCAGTTACATCATATATCTCTCTGGTTGTGTTGTAACATG     | 5340 |
| Db | 5545  | GTTGGAAATTTCTTTTGTGTCAGTTACATCATATATCTCTCTGGTTGTGTTGTAACATG     | 5604 |
| Oy | 5341  | TACATCGCGGTCACTCGAGAAACCTCAGTGTGTCTACTGAGAAAGTGCAGAGCCTCTG      | 5400 |
| Db | 5605  | TACATCGCGGTCACTCGAGAAACCTCAGTGTGTCTACTGAGAAAGTGCAGAGCCTCTG      | 5664 |
| Oy | 5401  | AGTAGAGATGACTTTGAGATGTTCTATGAGAGTTTGGGAAGATGTTGATCCCATCAACT     | 5460 |
| Db | 5665  | AGTAGAGATGACTTTGAGATGTTCTATGAGAGTTTGGGAAGATGTTGATCCCATCAACT     | 5724 |
| Oy | 5461  | CAGTTTATGAAATTTTGAAGAAATATATCAGATTGTCAGCTGCGCTTGAACCGCTCTCAAT   | 5520 |
| Db | 5725  | CAGTTTATGAAATTTTGAAGAAATATATCAGATTGTCAGCTGCGCTTGAACCGCTCTCAAT   | 5784 |
| Oy | 5521  | CTGCACAAACCAAAACATCCAGCTCATTTGCCATGATTTGCCATGATGATGCTGATC       | 5580 |

|    |      |   |      |
|----|------|---|------|
| Db | 5785 | CTGGCACAACCAACAAACTCCAGCTCATTTGCCATGGATTTCCTCCATGGTGGTGGTGC | 5844 |
| Oy | 5581 | CGGATCCACTGTCCTTGATATCTTATTTGCTTTTACAAAGCGGTTCTAGAGAGATGGA  | 5640 |
| Db | 5845 | CGGATCCACTGTCCTTGATATCTTATTTGCTTTTACAAAGCGGTTCTAGAGAGATGGA  | 5904 |
| Oy | 5641 | GAGATGGATGCTCTTCGAAATACAGATGGAGAGCGGATTCATGGCTTCCATCTTCCAG  | 5700 |
| Db | 5905 | GAGATGGATGCTCTTCGAAATACAGATGGAGAGCGGATTCATGGCTTCCATCTTCCAG  | 5964 |
| Oy | 5701 | GTCCTCTTACAGGCATACACTACTCTTAAAGGAAACAGAGAGATCTGCTGTC        | 5760 |
| Db | 5965 | GTCCTCTTACAGGCATACACTACTCTTAAAGGAAACAGAGAGATCTGCTGTC        | 6024 |
| Oy | 5761 | ATTATTCAGCGTGTCTTACAGACGCCACCTTTTAAAGCACTGTAAACAAAGCTTCTTT  | 5820 |
| Db | 6025 | ATTATTCAGCGTGTCTTACAGACGCCACCTTTTAAAGCACTGTAAACAAAGCTTCTTT  | 6084 |
| Oy | 5821 | ACGTCAATTAATAACAAAAATCAAAGTGGGCTAATCTTCTTAATAAAGACATGATA    | 5880 |
| Db | 6085 | ACGTCAATTAATAACAAAAATCAAAGTGGGCTAATCTTCTTAATAAAGACATGATA    | 6144 |
| Oy | 5881 | ATTGACAGATTAATGAAAACCTTTTCAGAAAAAATGATCTGACCATGTCGACTGA     | 5940 |
| Db | 6145 | ATTGACAGATTAATGAAAACCTTTTCAGAAAAAATGATCTGACCATGTCGACTGA     | 6204 |
| Oy | 5941 | GCTTGTCCACCTTCTTATGACCGGGTGAACAAGCCAAATGTGTGAAAAAATGAGACAGA | 6000 |
| Db | 6205 | GCTTGTCCACCTTCTTATGACCGGGTGAACAAGCCAAATGTGTGAAAAAATGAGACAGA | 6264 |
| Oy | 6001 | GGCAAAAGTGA AAAAGCCAAAGGAAATTA 6030                         |      |
| Db | 6265 | GGCAAAAGTGA AAAAGCCAAAGGAAATTA 6294                         |      |

|                            |   |   |      |        |                 |
|----------------------------|---|---|------|--------|-----------------|
| LOCUS                      | AX164172  | 8378 bp   | DNA  | linear | PAT 22-JUN-2001 |
| DEFINITION                 | Sequence 2 from Patent W00138564.   |   |      |        |                 |
| ACCESSION                  | AX164172  |   |      |        |                 |
| VERSION                    | AX164172.1  | GI:14545111   |      |        |                 |
| KEYWORDS                   |   |   |      |        |                 |
| SOURCE                     | human.  |   |      |        |                 |
| ORGANISM                   | Homo sapiens  |   |      |        |                 |
| REFERENCE                  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.         |   |      |        |                 |
| AUTHORS                    | Rouleau,G.A., Latrehiere,R.G., Rochefort,D., Cossette,P. and Ragsdale,D.  |   |      |        |                 |
| TITLE                      | Locoi for idiopathic generalized epilepsy, mutations thereof and method using same to assess, diagnose, prognosis or treat epilepsy |   |      |        |                 |
| JOURNAL                    | Patient: W0 0138564-A 2 31-MAY-2001; McGill University (CA)   |   |      |        |                 |
| FEATURES                   | location/qualifiers   |   |      |        |                 |
| Source                     | 1..8378   |   |      |        |                 |
|                            | /organism="Homo sapiens"  |   |      |        |                 |
|                            | /db_xref="taxon:9606"   |   |      |        |                 |
| BASE COUNT                 | 2498 a 1571 c 1775 g 2534 t   |   |      |        |                 |
| ORIGIN                     |   |   |      |        |                 |
| Query Match                | 81.2%; Score 4897; DB 6; Length 8378;   |   |      |        |                 |
| Best Local Similarity      | 99.9%; Pctid No. 0;   |   |      |        |                 |
| Matches 5337; Conservative | 0; Mismatches 4; Indels 2; Gaps 2;  |   |      |        |                 |
| OY                         | 688   | ATTCCAGGCGTGAACCACTTGTGGAGCGCCGATCCACAGTGTGTAGAGAGCTTCAGAT    | 747  |        |                 |
| DB                         | 953   | ATTCCAGGCGTGAACCACTTGTGGAGCGCCGATCCACAGTGTGTAGAGAGCTTCAGAT    | 1012 |        |                 |
| OY                         | 748   | GTAAATGATCCGACGTGTGTGTGTGTGAGCGATATTTGCTTAATTGGGCTGACGCTGTTT  | 807  |        |                 |
| DB                         | 1013  | GTAAATGATCCGACGTGTGTGTGTGTGAGCGCATTTTGTCTTAATTGGGCTGACGCTGTTT | 1072 |        |                 |

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|----|------|---|------|
| OY | 1888 | CGGATGCTGGAGCTGTTTCCAGCGAATGGAGAGATGCACAGCACTGTGGATTGCAATGGT    | 1947 |
| DB | 2092 | GTGCCCGAGCAGACAGGAGNAGNAGCAGAACCTGATGTCACAGCAGTAGTGATC          | 2151 |
| OY | 1828 | GTGCCCGAGCAGCAGGAGAGAGCAGCAACCTGATGTCACAGCAGTAGTGATC            | 1887 |
| DB | 2033 | TTTCGATATGTATGAGC-CACGACCCTTTGAGAGATTAAGAGAGCCGTGAGAGATTCCTTGTT | 2091 |
| OY | 1768 | TTTCGATATGTATGAGCAGCAGCAGCTTTGAGAGTAAAGAGCCGTGAGATTCCTTGTT      | 1827 |
| DB | 1973 | AGCAGAAACAAAGCCTTTTCACTTTAGAGGGCCAGCAAGATGTGGATCTTGAGACAC       | 2032 |
| OY | 1708 | AGCAGAACAAAGCCTTTTCAAGCTTTAGAGGGCAGCAAGAGATGTGGATCTTGAGACAC     | 1767 |
| DB | 1913 | TTCTCCCCACACCAAGCTTTGTTGAGAGATCCGTGGCTCCCTATTTTTCACAAAGGGAAT    | 1972 |
| OY | 1648 | TTCTCCCCACACCAAGCTTTTGTGAGAGATCCGTGGCTCCCTATTTTTCACAAAGGGAAT    | 1707 |
| DB | 1853 | AGGAGGAAGGTTTTCCTCTCTCATTTGAAGGGAACCGATATGAGAAAGAGATC           | 1912 |
| OY | 1598 | AGGAGGAAGGTTTTCCTCTCTCATTTGAAGGGAACCGATATGAGAAAGAGATC           | 1647 |
| DB | 1793 | TTCTGTGGGGAAGAAAGATGTAGAGTGAATTCAAAAATCTGAATCTGAGACAGCATC       | 1852 |
| OY | 1538 | TTCTGTGGGGAAGAAAGATGTAGAGTGAATTCAAAAATCTGAATCTGAGACAGCATC       | 1587 |
| DB | 1733 | AGTTCCAAAGTGTATAGAAAGAGAAATCCGAGGAGAAAGAAACAGAAAGACGAG          | 1732 |
| OY | 1468 | AGTTCCAAAGTGTATAGAAAGAGAAATCCGAGGAGAAAGAAAGAAAGACGAG            | 1537 |
| DB | 1673 | TTCCAGAGAGCCAGTGCAGAGAGGAGGCTCTCAGAGAGCTCATCTGAAAGCCTTAGATTG    | 1722 |
| OY | 1408 | TTCCAGAGAGCCAGTGCAGAGAGGAGGCTCTCAGAGAGCTCATCTGAAAGCCTTAGATTG    | 1467 |
| DB | 1613 | CAGCTTTAAAAAGCAACAGAGAGCAGCTCAGACAGGCAACGGCAACTGCTCAGAACAT      | 1672 |
| OY | 1348 | CAGCTTTAAAAAGCAACAGAGAGCAGCTCAGACAGGCAACGGCAACTGCTCAGAACAT      | 1407 |
| DB | 1553 | AATAGGCGCACCTTGGAAAGAGCAAGAAAGAGGCGGATTTTCAGACAGTAGTTGAA        | 1612 |
| OY | 1288 | AATAGGCGCACCTTGGAAAGAGCAAGAAAGAGGCGGATTTTCAGACAGTAGTTGAA        | 1347 |
| DB | 1493 | GGCTCATTTCTACCTAATAATTTGATCTCGGCTGTGTGTGGCCATGGCTCAGAGGACAG     | 1552 |
| OY | 1228 | GGCTCATTTCTACCTAATAATTTGATCTCGGCTGTGTGTGGCCATGGCTCAGAGGACAG     | 1287 |
| DB | 1433 | CTGACATTTAGCTGTCTGTGGAAAGGTCATGATATTTTGTATTTGGTCATTTTCTTG       | 1432 |
| OY | 1168 | CTGACATTTAGCTGTCTGTGGAAAGGTCATGATATTTTGTATTTGGTCATTTTCTTG       | 1227 |
| DB | 1373 | TGGGCTTTTGTCTCTTGTTCAGACTAATGACTCAGAGACTTCTGGGAAATCTTATCAA      | 1372 |
| OY | 1108 | TGGGCTTTTGTCTCTTGTTCAGACTAATGACTCAGAGACTTCTGGGAAATCTTATCAA      | 1167 |
| DB | 1313 | ATGTGTGAAAGCTGTGTAGAAATTCACATTTATGCTATACAAAGTTTGATACCTTCAGT     | 1312 |
| OY | 1048 | ATGTGTGAAAGCTGTGTAGAAATTCACATTTATGCTATACAAAGTTTGATACCTTCAGT     | 1107 |
| DB | 1253 | TTTTTAATGACACTACTATGTGTGAATAATGACTGTGATGAGGCCAAATGTCAGAGAGAT    | 1252 |
| OY | 988  | TTTTTAATGACACTACTATGTGTGAATAATGACTGTGATGAGGCCAAATGTCAGAGAGAT    | 1047 |
| DB | 1193 | TTTGAGTTTGACGTGAAGTCAATATATTCAAAGATTCACAGATATCATTTTCTGTGAGAGT   | 987  |
| OY | 928  | TTTGAGTTTGACGTGAAGTCAATATATTCAAAGATTCACAGATATCATTTTCTGTGAGAGT   | 927  |
| DB | 1133 | CATAGTATAGAAAAAGATATTAAGTGTGATTTAATAGTACACTATATAAGAAACTGTC      | 1132 |
| OY | 868  | CATAGTATAGAAAAAGATATTAAGTGTGATTTAATAGTACACTATATAAGAAACTGTC      | 867  |
| DB | 1073 | ATGGCAACCTGAGGAATTAATATATATACATATGAGCCCTCCACCAATGCTCTTGAGAGAA   | 1072 |
| OY | 808  | ATGGCAACCTGAGGAATTAATATATATACATATGAGCCCTCCACCAATGCTCTTGAGAGAA   | 807  |

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|----|------|---|-------|
| Db | 2152 | CGGATTCCTGGCAGTGTTCCAGCGAATGGAGAAATCCAGACACGTGTGATTCGAATGT      | 22111 |
| Qy | 1948 | GTGGTTTCCTGTTGGTGGACCTTCAGTTCCTACATCCCTGTTGGACAGCTTCTGGCA       | 20075 |
| Db | 2212 | GTGGTTTCCTGGTTGGTGGACCTTCAGTTCCTACATCCCTGTTGGACAGCTTCTGGCA      | 22711 |
| Qy | 2008 | GAGGTGATATAGTATAGCCACGCTACTGATGACATATGAGAACACCACTGAAACTGAATG    | 20675 |
| Db | 2272 | GAGGTGATATATAGTATAGCCACGCTACTGATGACAAATGGAACACCACTGAAACTGAATG   | 23311 |
| Qy | 2068 | AGAAAGAGAAAGGTCAACTCTTTCCACGTTTCCAGTTCAGTCTTCTGAAAGATCCCTGCCA   | 21275 |
| Db | 2332 | AGAAAGAGAAAGGTCAAGTCTTTCCACGTTTCCAGTTCAGTCTTCTGAAAGATCCCTGCCA   | 23911 |
| Qy | 2128 | AGGCACGAGCAATGAGTATATAGCCAGCAATTCCTAACAAATACAGTAGAGAAACCTTGAGAA | 21875 |
| Db | 2392 | AGGCACGAGCAATGAGTATATAGCCAGCAATTCCTAACAAATACAGTAGAGAAACCTTGAGAA | 24511 |
| Qy | 2188 | TTCCAGCGCAAAATGCCACCCCTGTGGTATAAATTTTCCAAACATATCTTAATCTGGGAC    | 22475 |
| Db | 2452 | TTCCAGCGCAAAATGCCACCCCTGTGGTATAAATTTTCCAAACATATCTTAATCTGGGAC    | 25111 |
| Qy | 2248 | TTGTTTCCTCATTTGGCTTAAAGGAAACAAATGTTTCCACCTGGTGTATATGACCACTTT    | 23075 |
| Db | 2512 | TTGTTTCCTCATTTGGCTTAAAGGAAACAAATGTTTCCACCTGGTGTATATGACCACTTT    | 25711 |
| Qy | 2308 | GTTTACCGTGGCATTACCACTCTGATTTGCTTAAATATCTTTTATGAGCCATATGAGAC     | 23675 |
| Db | 2572 | GTTTACCGTGGCATTACCACTCTGATTTGCTTAAATATCTTTTATGAGCCATATGAGAC     | 26311 |
| Qy | 2368 | TATCCAAATGACGGACATTTTCAATTAATGTGCTTACAGTAGAGAAACTGTGTTTCTACTGGG | 24275 |
| Db | 2632 | TATCCAAATGACGGACATTTTCAATTAATGTGCTTACAGTAGAGAAACTGTGTTTCTACTGGG | 26911 |
| Qy | 2428 | ATCTTTACAGCAAAATGTTTCTGAAAAATTTATGCGATGAGATCTTACTATTTATTTCCA    | 24875 |
| Db | 2692 | ATCTTTACAGCAAAATGTTTCTGAAAAATTTATGCGATGAGATCTTACTATTTATTTCCA    | 27511 |
| Qy | 2488 | GAAAGCTGAGAAATATCTTTGACGGTTTTATTTGTGACGCTTAGCCTGGTAGAATTTGGACTC | 25475 |
| Db | 2752 | GAAAGCTGAGAAATATCTTTGACGGTTTTATTTGTGACGCTTAGCCTGGTAGAATTTGGACTC | 28111 |
| Qy | 2548 | GCCAAATGTGAAGGATTAATCTGTTTCTCCGTTCAATTTGATGCTGCGAGCTTTTCAAGTTG  | 26075 |
| Db | 2812 | GCCAAATGTGAAGGATTAATCTGTTTCTCCGTTCAATTTGATGCTGCGAGCTTTTCAAGTTG  | 28711 |
| Qy | 2608 | GCAAAATCTTGGCCAAAGTTAAATATATGCTAAATAAATATATGCGCAATTCCTGGGGGCT   | 26675 |
| Db | 2872 | GCAAAATCTTGGCCAAAGTTAAATATATGCTAAATAAATATATGCGCAATTCCTGGGGGCT   | 29311 |
| Qy | 2668 | CTGGGAAATTTTAAACCTCGCTCTTGGGCATCATGCTTCAATTTTGGCCGTGTGGCGCANG   | 27275 |
| Db | 2932 | CTGGGAAATTTTAAACCTCGCTCTTGGGCATCATGCTTCAATTTTGGCCGTGTGGCGCANG   | 29911 |
| Qy | 2728 | CAGCTCTTGTGTAAGACTACAAAGATGTGCTGCAAGATCGCCAGTAGTATGTCACTC       | 27875 |
| Db | 2992 | CAGCTCTTGTGTAAGACTACAAAGATGTGCTGCAAGATCGCCAGTAGTATGTCAACTC      | 30511 |
| Qy | 2788 | CCAGGCTGGCATTGAATGACTTCTTCCACTCTTCTCTGATTTGTGTTCCGCTGCTGTGT     | 28475 |
| Db | 3052 | CCAGGCTGGCATTGAATGACTTCTTCCACTCTTCTCTGATTTGTGTTCCGCTGCTGTGT     | 31111 |
| Qy | 2848 | GGGGATGGATAGAGACCATGTGGGACGTATATGAGAGTTGCTGGTCCAAACCAATGTGCTT   | 29075 |
| Db | 3112 | GGGGATGGATAGAGACCATGTGGGACGTATATGAGAGTTGCTGGTCCAAACCAATGTGCTT   | 31711 |
| Qy | 2908 | ACTGCTTCATGATGATGTCATGTGATTTGGAAACCTATAGTGGTCTCTGATCTCTTTCTGGCC | 29675 |
| Db | 3172 | ACTGCTTCATGATGATGTCATGTGATTTGGAAACCTATAGTGGTCTCTGATCTCTTTCTGGCC | 32311 |
| Qy | 2968 | TTGCTTTTGAAGCTATTTTATGTCAGACACACCTTGCACCACTGATGATGATATGAATG     | 30275 |



Db 3332 TTGCTTGTGACCTCATTTAGTGCAGACACCTTGCACCCATGTATGATTAATGAATG 3391  
OY 3028 AATPATCTCCAAATTTGCTGTGATGAGATGCACAAAGAGATGTTATGTAAGAAAA 3087  
Db 3392 AATPATCTCCAAATTTGCTGTGATGAGATGCACAAAGAGATGTTATGTAAGAAAA 3351  
OY 3088 AATPATGAATTTATTAACAAGTCCCTTCATTAGGAACAAAAGATTTTATGTAATTTAA 3147  
Db 3352 AATPATGAATTTATTAACAAGTCCCTTCATTAGGAACAAAAGATTTTATGTAATTTAA 3411  
OY 3148 CCACTGTATCATCTAAACAACAAGAACAGATGTTATGTCACATCATACACAGAAAT 3207  
Db 3412 CCACTGTATCATCTAAACAACAAGAACAGATGTTATGTCACATCATACAGAAAT 3471  
OY 3208 GGGAAAGATCTGACATCTTAAGATGTAAGATGTAAGATGTAAGATGTAAGATGTA 3267  
Db 3472 GGGAAAGATCTGACATCTTAAGATGTAAGATGTAAGATGTAAGATGTAAGATGTA 3531  
OY 3268 AGCAGTGTGAAAAATATCATTTATGATGAAGATGATGATGATGATGATGATGATG 3327  
Db 3532 AGCAGTGTGAAAAATATCATTTATGATGAAGATGATGATGATGATGATGATGATG 3591  
OY 3328 AGCTTACTGTGACTGACCAATTTGCTGTAGAGACATCTGATGAAAAATTTAAACAG 3387  
Db 3592 AGCTTACTGTGACTGACCAATTTGCTGTAGAGACATCTGATGAAAAATTTAAACAG 3651  
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Db 3652 GAAGACTTTAGTATGTAATGGAATCTGTGAAGAAAGAAAGAAAGAAAGAAAGAAAG 3711  
OY 3448 AGCTCATCAGAAAGTACACTGTGTGACATGCGGCACCTGTAGAAAGAACGCCGTAGT 3507  
Db 3712 AGCTCATCAGAAAGTACACTGTGTGACATGCGGCACCTGTAGAAAGAACGCCGTAGT 3771  
OY 3508 GAACCTGAGAAACTCTTGAACCAAGAGCTTGTTCACGTGAAGCTGTGACAAAGATTC 3567  
Db 3772 GAACCTGAGAAACTCTTGAACCAAGAGCTTGTTCACGTGAAGCTGTGACAAAGATTC 3831  
OY 3568 AAGGTGTGAATCATGTGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAG 3627  
Db 3832 AAGGTGTGAATCATGTGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAG 3891  
OY 3628 ACGTGTTCGGAATAGTTGAACATTAACGTGTTGAGACCTTCATTTTCATGATTTCTC 3687  
Db 3892 ACGTGTTCGGAATAGTTGAACATTAACGTGTTGAGACCTTCATTTTCATGATTTCTC 3951  
OY 3688 CTTAGTAGTGTGCTGCGCATTTGAAGATTAATATATGATGATGATGATGATGATGAT 3747  
Db 3952 CTTAGTAGTGTGCTGCGCATTTGAAGATTAATATATGATGATGATGATGATGATGAT 4011  
OY 3748 ACGATGTGGAATATGCTGACAGAGTTTTCATTTTCATTTTCATTTTCATTTTCATTT 3807  
Db 4012 ACGATGTGGAATATGCTGACAGAGTTTTCATTTTCATTTTCATTTTCATTTTCATTT 4071  
OY 3808 AATGTGTCATATGCTCAATCAATATTTTCAACAATGCTGTGTGTGTGTGTGTGTGTG 3867  
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OY 3868 TTAATGTGTGATGTTTCATTTGCTGAGTTTAAACAGCAAAATGCTGTGTGTGTGTGTG 3927  
Db 4131 TTAATGTGTGATGTTTCATTTGCTGAGTTTAAACAGCAAAATGCTGTGTGTGTGTGTG 4190  
OY 3928 GAGGACATCAATCTCTACAGAGACATGAGAGCTGTGAGACCTTAAAGCCTTATCTCGA 3987  
Db 4191 GAGGACATCAATCTCTACAGAGACATGAGAGCTGTGAGACCTTAAAGCCTTATCTCGA 4250  
OY 3988 TTTGAAGGAGATGAGGATGTTGTGAATGCTTTTGAAGAGCAATTCATCATCATGAAT 4047  
Db 4251 TTTGAAGGAGATGAGGATGTTGTGAATGCTTTTGAAGAGCAATTCATCATCATGAAT 4310  
OY 4048 GTGCTCTGTGTTGTCTTATATCTGTGCTAAATTTTCAAGCATGAGGCTGTAATTTGT 4107  
Db 4311 GTGCTCTGTGTTGTCTTATATCTGTGCTAAATTTTCAAGCATGAGGCTGTAATTTGT 4370

OY 4108 GCTGGCAAAATCTCACACTGATTAACACCAACACTGCTGACAGGTTGACATGAGAC 4167  
Db 4371 GCTGGCAAAATCTCACACTGATTAACACCAACACTGCTGACAGGTTGACATGAGAC 4430  
OY 4168 GTGATATCATCTGATGATGCTTAAACTATATAGAAAGAAATGAGATGCTGATGAAA 4227  
Db 4431 GTGATATCATCTGATGATGCTTAAACTATATAGAAAGAAATGAGATGCTGATGAAA 4490  
OY 4228 AATGTGAAGTAACTTTGATATGATGATGATGATGATGATGATGATGATGATGATG 4287  
Db 4491 AATGTGAAGTAACTTTGATATGATGATGATGATGATGATGATGATGATGATGATG 4550  
OY 4288 ACATTCAGAGATGAGATGATATGATGATGATGATGATGATGATGATGATGATGATG 4347  
Db 4551 ACATTCAGAGATGAGATGATATGATGATGATGATGATGATGATGATGATGATGATG 4610  
OY 4348 CAGCCTAAGTATGAAAGAGCTGTACATGATGATGATGATGATGATGATGATGATGATG 4407  
Db 4611 CAGCCTAAGTATGAAAGAGCTGTACATGATGATGATGATGATGATGATGATGATGATG 4670  
OY 4408 GGTGCTCTTACCTTGAACCTGTTTATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4467  
Db 4671 GGTGCTCTTACCTTGAACCTGTTTATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4730  
OY 4468 AAAAAAGTTGGAGTCAAGACATCTTATGACAGAAAGAAAGAAAGAAAGAAAGAAAG 4527  
Db 4731 AAAAAAGTTGGAGTCAAGACATCTTATGACAGAAAGAAAGAAAGAAAGAAAGAAAG 4790  
OY 4528 GCAATGAAAAATTAAGATGAAAAAAGCAAAAGCTTATCTGACAGCAAGAAACAAA 4587  
Db 4791 GCAATGAAAAATTAAGATGAAAAAAGCAAAAGCTTATCTGACAGCAAGAAACAAA 4850  
OY 4588 TTTCAAGAAATGCTTGTGACTGTGATGACAGACAACTTTTGCATATGATGATGATGAT 4647  
Db 4851 TTTCAAGAAATGCTTGTGACTGTGATGACAGACAACTTTTGCATATGATGATGATGAT 4910  
OY 4648 CTGATCTGTATTAACATGTCACAAATGATGATGATGATGATGATGATGATGATGATGAT 4707  
Db 4911 CTGATCTGTATTAACATGTCACAAATGATGATGATGATGATGATGATGATGATGATGAT 4970  
OY 4708 ACTACATTTTTCACAGCATCAATCTGCTCATTTGCTATTTTACTGAGAGTGTGTA 4767  
Db 4971 ACTACATTTTTCACAGCATCAATCTGCTCATTTGCTATTTTACTGAGAGTGTGTA 5030  
OY 4768 CTGAACTCATCTCTACAGCATTAATTTTACATTTTACATTTTACATTTTACATTTT 4827  
Db 5031 CTGAACTCATCTCTACAGCATTAATTTTACATTTTACATTTTACATTTTACATTTT 5090  
OY 4828 GTGCTGTCAATCTCTCCTCATTTGATGATGATGATGATGATGATGATGATGATGATGAT 4887  
Db 5091 GTGCTGTCAATCTCTCCTCATTTGATGATGATGATGATGATGATGATGATGATGATGAT 5150  
OY 4888 GTGCTGTCAATCTCTCCTCATTTGATGATGATGATGATGATGATGATGATGATGATGAT 4947  
Db 5151 GTGCTGTCAATCTCTCCTCATTTGATGATGATGATGATGATGATGATGATGATGATGAT 5210  
OY 4948 ATCAAGAGCAAAAGGAGATCCGACAGCTCTCTTGTGTGTGTGTGTGTGTGTGTGTG 5007  
Db 5211 ATCAAGAGCAAAAGGAGATCCGACAGCTCTCTTGTGTGTGTGTGTGTGTGTGTGTG 5270  
OY 5008 TTTGTTTAACATGCGCTCTCTCATTTTGTGATGATGATGATGATGATGATGATGATGATG 5067  
Db 5271 TTTGTTTAACATGCGCTCTCTCATTTTGTGATGATGATGATGATGATGATGATGATGATG 5330  
OY 5068 TCCAACTTGTCTATGTTAAGAGGAAGTTGGATGATGATGATGATGATGATGATGATGATG 5127  
Db 5331 TCCAACTTGTCTATGTTAAGAGGAAGTTGGATGATGATGATGATGATGATGATGATGATG 5390  
OY 5128 TTTGGCAACAGCATGATCTGCTATTCCTCAATTTACAACCTCTGCTGCTGCTGCTGCTG 5187  
Db 5391 TTTGGCAACAGCATGATCTGCTATTCCTCAATTTACAACCTCTGCTGCTGCTGCTGCTG 5450



| QY  | 5188 | CTGACACCATTCTCACAAGTAAGCAACCCGACGTCAGTACCTTATTAAGTTAAACCCGGA    | 5247 |
|---|------|---|------|
| Db  | 5451 | CTGACACCATTCTCACAAGTAAGCAACCCGACGTCAGTACCTTATTAAGTTAAACCCGGA    | 5510 |
| QY  | 5248 | AGCTCAGTTAAGGAGACTGTGGGAACCCATCTGTGGAAATTTCTTTTGTGAGTTAC        | 5307 |
| Db  | 5511 | AGCTCAGTTAAGGAGACTGTGGGAACCCATCTGTGGAAATTTCTTTTGTGAGTTAC        | 5570 |
| QY  | 5308 | ATCATCATATCTCTTCGTTGTGTGTAACATGTACATCGCGTCACTCTGGAGACTTC        | 5367 |
| Db  | 5571 | ATCATCATATCTCTTCGTTGTGTGTAACATGTACATCGCGTCACTCTGGAGACTTC        | 5630 |
| QY  | 5368 | AGTGTGTCTACTGAAAGAAAGGACAGAGCCCTGTGATGAGTGAATTTGATATTTGAT       | 5427 |
| Db  | 5631 | AGTGTGTCTACTGAAAGAAAGGACAGAGCCCTGTGATGAGTGAATTTGATATTTGAT       | 5690 |
| QY  | 5428 | GAGGTTTGGGAAGATTGTGATCCGATGCACTAGTTCATGAGTAATTTGAAAATTAATCT     | 5487 |
| Db  | 5691 | GAGGTTTGGGAAGATTGTGATCCGATGCACTAGTTCATGAGTAATTTGAAAATTAATCT     | 5750 |
| QY  | 5488 | CAGTTTGACGCTGCGCTTGAAACCGCTCTCAATCTGCCACAACCAAACTCCAGCTC        | 5547 |
| Db  | 5751 | CAGTTTGACGCTGCGCTTGAAACCGCTCTCAATCTGCCACAACCAAACTCCAGCTC        | 5810 |
| QY  | 5548 | ATTGCGATGAGATTTCGCCCATGGTGAATGATGATACCGGATCCACTGCTGATATCTTAAT   | 5607 |
| Db  | 5811 | ATTGCGATGAGATTTCGCCCATGGTGAATGATGATACCGGATCCACTGCTGATATCTTAAT   | 5870 |
| QY  | 5608 | GCTTTTACAAAGCGGTTCTAGAGAGAGTGAAGATGATGATGCTCTACGATACAGATG       | 5667 |
| Db  | 5871 | GCTTTTACAAAGCGGTTCTAGAGAGAGTGAAGATGATGATGCTCTACGATACAGATG       | 5930 |
| QY  | 5668 | GAAGAGCGATTCATGGCTTCCATCTCCAAAGTCTCCATACAGCAATCAGTACTACT        | 5727 |
| Db  | 5931 | GAAGAGCGATTCATGGCTTCCATCTCCAAAGTCTCCATACAGCAATCAGTACTACT        | 5990 |
| QY  | 5728 | TTTAAACGAAAAACAAGAGAGATATCTGCTGATATTTCAGCCGTCTTACAGAGCCAC       | 5787 |
| Db  | 5991 | TTTAAACGAAAAACAAGAGAGATATCTGCTGATATTTCAGCCGTCTTACAGAGCCAC       | 6050 |
| QY  | 5788 | CTTTTAAAGCGCACTGTAAACAACAGCTTCCTTACGTACATTAATAAACAATAACAAAGT    | 5847 |
| Db  | 6051 | CTTTTAAAGCGCACTGTAAACAACAGCTTCCTTACGTACATTAATAAACAATAACAAAGT    | 6110 |
| QY  | 5848 | GGGGCTAATCTTCTTATTAAGAAGACATGATTAATGACAGATTAATGAAAATCTTAAT      | 5907 |
| Db  | 6111 | GGGGCTAATCTTCTTATTAAGAAGACATGATTAATGACAGATTAATGAAAATCTTAAT      | 6170 |
| QY  | 5908 | ACAGAAAAAATCGATCTGACCATGTGCCATGTGAGCTTGTCCACTTCTTATGACCGGGTG    | 5967 |
| Db  | 6171 | ACAGAAAAAATCGATCTGACCATGTGCCATGTGAGCTTGTCCACTTCTTATGACCGGGTG    | 6230 |
| QY  | 5968 | ACAAAGCCCAATTTGTGGAAAAACATGACAGCAAGAGCAAAAGATGAAGAAAGCCAAAGGAAA | 6027 |
| Db  | 6231 | ACAAAGCCCAATTTGTGGAAAAACATGACAGCAAGAGCAAAAGATGAAGAAAGCCAAAGGAAA | 6290 |
| QY  | 6028 | TAA 6030  |      |
| Db  | 6291 | TAA 6293  |      |
| <p>RESULT 5<br/>           AX391144 4362 bp DNA linear PAT 19-MAR-2002<br/>           LOCUS AX391144<br/>           DEFINITION Sequence 15 from Patent W00214498.<br/>           ACCESSION AX391144<br/>           VERSION AX391144.1 GI:19584239<br/>           KEYWORDS<br/>           SOURCE human.<br/>           ORGANISM Homo sapiens<br/>           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;<br/>           Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.</p> |      |   |      |
| REFERENCE   | 1    |   |      |

| FEATURES              | source  | 1. .4362   | /organism="Homo sapiens" | /db_xref="taxon:9606" | 3 others |
|-----------------------|---|--|--------------------------|-----------------------|----------|
| JOURNAL               | same  | Patent: WO 0214498-A 15 21-FEB-2002;                           |                          |                       |          |
| TITLE                 | Novel human ion channel proteins and polynucleotides encoding the |  |                          |                       |          |
| AUTHORS               | Turner, C.A., Mathur, B. and Mathur, D.                           |  |                          |                       |          |
| BASE COUNT            | 1300 a  | 845 c  | 995 g                    | 1219 t                | 3 others |
| ORIGIN                |   |  |                          |                       |          |
| Query Match           | 71.9%;  | Score 4338;  | DB 6;                    | Length 4362;          |          |
| Best Local Similarity | 100.0%;   | Prod. No. 0;   |                          |                       |          |
| Matches 4338;         | Conservative 0;   | Mismatches 0;  | Indels 0;                | Gaps 0;               |          |
| QY                    | 1   | ATGGAGCAACAGCTGCTTGTACCAACAGACCTGACAGCTTCACCTTCCACAGAGAA       | 60                       |                       |          |
| Db                    | 1   | ATGGAGCAACAGCTGCTTGTACCAACAGACCTGACAGCTTCACCTTCCACAGAGAA       | 60                       |                       |          |
| QY                    | 61  | TCTCTGGCGCTATTGAAAGACGCATTGCAAGAAAAAGCAAGATCCCAACACGAC         | 120                      |                       |          |
| Db                    | 61  | TCTCTGGCGCTATTGAAAGACGCATTGCAAGAAAAAGCAAGATCCCAACACGAC         | 120                      |                       |          |
| QY                    | 121   | AAAAAAGTGCAGCAGAAAAATGGCCCAAGCCAAATAGTACTTGGAAGCTGGAAGAAC      | 180                      |                       |          |
| Db                    | 121   | AAAAAAGTGCAGCAGAAAAATGGCCCAAGCCAAATAGTACTTGGAAGCTGGAAGAAC      | 180                      |                       |          |
| QY                    | 181   | CTTCCATTAAATTAAGAGACATTTCTCCAGAGATGCTGCAGAGCCCTCGAGAGACCTG     | 240                      |                       |          |
| Db                    | 181   | CTTCCATTAAATTAAGAGACATTTCTCCAGAGATGCTGCAGAGCCCTCGAGAGACCTG     | 240                      |                       |          |
| QY                    | 241   | GACCCCTACTATATCAATPAGAAAACTTTATAGTATGATPAGAAAAAGGAGCCATCTTC    | 300                      |                       |          |
| Db                    | 241   | GACCCCTACTATATCAATPAGAAAACTTTATAGTATGATPAGAAAAAGGAGCCATCTTC    | 300                      |                       |          |
| QY                    | 301   | CGGTCACTGCACCTGCGCCCTGTACATTTAACTCCCTCCATCCCTTGAGAAAAATA       | 360                      |                       |          |
| Db                    | 301   | CGGTCACTGCACCTGCGCCCTGTACATTTAACTCCCTCCATCCCTTGAGAAAAATA       | 360                      |                       |          |
| QY                    | 361   | GCTATTAGATTTTGGTACATTCATTATTCAGACATGCTCAATTAATGTCACCTATTTTGACA | 420                      |                       |          |
| Db                    | 361   | GCTATTAGATTTTGGTACATTCATTATTCAGACATGCTCAATTAATGTCACCTATTTTGACA | 420                      |                       |          |
| QY                    | 421   | AACCTGTGTATTATGACAAATGATTAACCTCCTGATGAGCAAGAAATGTAGAAATCACCC   | 480                      |                       |          |
| Db                    | 421   | AACCTGTGTATTATGACAAATGATTAACCTCCTGATGAGCAAGAAATGTAGAAATCACCC   | 480                      |                       |          |
| QY                    | 481   | TTCAAGAGAAATTAATTAATTTGAACACTTAAATAAATTAATGCAAGGGGATTCCTTTA    | 540                      |                       |          |
| Db                    | 481   | TTCAAGAGAAATTAATTAATTTGAACACTTAAATAAATTAATGCAAGGGGATTCCTTTA    | 540                      |                       |          |
| QY                    | 541   | GAAAGATTTTACTTCTCTCGGATCCATGGAATGGAATGCTGATTCATTAATTT          | 600                      |                       |          |
| Db                    | 541   | GAAAGATTTTACTTCTCTCGGATCCATGGAATGGAATGCTGATTCATTAATTT          | 600                      |                       |          |
| QY                    | 601   | GGTACGTCACAGAGTTTGTGACACCGGCAATGCTCGGCATTTGGAACATTCACAGATT     | 660                      |                       |          |
| Db                    | 601   | GGTACGTCACAGAGTTTGTGACACCGGCAATGCTCGGCATTTGGAACATTCACAGATT     | 660                      |                       |          |
| QY                    | 661   | CTCCAGAGCAATTAAGACAACTTCAGATTCACAGAGCTCAAAAAACATTTGGGAGGCCCTG  | 720                      |                       |          |
| Db                    | 661   | CTCCAGAGCAATTAAGACAACTTCAGATTCACAGAGCTCAAAAAACATTTGGGAGGCCCTG  | 720                      |                       |          |
| QY                    | 721   | ATCCAGTCTGTGAAGAGCTCTCAGATGTAATGATCTCACTGTCTCTGTCGACGCTA       | 780                      |                       |          |
| Db                    | 721   | ATCCAGTCTGTGAAGAGCTCTCAGATGTAATGATCTCACTGTCTCTGTCGACGCTA       | 780                      |                       |          |
| QY                    | 781   | TTTGGCTTAATTTGGGCTGCAGCTGTTCAATGAGCAACCTGAGCAATTAATGATTAATG    | 840                      |                       |          |
| Db                    | 781   | TTTGGCTTAATTTGGGCTGCAGCTGTTCAATGAGCAACCTGAGCAATTAATGATTAATG    | 840                      |                       |          |
| QY                    | 841   | CCTCCACCAATGCTCTTGGAGAGCAATGATTAAGAAAAAATTAATTAATGATTAATG      | 900                      |                       |          |

|    |      |   |      |
|----|------|---|------|
| Db | 841  | CTCTCCACCAATGCTTCTTGAGGAAACATGATATAGAAAGAAATATACCTGTGAATAT    | 900  |
| Oy | 901  | AATGCTACACTTATAAATGAAACTGTCTTTGACTTTGACTGGAAGTCATATATTTCAAGAT | 960  |
| Db | 901  | AATGCTACACTTATAAATGAAAGCTGTCTTTGACTTTGACTGGAAGTCATATTTCAAGAT  | 960  |
| Oy | 961  | TCAAGATATCTATTATTTCTTGAGGGTTTTTATGATGACACACTATGTGGAATATGCTCT  | 1020 |
| Db | 961  | TCAAGATATCTATTATTTCTTGAGGGTTTTTATGATGACACTATATGTGGAATATGCTCT  | 1020 |
| Oy | 1021 | GATCGAGGCCAAATGCTCCAGAGGGATATATGTGTGAAGCTGTGAATATCCCAATAT     | 1080 |
| Db | 1021 | GATCGAGGCCAAATGCTCCAGAGGGATATATGTGTGAAGCTGTGAATATCCCAATAT     | 1080 |
| Oy | 1081 | GGCTACACAAAGCTTTGATACCTTCAGTGGGCTTTTGTGCTTGTTGACTAATGACT      | 1140 |
| Db | 1081 | GGCTACACAAAGCTTTGATACCTTCAGTGGGCTTTTGTGCTTGTTGACTAATGACT      | 1140 |
| Oy | 1141 | CAGGACTTTGEGGAAATCTTTATCACTGACATTAACGTGCTGTGGGAAACGTACATG     | 1200 |
| Db | 1141 | CAGGACTTTGEGGAAATCTTTATCACTGACATTAACGTGCTGTGGGAAACGTACATG     | 1200 |
| Oy | 1201 | ATATTTTGTGTGTGTCATTTTCTTG6GCTCATTTCTACCTAATTAATTTGATCTGCT     | 1260 |
| Db | 1201 | ATATTTTGTGTGTGTCATTTTCTTG6GCTCATTTCTACCTAATTAATTTGATCTGCT     | 1260 |
| Oy | 1261 | GTGTGGGCAATGGCTGACGAGGAAACGAATACAGGCCACCTTGGAAGAACACAAAGAA    | 1320 |
| Db | 1261 | GTGTGGGCAATGGCTGACGAGGAAACGAATACAGGCCACCTTGGAAGAACACAAAGAA    | 1320 |
| Oy | 1321 | GAGGCCGAATTTACGAGATGATTTGAACACTTAAAAACAAACAGAGGCACTCAGAG      | 1380 |
| Db | 1321 | GAGGCCGAATTTACGAGATGATTTGAACACTTAAAAACAAACAGAGGCACTCAGAG      | 1380 |
| Oy | 1381 | GCAGCAACGGCACTGCTCTAGAAACATTCAGAGAGCCAGTGCACGACGACGAGCTCTCA   | 1440 |
| Db | 1381 | GCAGCAACGGCACTGCTCTAGAAACATTCAGAGAGCCAGTGCACGACGACGAGCTCTCA   | 1440 |
| Oy | 1441 | GACAGCTCATGTGAAGCTCTGAAGTTAGTTCCAAAGAGCTTAAGGAAAGAAATATGG     | 1500 |
| Db | 1441 | GACAGCTCATGTGAAGCTCTGAAGTTAGTTCCAAAGAGCTTAAGGAAAGAAATATGG     | 1500 |
| Oy | 1501 | AGGAGAGAAAGAAACAGAAAGAGCACTGTGTGGGGAGAGAAAGATGAGGATGAATTC     | 1560 |
| Db | 1501 | AGGAGAGAAAGAAACAGAAAGAGCACTGTGTGGGGAGAGAAAGATGAGGATGAATTC     | 1560 |
| Oy | 1561 | CAAAAATCTGATCTGAGGACAGCATCAGAGGAAAGTTTTGCTTCCATTAAGAGG        | 1620 |
| Db | 1561 | CAAAAATCTGATCTGAGGACAGCATCAGAGGAAAGTTTTGCTTCCATTAAGAGG        | 1620 |
| Oy | 1621 | AACGGATGACATTAAGAAAGAGTACTCTCCGCCACACAGCTTTGTTGAGCAATCCGT     | 1680 |
| Db | 1621 | AACGGATGACATTAAGAAAGAGTACTCTCCGCCACACAGCTTTGTTGAGCAATCCGT     | 1680 |
| Oy | 1681 | GGCTCCCTATTTTACCAGAGGCGAAATAGCAGAAACAGCTTTACGTTTAGAGGGCA      | 1740 |
| Db | 1681 | GGCTCCCTATTTTACCAGAGGCGAAATAGCAGAAACAGCTTTTACGTTTAGAGGGCA     | 1740 |
| Oy | 1741 | GCAAAAGATGTGGATCTGAGAACACTTGCGAGATGATGAGACACAGCACTTTAGAGAT    | 1800 |
| Db | 1741 | GCAAAAGATGTGGATCTGAGAACACTTGCGAGATGATGAGACACAGCACTTTAGAGAT    | 1800 |
| Oy | 1801 | AACGAGAGCCGTAGAGATTCCTTTGTGTGCCCGGACGACAGGAGAGAGCAACAGC       | 1860 |
| Db | 1801 | AACGAGAGCCGTAGAGATTCCTTTGTGTGCCCGGACGACAGGAGAGAGCAACAGC       | 1860 |
| Oy | 1861 | AACCTGATCTAGACACAGTAGGTCAATCCCGGATCTGTGGACGTGTTCCACGAGATGGAG  | 1920 |
| Db | 1861 | AACCTGATCTAGACACAGTAGGTCAATCCCGGATCTGTGGACGTGTTCCACGAGATGGAG  | 1920 |
| Oy | 1921 | ATGCAACGACTGTGATGTGCAATGTGTGTCTTGTGGTTGTGGACCTTCAGTTCTCT      | 1980 |
| Db | 1921 | ATGCAACGACTGTGATGTGCAATGTGTGTCTTGTGGTTGTGGACCTTCAGTTCTCT      | 1980 |

|    |      |   |      |
|----|------|---|------|
| Db | 1921 | ATGCATAGACACTGTGGATTGGCAATGGGTGTGGTTCTTGGTTGGTGGACCTTCAAGTTCCT  | 1980 |
| Qy | 1981 | ACATGCGCTGTGGAGACAGCTTTCGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC   | 2040 |
| Db | 1981 | ACATGCGCTGTGGAGAGCTTTCGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC     | 2040 |
| Qy | 2041 | AATGGAACAACCACTGAAACTGAAATGAGAAAGAAAGTTCAGTTCCTTCCACGTTTCC      | 2100 |
| Db | 2041 | AATGGAACAACAACCTGAAACTGAAATGAGAAAGAAAGTTCAGTTCCTTCCACGTTTCC     | 2100 |
| Qy | 2101 | ATGGACCTTCTCAAGAACCTTCCTCCAAAGCAAGCAATGAGTATAGCAGCATTCCTA       | 2160 |
| Db | 2101 | ATGGACCTTCTCAAGAACCTTCCTCCAAAGCAAGCAATGAGTATAGCAGCATTCCTA       | 2160 |
| Qy | 2161 | ACAAATACAGTAGAAGAACTTGAAGAATCCAGGACAGAAAGCCCAACCTGTGGTATATAA    | 2220 |
| Db | 2161 | ACAAATACAGTAGAAGAACTTGAAGAATCCAGGACAGAAAGCCCAACCTGTGGTATATAA    | 2220 |
| Qy | 2221 | TTTTCCACATATTTCTTAATCTGGGAGCTGTTCTCCATATTTGGTTAAAAATGAAACATGTT  | 2280 |
| Db | 2221 | TTTTCCACATATTTCTTAATCTGGGAGCTGTTCTCCATATTTGGTTAAAAATGAAACATGTT  | 2280 |
| Qy | 2281 | GTCAACCTGTTGTGATGAGACCAATTTGTTGACCTGGCCATCACACTGTATGTCTTA       | 2340 |
| Db | 2281 | GTCAACCTGTTGTGATGAGACCAATTTGTTGACCTGGCCATCACACTGTATGTCTTA       | 2340 |
| Qy | 2341 | AATACCTTTTCATGAGCAATGAGACACTATCCATGACGAGCAATTCATTAATAGTCTT      | 2400 |
| Db | 2341 | AATACCTTTTCATGAGCAATGAGACACTATCCATGACGAGCAATTCATTAATAGTCTT      | 2400 |
| Qy | 2401 | ACAGTAGAAGAACTGTGTTTTCATCTGGGATCTTTCACAGCAAGAAATGTTTCGAAAAATATT | 2460 |
| Db | 2401 | ACAGTAGAAGAACTGTGTTTTCATCTGGGATCTTTCACAGCAAGAAATGTTTCGAAAAATATT | 2460 |
| Qy | 2461 | GCCATGGAATCTTACTATATATTTCCAAAGAGCTGGAAATATCTTGAACGTTTTATTTGG    | 2520 |
| Db | 2461 | GCCATGGAATCTTACTATATATTTCCAAAGAGCTGGAAATATCTTGAACGTTTTATTTGG    | 2520 |
| Qy | 2521 | ACGCTTAGCCTGTGTAGAACTGGACATCGGCCAATGTGGAAAGATTAATCTGTTCCCGTTCA  | 2580 |
| Db | 2521 | ACGCTTAGCCTGTGTAGAACTGGACATCGGCCAATGTGGAAAGATTAATCTGTTCCCGTTCA  | 2580 |
| Qy | 2581 | TTTTGATTCGTGCGAGTTTTCAAGTTGGCAAAATCTTTGGCAACGTTAAATATGCTATATA   | 2640 |
| Db | 2581 | TTTTGATTCGTGCGAGTTTTCAAGTTGGCAAAATCTTTGGCAACGTTAAATATGCTATATA   | 2640 |
| Qy | 2641 | AAGATCATGCGCAATTCCTGGGGGGCTGTGGAAATTTAAACCTCGTCTTGGCCATCATC     | 2700 |
| Db | 2641 | AAGATCATGCGCAATTCCTGGGGGGCTGTGGAAATTTAAACCTCGTCTTGGCCATCATC     | 2700 |
| Qy | 2701 | GTCTCATTTTTCGCGGTGGCGGCAATGCAACTCTTTGGTAAAGCTACAAAGATTTGTC      | 2760 |
| Db | 2701 | GTCTCATTTTTCGCGGTGGCGGCAATGCAACTCTTTGGTAAAGCTACAAAGATTTGTC      | 2760 |
| Qy | 2761 | TGCAAGATGCGCAGTATTTGTCAACTCCACGCTGGCAGCATGATGACTTCTTCCACTCC     | 2820 |
| Db | 2761 | TGCAAGATGCGCAGTATTTGTCAACTCCACGCTGGCAGCATGATGACTTCTTCCACTCC     | 2820 |
| Qy | 2821 | TTTCTGATTTGTTCGCGGTGTGTGTGGGAGTGATAGAGACCATGTGGAGCTGTATG        | 2880 |
| Db | 2821 | TTTCTGATTTGTTCGCGGTGTGTGTGGGAGTGATAGAGACCATGTGGAGCTGTATG        | 2880 |
| Qy | 2881 | GAGGTGTGCTGAACCAATGCTACCTGCTCACTGATGAGTGAAGCATGTGGAAAC          | 2940 |
| Db | 2881 | GAGGTGTGCTGAACCAATGCTACCTGCTCACTGATGAGTGAAGCATGTGGAAAC          | 2940 |
| Qy | 2941 | CTAGTGTCTGTGATCTCTTTCTGGCGCTTCTMTGAGCTCATTTTATGTGACAGCAACCTT    | 3000 |
| Db | 2941 | CTAGTGTCTGTGATCTCTTTCTGGCGCTTCTMTGAGCTCATTTTATGTGACAGCAACCTT    | 3000 |
| Qy | 3001 | GCAAGCACTGATGATGATAATGAATGAATATATCTCCAAATTCGCTGTGGATAGAGATCAC   | 3060 |
| Db | 3001 | GCAAGCACTGATGATGATAATGAATGAATATATCTCCAAATTCGCTGTGGATAGAGATCAC   | 3060 |

QY 3061 AAAAGAGTACCTTATGTGAAAAAGAAAAATATATGAAATTTATTCACAGTCCCTTCATTAGG 3120  
 DB 3061 AAAAGAGTACCTTATGTGAAAAAGAAAAATATATGAAATTTATTCACAGTCCCTTCATTAGG 3120  
 QY 3121 AAAAGAGTACCTTATGTGAAAAAGAAAAATATATGAAATTTATTCACAGTCCCTTCATTAGG 3180  
 DB 3121 AAAAGAGTACCTTATGTGAAAAAGAAAAATATATGAAATTTATTCACAGTCCCTTCATTAGG 3180  
 QY 3181 TGTATGTCCATCATTCACAGAAATTTGGAAAAATCTTACATCTCTTAAAGATGTAAAT 3240  
 DB 3181 TGTATGTCCATCATTCACAGAAATTTGGAAAAATCTTACATCTCTTAAAGATGTAAAT 3240  
 QY 3241 GGAAGTACAAAGTGTATAGAACTGGACAGTGTGAAAAATACATATTATGTAGAAAGT 3300  
 DB 3241 GGAAGTACAAAGTGTATAGAACTGGACAGTGTGAAAAATACATATTATGTAGAAAGT 3300  
 QY 3301 GATTACATGCTATTCATTAACAAACCCAGCTTACTGTGACTGTACCAATTTGCTAGGA 3360  
 DB 3301 GATTACATGCTATTCATTAACAAACCCAGCTTACTGTGACTGTACCAATTTGCTAGGA 3360  
 QY 3361 GAATCTGACTTTGAAAATTTAAACACGGAAAGCTTTAGTAGATCGAATCTGGAAAGAA 3420  
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QY 4141 ACTGTGACAGGTTTGTGACATCGAAGAGCTGAATATCATCTGATTCCTTAAACTAATA 4200  
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 RESULT 6  
 AX391146 4179 bp DNA linear PAT 19-MAR-2002  
 LOCUS AX391146  
 DEFINITION Sequence 17 from Patent WO0214498.  
 ACCESSION AX391146  
 VERSION AX391146.1 GI:19584240  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1  
 AUTHORS Turner, C.A., Mathur, B. and Mathur, D.  
 TITLE Novel human ion channel proteins and polynucleotides encoding the  
 same  
 JOURNAL Patent: WO 0214498-A 17 21-FEB-2002;  
 FEATURES  
 source 1. 4179  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 BASE COUNT 1239 a 815 c 958 g 1164 t 3 others  
 ORIGIN  
 Query Match 68.9%; Score 4152; DB 6; Length 4179;  
 Best local similarity 100.0%; Pred. No. 0;  
 Matches 4152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ATGAGCAAAACAGTGTGTGACACGAGACGTGACAGCTTCACTTCCACAGAGAA 60  
 DB 1 ATGAGCAAAACAGTGTGTGACACGAGACGTGACAGCTTCACTTCCACAGAGAA 60  
 QY 61 TCTCTGCGCTATTTGAAAGAGCATTTGCAAGAAAGGCAAAAGATCCCAACAGAC 120  
 DB 61 TCTCTGCGCTATTTGAAAGAGCATTTGCAAGAAAGGCAAAAGATCCCAACAGAC 120  
 QY 121 AAAAAGATGACGAGAAATGAGCCCAAGCCAAATAGTACTGTGAAGCTGAAAGAC 180  
 DB 121 AAAAAGATGACGAGAAATGAGCCCAAGCCAAATAGTACTGTGAAGCTGAAAGAC 180  
 QY 181 CTTCATTTATTTATGAGAGCATTTCTCCAGAGATGCTGACAGCCCTGAGAGACTG 240  
 DB 181 CTTCATTTATTTATGAGAGCATTTCTCCAGAGATGCTGACAGCCCTGAGAGACTG 240  
 QY 241 GACCCCTACTATATCATTAAGAAACTTTATATGATTAAGTAAGGAAGGCCATCTC 300  
 DB 241 GACCCCTACTATATCATTAAGAAACTTTATATGATTAAGTAAGGAAGGCCATCTC 300  
 QY 301 CGGTTCACTGACACCTGCTGCTGATCAATTTAATCTTCAATCTCTTAGAAATA 360  
 DB 301 CGGTTCACTGACACCTGCTGCTGATCAATTTAATCTTCAATCTCTTAGAAATA 360  
 QY 361 GCTATTAAGATTTGTTGATCAATTCATTAATGACATGCTAATATGTCACATTTTGA 420  
 DB 361 GCTATTAAGATTTGTTGATCAATTCATTAATGACATGCTAATATGTCACATTTTGA 420

|    |      |  |      |
|----|------|--|------|
| Oy | 421  | AAAGTGTTTATGACATGAGTAAACCTCCTGATTTGACAAAGAAATGTTGATTAAC          | 480  |
| Oy | 421  | AAAGTGTTTATGACATGAGTAAACCTCCTGATTTGACAAAGAAATGTTGATTAAC          | 480  |
| Oy | 421  | AAAGTGTTTATGACATGAGTAAACCTCCTGATTTGACAAAGAAATGTTGATTAAC          | 480  |
| Oy | 481  | TTCCACAGGAATATATCTTTTGAATACCTATATAAAAATTATGCAAGGAGCTTCTGTTTA     | 540  |
| Oy | 481  | TTCCACAGGAATATATCTTTTGAATACCTATATAAAAATTATGCAAGGAGCTTCTGTTTA     | 540  |
| Oy | 481  | TTCCACAGGAATATATCTTTTGAATACCTATATAAAAATTATGCAAGGAGCTTCTGTTTA     | 540  |
| Oy | 541  | GAAGATTTTACTTTCCTTGGGGATCCATGGAACCTGGCTGATTTCACTGTCATTACATTT     | 600  |
| Oy | 541  | GAAGATTTTACTTTCCTTGGGGATCCATGGAACCTGGCTGATTTCACTGTCATTACATTT     | 600  |
| Oy | 541  | GAAGATTTTACTTTCCTTGGGGATCCATGGAACCTGGCTGATTTCACTGTCATTACATTT     | 600  |
| Oy | 601  | GGGAGCTCAACAGTTTGTGGACCTGGGCAATGTCCTGGCATTTGAGAACCTTAGAGTT       | 660  |
| Oy | 601  | GGGAGCTCAACAGTTTGTGGACCTGGGCAATGTCCTGGCATTTGAGAACCTTAGAGTT       | 660  |
| Oy | 601  | GGGAGCTCAACAGTTTGTGGACCTGGGCAATGTCCTGGCATTTGAGAACCTTAGAGTT       | 660  |
| Oy | 661  | CTCCGACATTTGAAGACGATTCAGACATTTCCAGGCTCGAAACCATTTGTGGAGCCCTG      | 720  |
| Oy | 661  | CTCCGACATTTGAAGACGATTCAGACATTTCCAGGCTCGAAACCATTTGTGGAGCCCTG      | 720  |
| Oy | 661  | CTCCGACATTTGAAGACGATTCAGACATTTCCAGGCTCGAAACCATTTGTGGAGCCCTG      | 720  |
| Oy | 721  | ATCCAGTCTGTGAAGAAGCTCTCAGATGTAAATGATCTGACTGTGTCTGTGAGGCTA        | 780  |
| Oy | 721  | ATCCAGTCTGTGAAGAAGCTCTCAGATGTAAATGATCTGACTGTGTCTGTGAGGCTA        | 780  |
| Oy | 721  | ATCCAGTCTGTGAAGAAGCTCTCAGATGTAAATGATCTGACTGTGTCTGTGAGGCTA        | 780  |
| Oy | 781  | TTTGCTCTAATTTGGGCTGCAAGCTGTTCATGGCAACTGAGAGATTAATGTATCAATGG      | 840  |
| Oy | 781  | TTTGCTCTAATTTGGGCTGCAAGCTGTTCATGGCAACTGAGAGATTAATGTATCAATGG      | 840  |
| Oy | 781  | TTTGCTCTAATTTGGGCTGCAAGCTGTTCATGGCAACTGAGAGATTAATGTATCAATGG      | 840  |
| Oy | 841  | CCCTCCACCAATCTCTCTGGGAGCAATPATATAGAAAAAATATATACGTGAATTTAT        | 900  |
| Oy | 841  | CCCTCCACCAATCTCTCTGGGAGCAATPATATAGAAAAAATATATACGTGAATTTAT        | 900  |
| Oy | 841  | CCCTCCACCAATCTCTCTGGGAGCAATPATATAGAAAAAATATATACGTGAATTTAT        | 900  |
| Oy | 901  | AATGGTACACTTATTAATGAAACTGTCTTGTGAGTTTGAAGTCAATATATTTCAAGAT       | 960  |
| Oy | 901  | AATGGTACACTTATTAATGAAACTGTCTTGTGAGTTTGAAGTCAATATATTTCAAGAT       | 960  |
| Oy | 901  | AATGGTACACTTATTAATGAAACTGTCTTGTGAGTTTGAAGTCAATATATTTCAAGAT       | 960  |
| Oy | 961  | TCAAGATATCATTTATTTCTGAGGGTTTTTATGATGCACACTATGTGTGAATATGCTCT      | 1020 |
| Oy | 961  | TCAAGATATCATTTATTTCTGAGGGTTTTTATGATGCACACTATGTGTGAATATGCTCT      | 1020 |
| Oy | 961  | TCAAGATATCATTTATTTCTGAGGGTTTTTATGATGCACACTATGTGTGAATATGCTCT      | 1020 |
| Oy | 1021 | GATCAGAGGCAATGTCAGAGGGATPATGTGTGAAGAAAGCGTAGAAGAAATCCCAATTTAT    | 1080 |
| Oy | 1021 | GATCAGAGGCAATGTCAGAGGGATPATGTGTGAAGAAAGCGTAGAAGAAATCCCAATTTAT    | 1080 |
| Oy | 1021 | GATCAGAGGCAATGTCAGAGGGATPATGTGTGAAGAAAGCGTAGAAGAAATCCCAATTTAT    | 1080 |
| Oy | 1081 | GGCTACACCAAGCTTTGATACCTTCAGTTCAGTTCGGGCTTTTGTCTGCTTTCGACTAATGACT | 1140 |
| Oy | 1081 | GGCTACACCAAGCTTTGATACCTTCAGTTCAGTTCGGGCTTTTGTCTGCTTTCGACTAATGACT | 1140 |
| Oy | 1081 | GGCTACACCAAGCTTTGATACCTTCAGTTCAGTTCGGGCTTTTGTCTGCTTTCGACTAATGACT | 1140 |
| Oy | 1141 | CAGGACTTGTGGAAATCTTTATYCAACTGACATTACGTGCTGTGGAAACGTACATG         | 1200 |
| Oy | 1141 | CAGGACTTGTGGAAATCTTTATYCAACTGACATTACGTGCTGTGGAAACGTACATG         | 1200 |
| Oy | 1141 | CAGGACTTGTGGAAATCTTTATYCAACTGACATTACGTGCTGTGGAAACGTACATG         | 1200 |
| Oy | 1201 | ATATTTTGTGTGGCAATTTCTTGGGCTCATTTCTACCTAATATTAATTAATCTTGCT        | 1260 |
| Oy | 1201 | ATATTTTGTGTGGCAATTTCTTGGGCTCATTTCTACCTAATATTAATTAATCTTGCT        | 1260 |
| Oy | 1201 | ATATTTTGTGTGGCAATTTCTTGGGCTCATTTCTACCTAATATTAATTAATCTTGCT        | 1260 |
| Oy | 1261 | GTGGTGCCATGCGCTACGAGAACGAAATTCAGGCCACCTTGTGGAAGACGAAACAGAAA      | 1320 |
| Oy | 1261 | GTGGTGCCATGCGCTACGAGAACGAAATTCAGGCCACCTTGTGGAAGACGAAACAGAAA      | 1320 |
| Oy | 1261 | GTGGTGCCATGCGCTACGAGAACGAAATTCAGGCCACCTTGTGGAAGACGAAACAGAAA      | 1320 |
| Oy | 1321 | GAGCGCAATTTACAGCAGATGATTGAACAGCTTTAAAAAGCAACAGAGAGCGCTACAGAG     | 1380 |
| Oy | 1321 | GAGCGCAATTTACAGCAGATGATTGAACAGCTTTAAAAAGCAACAGAGAGCGCTACAGAG     | 1380 |
| Oy | 1321 | GAGCGCAATTTACAGCAGATGATTGAACAGCTTTAAAAAGCAACAGAGAGCGCTACAGAG     | 1380 |
| Oy | 1381 | GCACACAGGCACTGCTCAGAACCTTCCAGAGGCCAGTGCAGCAGGACGAGCTCTCA         | 1440 |
| Oy | 1381 | GCACACAGGCACTGCTCAGAACCTTCCAGAGGCCAGTGCAGCAGGACGAGCTCTCA         | 1440 |
| Oy | 1381 | GCACACAGGCACTGCTCAGAACCTTCCAGAGGCCAGTGCAGCAGGACGAGCTCTCA         | 1440 |
| Oy | 1441 | GACAGCTATCTGAAGCTCTTAAGTTGAGTTTCCAAAGTGTCTAAGAGAAAGAAATATGG      | 1500 |
| Oy | 1441 | GACAGCTATCTGAAGCTCTTAAGTTGAGTTTCCAAAGTGTCTAAGAGAAAGAAATATGG      | 1500 |
| Oy | 1441 | GACAGCTATCTGAAGCTCTTAAGTTGAGTTTCCAAAGTGTCTAAGAGAAAGAAATATGG      | 1500 |
| Oy | 1501 | AGGAGAAAAAGAAACAGAAAGACAGTCTGTGGGGAGAGAAAGATGAGATGAATTC          | 1560 |

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|----|------|---|------|
| Db | 1501 | AGGAAGAAAAGAAAAACGAAAAGCAGACTCTGGTGGGGAAGAAAGATGAGATCAATTC    | 1500 |
| Qy | 1561 | CAAAAATCTGAATCTGAGGAGCAGCATCAGAGGAAAGTTTTGCTTCATTCGAAAGG      | 1620 |
| Db | 1561 | CAAAAATCTGAATCTGAGGAGCAGCATCAGAGGAAAGTTTTGCTTCATTCGAAAGG      | 1620 |
| Qy | 1621 | AACCGATTGACATTTGAAAAGAGGACTCTCCCAACCAAGCTTTGTGTGACATCCGT      | 1680 |
| Db | 1621 | AACCGATTGACATTTGAAAAGAGGACTCTCCCAACCAAGCTTTGTGTGAGCATCCGT     | 1680 |
| Qy | 1681 | GGCTCCCAATTTTACCAAGGCGGAATAGCAACAGCTTTCAAGCTTTAGAGGGGA        | 1740 |
| Db | 1681 | GGCTCCCAATTTTACCAAGGCGGAATAGCAACAGCTTTCAAGCTTTAGAGGGGA        | 1740 |
| Qy | 1741 | GCAAGGATGTGGGATCTGAGAAAGCATTCGCGAGATGAGACAGCAGCTTTGAGAT       | 1800 |
| Db | 1741 | GCAAGGATGTGGGATCTGAGAAAGCATTCGCGAGATGAGACAGCAGCTTTGAGAT       | 1800 |
| Qy | 1801 | AACGAGAGCCGTAGAGATTCCTTGTGTCGCCGACGACGAGAGAGAGCAACAGC         | 1860 |
| Db | 1801 | AACGAGAGCCGTAGAGATTCCTTGTGTCGCCGACGACGAGAGAGAGCAACAGC         | 1860 |
| Qy | 1861 | AACCGAGTCAAGACCACTAGGTCATCCCGATTCGCGAGTGTTCAGCGCAATGGGAG      | 1920 |
| Db | 1861 | AACCGAGTCAAGACCACTAGGTCATCCCGATTCGCGAGTGTTCAGCGCAATGGGAG      | 1920 |
| Qy | 1921 | ATGCACAGCACTGTGGATATGCAATGGTGTGTTCTTGGTTGGTGAGACTTCAGTTCT     | 1980 |
| Db | 1921 | ATGCACAGCACTGTGGATATGCAATGGTGTGTTCTTGGTTGGTGAGACTTCAGTTCT     | 1980 |
| Qy | 1981 | ACATGCGCTGTTGGACAGACTTCTGCCAGAGGTATATAGATTAAGCCACTAGTATAC     | 2040 |
| Db | 1981 | ACATGCGCTGTTGGACAGACTTCTGCCAGAGGTATATAGATTAAGCCACTAGTATAC     | 2040 |
| Qy | 2041 | AATGGAACACCACTGAAATCTGAAATGAGAAAGAAAGTCAAGTTCTTCCAGCTTTCC     | 2100 |
| Db | 2041 | AATGGAACACCACTGAAATCTGAAATGAGAAAGAAAGTCAAGTTCTTCCAGCTTTCC     | 2100 |
| Qy | 2101 | ATGGAATCTTGAAGAGATCCCTCCCAAGGCAAGAGCATGAGTATAGCCAGCAATCTTA    | 2160 |
| Db | 2101 | ATGGAATCTTGAAGAGATCCCTCCCAAGGCAAGAGCATGAGTATAGCCAGCAATCTTA    | 2160 |
| Qy | 2161 | ACAATATACAGTAGAAGAACTTGAAATCCAGGACAGAAATGCCACCCGTTGGTATAA     | 2220 |
| Db | 2161 | ACAATATACAGTAGAAGAACTTGAAATCCAGGACAGAAATGCCACCCGTTGGTATAA     | 2220 |
| Qy | 2221 | TTTTTCAACATATTTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAGTGAACATGTT   | 2280 |
| Db | 2221 | TTTTTCAACATATTTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAGTGAACATGTT   | 2280 |
| Qy | 2281 | GTCACATGCTGTGTGATGAGAACCCATTTGTTGACCTGGCCATCCCACTCTGTATCTCTTA | 2340 |
| Db | 2281 | GTCACATGCTGTGTGATGAGAACCCATTTGTTGACCTGGCCATCCCACTCTGTATCTCTTA | 2340 |
| Qy | 2341 | AATACTCTTTTCAATGGCCATGAGCACTATCAATGAGGACCATTTCAATATGCTT       | 2400 |
| Db | 2341 | AATACTCTTTTCAATGGCCATGAGCACTATCAATGAGGACCATTTCAATATGCTT       | 2400 |
| Qy | 2401 | ACAGTAGAAGAACTTGGTTTCACTGGGATCTTTACAGCAAGAAATGTTTGTGAAAATATTT | 2460 |
| Db | 2401 | ACAGTAGAAGAACTTGGTTTCACTGGGATCTTTACAGCAAGAAATGTTTGTGAAAATATTT | 2460 |
| Qy | 2461 | GCCATGATTCCTTCAATATTTTCAAGAAAGGCTGGAAATATCTTTGAGGGTTTATGAG    | 2520 |
| Db | 2461 | GCCATGATTCCTTCAATATTTTCAAGAAAGGCTGGAAATATCTTTGAGGGTTTATGAG    | 2520 |
| Qy | 2521 | ACGCTTACCTGTGAGAACTTGGACTGCCAATGTGGAAGATATCTTCTCCGTCA         | 2580 |
| Db | 2521 | ACGCTTACCTGTGAGAACTTGGACTGCCAATGTGGAAGATATCTTCTCCGTCA         | 2580 |
| Qy | 2581 | TTTGATTTGCTGCGAGTTTCAAGTTGGCAAAATCTTGGCAAGTTAAATGCTATA        | 2640 |
| Db | 2581 | TTTGATTTGCTGCGAGTTTCAAGTTGGCAAAATCTTGGCAAGTTAAATGCTATA        | 2640 |

Db 2581 TTTCGATTCGTCGAGTTTCAGTTGCGCAAAATCTTGCCAGCTTAATATGCTAATA 2640  
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 Db 2641 AAGATTCATCCGCAATTCGCGTGGGGCTGTGGAAATTTAAACCTGCTGGCCATCATTC 2700  
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 QY 3121 AAACAAAAGATTTAGATGAATTAACACCTGATGATGATGATGATGATGATGATGAT 3180  
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 QY 3181 TGTATGTCATCATACACACAGAAATTTGGGAAAGATCTTGACTATCTTAAAGATTAAT 3240  
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 QY 3241 GGAATCTACAGTGTATGGAAGTGGAGCTGGAGAGCTGTGTAAGAAATACATTTATGATGA 3300  
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 ACCESSION AX391148  
 VERSION AX391148.1 GI:19584241  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1  
 TURNER, C.A., Mathur, B. and Mathur, D.  
 Novel human ion channel proteins and polynucleotides encoding the  
 same  
 JOURNAL Patent: WO 0214498-A 19 21-FEB-2002;  
 LEXICON Genetics Incorporated (US)  
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 Db 1 ATGAGACCAACAGTGTGTATCCACAGACGTGACAGCTTCACTTTCACAGAGAA 60  
 QY 61 TCTCTGGCGCTATTTAAAGAGAGCATTTGCAAGAAAGGCAAGATCCCAACAGAC 120  
 Db 61 TCTCTGGCGCTATTTAAAGAGAGCATTTGCAAGAAAGGCAAGATCCCAACAGAC 120  
 QY 121 AAAAAAGATGACAGCAAAATGCCCCCAAGCCAAATAGTACTTGGAACTGGAAAGAC 180  
 Db 121 AAAAAAGATGACAGCAAAATGCCCCCAAGCCAAATAGTACTTGGAACTGGAAAGAC 180



OY 181 CTTCATTATATGAGACATTCCTCCAGAGATGATGTCAGAGCCCTCGAGACCTG 240  
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OY 1081 GAGCTACACAGCTTTGATACCTTCAGTTGGGCTTTTGTCTGTTGAGCAATTAAGACT 1140  
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DB 1381 GAGGAGGAGGCAATGCTCTCAGAACTTCCAGAGAGCCCAAGTGCAGAGGAGGCTCTCA 1440  
OY 1441 GACAGCTCATCTGAAGCCCTTAAGTTGAGTTCCAAGATGCTTAAGGAAAGAAATTCGG 1500  
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OY 1621 AACCAGTATGCAATATGAAAAAGAGTATCTCCGACACAGAGCTTTGTTGAGCAATCGGT 1680  
DB 1621 AACCAGTATGCAATATGAAAAAGAGTATCTCCGACACAGAGCTTTGTTGAGCAATCGGT 1680  
OY 1681 GGTCTCCATTTTTCACCAAGGCGAAATATACAGAAAGCCTTTTACGTTTGAAGGGCGA 1740  
DB 1681 GGTCTCCATTTTTCACCAAGGCGAAATATACAGAAAGCCTTTTACGTTTGAAGGGCGA 1740  
OY 1741 GCAGAGATGTGGGATCTGAGAACGATTCGAGATGATGAGACGACACTTTGAGAT 1800  
DB 1741 GCAGAGATGTGGGATCTGAGAACGATTCGAGATGATGAGACGACACTTTGAGAT 1800  
OY 1801 AACGAGAGGCGTATGAGATTCCTGTTTGTGCGCCGAGAGACGAGAGAGAGCAACAG 1860  
DB 1801 AACGAGAGGCGTATGAGATTCCTGTTTGTGCGCCGAGAGAGACGAGAGAGAGCAACAG 1860  
OY 1861 AACCTGAGTCAGACAGCATGATGATCCGAGATGCTGGAGTGTTCACAGGAATGGGAAG 1920  
DB 1861 AACCTGAGTCAGACAGCATGATGATCCGAGATGCTGGAGTGTTCACAGGAATGGGAAG 1920  
OY 1921 ATGCAAGACATGCTGATTTGCAATGCTGTGCTTCTGCTGTGCTGACCTTCACTTCT 1980  
DB 1921 ATGCAAGACATGCTGATTTGCAATGCTGTGCTTCTGCTGTGCTGACCTTCACTTCT 1980  
OY 1981 ACATGCTGCTGTTGAGACAGCTTCTGCCAGAGAGTATATATGATATAGCCAGCTATGATGAC 2040  
DB 1981 ACATGCTGCTGTTGAGACAGCTTCTGCCAGAGAGTATATATGATATAGCCAGCTATGATGAC 2040  
OY 2041 AATGAAACAACCACTGAACCTGAATGAGAAAGAGAGGTCAGATTCCTTCCACGTTTCC 2100  
DB 2041 AATGAAACAACCACTGAACCTGAATGAGAAAGAGAGGTCAGATTCCTTCCACGTTTCC 2100  
OY 2101 ATGGAATTTCTAGAAATCTCTCCAAAGGCAACGAGCAATGATATAGCCAGATTTCA 2160  
DB 2101 ATGGAATTTCTAGAAATCTCTCCAAAGGCAACGAGCAATGATATAGCCAGATTTCA 2160  
OY 2161 ACAATATGAGTAAAGAACTTGAAGAAATCCAGGCAAAATGCCCACCTGTTGATTAATA 2220  
DB 2161 ACAATATGAGTAAAGAACTTGAAGAAATCCAGGCAAAATGCCCACCTGTTGATTAATA 2220  
OY 2221 TTTTCCAAATATTTCTTAATCTGGAAGTGTCTCATTTGTTGTTAAAGTGAACAATGTT 2280  
DB 2221 TTTTCCAAATATTTCTTAATCTGGAAGTGTCTCATTTGTTGTTAAAGTGAACAATGTT 2280  
OY 2281 GTCAACCTGTGTGTGATGAGACCATTTTGTGACCTGGCATACCATCTGATTTGCTTA 2340  
DB 2281 GTCAACCTGTGTGTGATGAGACCATTTTGTGACCTGGCATACCATCTGATTTGCTTA 2340  
OY 2341 AATATCTTTTATGAGGCAATGAGACATATCCAAATGACGAGACATTTCAATATATGCTT 2400



|    |      |   |      |
|----|------|---|------|
| Db | 2341 | AAATCTTTTCAATGCGCATGGAGCACTATCCAAATGACGACATTCCTCAATATATGCTGT  | 2400 |
| Qy | 2401 | ACAGTAGGAAACCTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTTCTGAAATTAAT  | 2460 |
| Db | 2401 | ACAGTAGGAAACCTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTTCTGAAATTAAT  | 2460 |
| Qy | 2461 | GCACATGATCCTTACTATTAATTTCCAAAGAAAGCTGGAAATCTTGACGGTTTATATGTCG | 2520 |
| Db | 2461 | GCACATGATCCTTACTATTAATTTCCAAAGAAAGCTGGAAATCTTGACGGTTTATATGTCG | 2520 |
| Qy | 2521 | ACGGTTAGCCGTGGTAGAACTTGGACATCGCAATGTGGAGATTAATCTGTTCCGTCCA    | 2580 |
| Db | 2521 | ACGGTTAGCCGTGGTAGAACTTGGACATCGCAATGTGGAGATTAATCTGTTCCGTCCA    | 2580 |
| Qy | 2581 | TTTCGATTTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAAAGTTAAATATGCTAATA | 2640 |
| Db | 2581 | TTTCGATTTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAAAGTTAAATATGCTAATA | 2640 |
| Qy | 2641 | AAAGTCAATCGGCAATTCCTGGGGGCGCTGAGGAAATTAACCTCGTCTGGCCATCATC    | 2700 |
| Db | 2641 | AAAGTCAATCGGCAATTCCTGGGGGCGCTGAGGAAATTAACCTCGTCTGGCCATCATC    | 2700 |
| Qy | 2701 | GTCCTCAATTTTGCCCGGCGGCGGCAATGCAAGCTTTGGTAAAGCTACAAAGATGTGTC   | 2760 |
| Db | 2701 | GTCCTCAATTTTGCCCGGCGGCGGCAATGCAAGCTTTGGTAAAGCTACAAAGATGTGTC   | 2760 |
| Qy | 2761 | TGCAGATTCGCCAGTGAATTTCTCAACTCCACGCTGGCAGATGAATAGCTCTTCCACATCC | 2820 |
| Db | 2761 | TGCAGATTCGCCAGTGAATTTCTCAACTCCACGCTGGCAGATGAATAGCTCTTCCACATCC | 2820 |
| Qy | 2821 | TTTCGTATTTGTTCGCGCTGCTGTGTGGGAGTAGATAGAGACCATGTGGCATGTATG     | 2880 |
| Db | 2821 | TTTCGTATTTGTTCGCGCTGCTGTGTGGGAGTAGATAGAGACCATGTGGCATGTATG     | 2880 |
| Qy | 2881 | GAGGTCTGTGCTCAAGCCATGTGCGCTTACTGTCTTATATGTCATGGTATTTGGAAAC    | 2940 |
| Db | 2881 | GAGGTCTGTGCTCAAGCCATGTGCGCTTACTGTCTTATATGTCATGGTATTTGGAAAC    | 2940 |
| Qy | 2941 | CTAGTGGCCGATCTCTTCTGCGCTTGTAGCTCAATTTAGTCAACAAACCTT           | 3000 |
| Db | 2941 | CTAGTGGCCGATCTCTTCTGCGCTTGTAGCTCAATTTAGTCAACAAACCTT           | 3000 |
| Qy | 3001 | GCAGCCACTGATGATGATTAATGAAATGATATCTCCAAATTCGTGTGATAGATGAC      | 3060 |
| Db | 3001 | GCAGCCACTGATGATGATTAATGAAATGATATCTCCAAATTCGTGTGATAGATGAC      | 3060 |
| Qy | 3061 | AAAGAGTAGCTTATGTGAAAAAATAATATGATTTATTCACACAGTCTTCAATAGG       | 3120 |
| Db | 3061 | AAAGAGTAGCTTATGTGAAAAAATAATATGATTTATTCACACAGTCTTCAATAGG       | 3120 |
| Qy | 3121 | AAACAAAGATTTAGATGAAATTTAAACCACTGATGATCTTAAACAAGAAACAGT        | 3180 |
| Db | 3121 | AAACAAAGATTTAGATGAAATTTAAACCACTGATGATCTTAAACAAGAAACAGT        | 3180 |
| Qy | 3181 | TGTATGTCCAAATCATACARCAGAAATTTGGAAAGATCTTGACTATCTTAAAGATTAAT   | 3240 |
| Db | 3181 | TGTATGTCCAAATCATACARCAGAAATTTGGAAAGATCTTGACTATCTTAAAGATTAAT   | 3240 |
| Qy | 3241 | GGAACTACAACTGTATAGAACTGTGGAGCAGTGTGAAAAATACATTAATGATAAAGT     | 3300 |
| Db | 3241 | GGAACTACAACTGTATAGAACTGTGGAGCAGTGTGAAAAATACATTAATGATAAAGT     | 3300 |
| Qy | 3301 | GATTACATGTCAATCATAAACAACCCAGCTTACTGTACAGTGAACCAATTCCTGTAGGA   | 3360 |
| Db | 3301 | GATTACATGTCAATCATAAACAACCCAGCTTACTGTACAGTGAACCAATTCCTGTAGGA   | 3360 |
| Qy | 3361 | GAATCTGACTTTGAAATTTTAAACAGGAGACTTTAGTAGTGAATCGGATCTGGAGAA     | 3420 |
| Db | 3361 | GAATCTGACTTTGAAATTTTAAACAGGAGACTTTAGTAGTGAATCGGATCTGGAGAA     | 3420 |
| Qy | 3421 | AGCAAGAGAACTGAATGAAAGCAGTAGCTCATCGAAGTAGACCTGTGGACATGGGC      | 3480 |
| Db | 3421 | AGCAAGAGAACTGAATGAAAGCAGTAGCTCATCGAAGTAGACCTGTGGACATGGGC      | 3480 |

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|----|------|--|------|
| Dd | 3421 | AGCAAGAGAAACGAAAGAAAGAGAGAGTAGTCATCAGAAAGGTAGACATGCTGGACATCGGC | 3480 |
| Qy | 3481 | GCACCTGTAGAAGAACAGACCCCGTAGTGGACACCTGTAGAAACTCTTGAACCGAAGCTTGT | 3540 |
| Dd | 3481 | GCACCTGTAGAAGAACACCCCGTAGTGGACACCTGTAGAAACTCTTGAACCGAAGCTTGT   | 3540 |
| Qy | 3541 | TTCACTGAAGGCTGTGTCAAAAGATTCAAAGTGGTTCAAATCATGTGGAAGAGGCAGA     | 3600 |
| Dd | 3541 | TTCACTGAAGGCTGTGTCAAAAGATTCAAAGTGGTTCAAATCATGTGGAAGAGGCAGA     | 3600 |
| Qy | 3601 | GGAAACAAATGCTGGAACCTGAGAAAGACAGCTGTTCCGAATAGTGTGAACATPAACGTGTT | 3660 |
| Dd | 3601 | GGAAACAAATGCTGGAACCTGAGAAAGACAGCTGTTCCGAATAGTGTGAACATPAACGTGTT | 3660 |
| Qy | 3661 | GAGACCTTCATTTGTTTCATGATTCCTCCTAGTAGTGGTGCCTGGCATTTGAAGATATA    | 3720 |
| Dd | 3661 | GAGACCTTCATTTGTTTCATGATTCCTCCTAGTAGTGGTGCCTGGCATTTGAAGATATA    | 3720 |
| Qy | 3721 | TATATTGATCGCGCAAGAACGATTAAACGATTTGGAAATATGCTGACAGGTTTCACT      | 3780 |
| Dd | 3721 | TATATTGATCGCGCAAGAACGATTAAACGATTTGGAAATATGCTGACAGGTTTCACT      | 3780 |
| Qy | 3781 | TACATTTTCATTTTCGGAATGCTTCTAAAGGGGGCATATAGCTATACCAACAATATTC     | 3840 |
| Dd | 3781 | TACATTTTCATTTTCGGAATGCTTCTAAAGGGGGCATATAGCTATACCAACAATATTC     | 3840 |
| Qy | 3841 | ACCAATGCGCTGGTGTGGCTGACCTCTTAATATTTGATGTTTCATTTGGTCAGTTTACA    | 3900 |
| Dd | 3841 | ACCAATGCGCTGGTGTGGCTGACCTCTTAATATTTGATGTTTCATTTGGTCAGTTTACA    | 3900 |
| Qy | 3901 | GCAAATGCGCTTGGTGTACTCAGAACTTTCGAGACCAATCTCTCAGACACTTAAGACT     | 3960 |
| Dd | 3901 | GCAAATGCGCTTGGTGTACTCAGAACTTTCGAGACCAATCTCTCAGACACTTAAGACT     | 3960 |
| Qy | 3961 | CTGAGACCTCTTAAGACCTTATCTCGATTTTGAAGGATGAGGG                    | 4003 |
| Dd | 3961 | CTGAGACCTCTTAAGACCTTATCTCGATTTTGAAGGATGAGGG                    | 4003 |

| LOCUS                      | AX391130   | 5997 bp     | DNA     | linear | PAT 19-MAR-2002 |
|----------------------------|--|-------------|---------|--------|-----------------|
| DEFINITION                 | Sequence 1 from Patent WO0214498.                                      |             |         |        |                 |
| ACCESSION                  | AX391130   |             |         |        |                 |
| VERSION                    | AX391130.1   | GI:19584232 |         |        |                 |
| KEYWORDS                   |  |             |         |        |                 |
| SOURCE                     | human.   |             |         |        |                 |
| ORGANISM                   | Homo sapiens   |             |         |        |                 |
| REFERENCE                  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;      |             |         |        |                 |
| AUTHORS                    | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.             |             |         |        |                 |
| TITLE                      | 1 Turner, C.A., Mathur, B. and Mathur, D.                              |             |         |        |                 |
| JOURNAL                    | Novel human ion channel proteins and polynucleotides encoding the same |             |         |        |                 |
| FEATURES                   | Patent: WO 0214498-A 1 21-FEB-2002;                                    |             |         |        |                 |
| source                     | Lexicon Genetics Incorporated (US)                                     |             |         |        |                 |
|                            | Location/Qualifiers  |             |         |        |                 |
|                            | 1..5997  |             |         |        |                 |
|                            | /organism="Homo sapiens"   |             |         |        |                 |
|                            | /db_xref="taxon:9606"  |             |         |        |                 |
| BASE COUNT                 | 1773 a 1185 c 1338 g 1698 t  | 3 others    |         |        |                 |
| ORIGIN                     |  |             |         |        |                 |
| Query Match                | 66.1%; Score 3987; DB 6; Length 5997;                                  |             |         |        |                 |
| Best Local Similarity      | 100.0%; Pred. No. 0;   |             |         |        |                 |
| Matches 3987; Conservative | 0; Mismatches  | 0; Indels   | 0; Gaps | 0;     |                 |
| QY 2044                    | GSAGACACCACTGAAGTGAATGAGAAAGAGAGAGTCAAGTTCTTCCACGTTCCATG               | 2103        |         |        |                 |
| Db 2011                    | GSAGACACCACTGAAGTGAATGAGAAAGAGAGAGTCAAGTTCTTCCACGTTCCATG               | 2070        |         |        |                 |
| QY 2104                    | GACCTTGAGAGATCGTCCCAAGGACAGAGCAATGATATAGCCAGATTTCAAC                   | 2163        |         |        |                 |

Db 2071 GACTTCTAGAGATCTCTCCAAAGGCAAGACATGATATAGCAGATTTCTAACA 2130  
OY 2164 AATACAGTAGAGACTTGAAGAAATCCAGCAGAAATCCACCCTGTGTATATAATTT 2223  
Db 2131 AATACAGTAGAGAACTTGAAGAAATCCAGCAGAAATCCACCCTGTGTATATAATTT 2190  
OY 2224 TCCAGCATATTTCTAATCTGGAGCTGTTCACATATGTTTAAAGGAAACATGTTGTC 2283  
Db 2191 TCCAGCATATTTCTAATCTGGAGCTGTTCACATATGTTTAAAGGAAACATGTTGTC 2250  
OY 2284 AACCTGTGTGATGAGACCCATTTGTTGACCTGGCCATTCACATCTGTATTTGTTAAAT 2343  
Db 2251 AACCTGTGTGATGAGACCCATTTGTTGACCTGGCCATTCACATCTGTATTTGTTAAAT 2310  
OY 2344 ACTCTTTTCATGCGCATGAGACACTATTCATGACGACATTTCAATTAATGTCCTTACA 2403  
Db 2311 ACTCTTTTCATGCGCATGAGACACTATTCATGACGACATTTCAATTAATGTCCTTACA 2370  
OY 2404 GTAGGAACCTGTTTCTACCTGGGATCTTACACAGCAAAATGTTTGAATAATATATGCC 2463  
Db 2371 GTAGGAACCTGTTTCTACCTGGGATCTTACACAGCAAAATGTTTGAATAATATATGCC 2430  
OY 2464 ATGATGCTTACTATTTATTTTCCAGAGGCTGGAATATCTTTGACGGTTTATTTGAGC 2523  
Db 2431 ATGATGCTTACTATTTATTTTCCAGAGGCTGGAATATCTTTGACGGTTTATTTGAGC 2490  
OY 2524 CTTAGCTGTAGAACCTTGACATCCGCAATGTGGAAGCAATATCTGTTCCGTTCAATTT 2583  
Db 2491 CTTAGCTGTAGAACCTTGACATCCGCAATGTGGAAGCAATATCTGTTCCGTTCAATTT 2550  
OY 2584 CGATTTGCTGGAGTTTTCAGATTTGGCAAAATCTTGGCCAACTTAAATATGCTAATTAAG 2643  
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OY 2644 ATCATGCGCAATTTCCGTGGGGCTCTGGGAAATTTAACCCCTGCTGGCCATCATCTGTC 2703  
Db 2611 ATCATGCGCAATTTCCGTGGGGCTCTGGGAAATTTAACCCCTGCTGGCCATCATCTGTC 2670  
OY 2704 TTCAATTTTGGCTGTGGCGCATGCACTCTTTGTTAAAGCTAACAAAGATTTGTCTGC 2763  
Db 2671 TTCAATTTTGGCTGTGGCGCATGCACTCTTTGTTAAAGCTAACAAAGATTTGTCTGC 2730  
OY 2764 AAGATGCGCATGATTTGTCACATCCACGCGTGGCAATGATGATGCTTCCACATCTTC 2823  
Db 2731 AAGATGCGCATGATTTGTCACATCCACGCGTGGCAATGATGATGCTTCCACATCTTC 2790  
OY 2824 CTGATTTGTTCCGCTGTCTGTGTGGGAGATGATAGAGACATGTCGACTGTATGAG 2883  
Db 2791 CTGATTTGTTCCGCTGTCTGTGTGGGAGATGATAGAGACATGTCGACTGTATGAG 2850  
OY 2884 GTTGTGCTGTCAGACCATGATGCTTACTGTCTTCATGATGATGATGATGATGATGATGAT 2943  
Db 2851 GTTGTGCTGTCAGACCATGATGCTTACTGTCTTCATGATGATGATGATGATGATGATGAT 2910  
OY 2944 GTTGTGCTGTCATCTTCTTGGGCTTGTGCTTGTGATGATGATGATGATGATGATGATGAT 3003  
Db 2911 GTTGTGCTGTCATCTTCTTGGGCTTGTGCTTGTGATGATGATGATGATGATGATGATGAT 2970  
OY 3004 GGCACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3063  
Db 2971 GGCACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3030  
OY 3064 GAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3123  
Db 3031 GAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3090  
OY 3124 CAAGAATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3183  
Db 3091 CAAGAATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3150  
OY 3184 ATGTGCAATCATACAGAGAAATTTGGGAAAGATCTTGTGATGATGATGATGATGATGAT 3243  
Db 3151 ATGTGCAATCATACAGAGAAATTTGGGAAAGATCTTGTGATGATGATGATGATGATGATGAT 3210

OY 3244 ACTACAGTGTATAGAGACTGGCAGAGCTGTGAAAAATACATATATGATGAAATGAT 3303  
Db 3211 ACTACAGTGTATAGAGACTGGCAGAGCTGTGAAAAATACATATATGATGAAATGAT 3270  
OY 3304 TACATGATTTCAATTAACCAACCCAGCTTACTGTGACTGTACCAATTTGCTGTAGAGAA 3363  
Db 3271 TACATGATTTCAATTAACCAACCCAGCTTACTGTGACTGTACCAATTTGCTGTAGAGAA 3330  
OY 3364 TGTGACTTTGAAAAATTTAAACAGGAAAGACTTATGATGATGATGATGATGATGATGATGAT 3423  
Db 3331 TGTGACTTTGAAAAATTTAAACAGGAAAGACTTATGATGATGATGATGATGATGATGATGAT 3390  
OY 3424 AAAGAGAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3483  
Db 3391 AAAGAGAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3450  
OY 3484 CCTGTAGAGAACGCGCTGATGAGAACCTGGAAGAACTCTTGACAGAAAGCTGTTTC 3543  
Db 3451 CCTGTAGAGAACGCGCTGATGAGAACCTGGAAGAACTCTTGACAGAAAGCTGTTTC 3510  
OY 3544 ACTGAAGCTGTGTACAAAGATTCAGTGTGTGCAATATCATATGTGAGAGAGCAGAGGA 3603  
Db 3511 ACTGAAGCTGTGTACAAAGATTCAGTGTGTGCAATATCATATGTGAGAGAGCAGAGGA 3570  
OY 3604 AAACATGTTGGAACCTGAGAGAGAGCTGTTCCGAATAGTTGAAACATTAAGCTGTTGAG 3663  
Db 3571 AAACATGTTGGAACCTGAGAGAGAGCTGTTCCGAATAGTTGAAACATTAAGCTGTTGAG 3630  
OY 3664 ACCCTCATTTGTTTCAATGATTCCTTACATGATGATGATGATGATGATGATGATGATGAT 3723  
Db 3631 ACCCTCATTTGTTTCAATGATTCCTTACATGATGATGATGATGATGATGATGATGATGAT 3690  
OY 3724 ATGATCAGAGGAAAGACATTAAGACATGTTGGAATATGTCAGCAAGTTTTCACCTAC 3783  
Db 3691 ATGATCAGAGGAAAGACATTAAGACATGTTGGAATATGTCAGCAAGTTTTCACCTAC 3750  
OY 3784 ATTTTCATTTGGAATGCTTCTTAAATGAGGTGATGATGATGATGATGATGATGATGATGAT 3843  
Db 3751 ATTTTCATTTGGAATGCTTCTTAAATGAGGTGATGATGATGATGATGATGATGATGATGAT 3810  
OY 3844 AATGCTGTGTTGGCTGGGACTTCTTAATGATGATGATGATGATGATGATGATGATGATGAT 3903  
Db 3811 AATGCTGTGTTGGCTGGGACTTCTTAATGATGATGATGATGATGATGATGATGATGATGAT 3870  
OY 3904 AATGCTGTGTTGGCTGGGACTTCTTAATGATGATGATGATGATGATGATGATGATGATGAT 3963  
Db 3871 AATGCTGTGTTGGCTGGGACTTCTTAATGATGATGATGATGATGATGATGATGATGATGAT 3930  
OY 3964 AGACCTTAAAGAGCTTATCTCGATTTGAAAGGATGAGGTGTTGATGATGATGATGATGAT 4023  
Db 3931 AGACCTTAAAGAGCTTATCTCGATTTGAAAGGATGAGGTGTTGATGATGATGATGATGAT 3990  
OY 4024 GAGCAATTCATCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4083  
Db 3991 GAGCAATTCATCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4050  
OY 4084 AGCATATGAGGCTGTAATTTGTTGCTGGCAAAATTTTACACAGTATTAACACACAACT 4143  
Db 4051 AGCATATGAGGCTGTAATTTGTTGCTGGCAAAATTTTACACAGTATTAACACACAACT 4110  
OY 4144 GGTGACAGGTTTGAATGAGAGAGCTGATATATCATATCTGATTTGCTTAAACTATATGAA 4203  
Db 4111 GGTGACAGGTTTGAATGAGAGAGCTGATATATCATATCTGATTTGCTTAAACTATATGAA 4170  
OY 4204 AGAATGAGAGCTGCTGATGAG 4263  
Db 4171 AGAATGAGAGCTGCTGATGAG 4230  
OY 4264 TATCTCTTCTTCTTCAAGTTGACATTCAAAGATGATGATGATGATGATGATGATGATGAT 4323  
Db 4231 TATCTCTTCTTCTTCAAGTTGACATTCAAAGATGATGATGATGATGATGATGATGATGATGAT 4290

|    |      |   |      |
|----|------|---|------|
| 0Y | 4324 | GTATTCGACGAANAATGTGAACTCCAGGCTAAGTATGAAGAAATCTGTACATGTA       | 4383 |
| Db | 4291 | GTGTATTCGCGAANAATGTGAACTCCAGGCTAAGTATGAAGAAATCTGTACATGTA      | 4350 |
| 0Y | 4384 | TACTGTGTATTTTCACATCTTTGGGCTCTTCACCTTGAACCTGTATATGGTGC         | 4443 |
| Db | 4351 | TACTGTGTATTTTCACATCTTTGGGCTCTTCACCTTGAACCTGTATATGGTGC         | 4410 |
| 0Y | 4444 | ATCATGATATTTTCAACGACAGCAAGAAAGATTGGAGGTCAAGACATCTTATGACA      | 4503 |
| Db | 4411 | ATCATGATATTTTCAACGACAGCAAGAAAGATTGGAGGTCAAGACATCTTATGACA      | 4470 |
| 0Y | 4504 | GAGACACAGAAAGATCTATATGCAATGAAAAATTATGATGAAAAACCGCAAAAG        | 4563 |
| Db | 4471 | GAAACACAGAAAGATCTATATGCAATGAAAAATTATGATGAAAAACCGCAAAAG        | 4530 |
| 0Y | 4564 | CCATACCTGACACGAGAAACAAATTTCAAGAAATGGCTTTTGACTTCGTACACAGAA     | 4623 |
| Db | 4531 | CCATACCTGACACGAGAAACAAATTTCAAGAAATGGCTTTTGACTTCGTACACAGAA     | 4590 |
| 0Y | 4624 | GTATTTGACATTAAGCATCATGATTTCATCTGTCTTAAACATGTCACAAATGATGGTAA   | 4683 |
| Db | 4591 | GTATTTGACATTAAGCATCATGATTTCATCTGTCTTAAACATGTCACAAATGATGGTAA   | 4650 |
| 0Y | 4684 | ACAGATGACAGAGTGAATATGTGACTACCATTTTGTACAGCATATATCTGGTTCAT      | 4743 |
| Db | 4651 | ACAGATGACAGAGTGAATATGTGACTACCATTTTGTACAGCATATATCTGGTTCAT      | 4710 |
| 0Y | 4744 | GTGTAATTTACTGAGAGTGTGTGACGAACATCTGTCACGATCATATTAATTTTACC      | 4803 |
| Db | 4711 | GTGTAATTTACTGAGAGTGTGTGACGAACATCTGTCACGATCATATTAATTTTACC      | 4770 |
| 0Y | 4804 | ATTCGATGAGATATTTTGAATTTGTGTGTGTCATCTCTCCATTTGATGATGTTCCT      | 4863 |
| Db | 4771 | ATTCGATGAGATATTTTGAATTTGTGTGTGTCATCTCTCCATTTGATGATGTTCCT      | 4830 |
| 0Y | 4864 | GCCAGACTGATAGAAAGTATTTGCTGTGCCCTACCCGTTCGAGTATCCGCTTGTCT      | 4923 |
| Db | 4831 | GCCAGACTGATAGAAAGTATTTGCTGTGCCCTACCCGTTCGAGTATCCGCTTGTCT      | 4890 |
| 0Y | 4924 | AGGANTGGCCCAATCCATACCTGTGATCCAAAGGAGGAAATCCGACGCTGCTCTT       | 4983 |
| Db | 4891 | AGGANTGGCCCAATCCATACCTGTGATCCAAAGGAGGAAATCCGACGCTGCTCTT       | 4950 |
| 0Y | 4984 | GCTTTGATGATGTCCCTTCCTGCTGGTGTATTAACATGGGCTCCTACTCTTCTAGTCATG  | 5043 |
| Db | 4951 | GCTTTGATGATGTCCCTTCCTGCTGGTGTATTAACATGGGCTCCTACTCTTCTAGTCATG  | 5010 |
| 0Y | 5044 | TTCATCTACGCCATCTTTGGAGATGCCAATCTTGCTATGTTAAGAGGAAATGGGATC     | 5103 |
| Db | 5011 | TTCATCTACGCCATCTTTGGAGATGCCAATCTTGCTATGTTAAGAGGAAATGGGATC     | 5070 |
| 0Y | 5104 | GATGACAGTTCACATTTTGAGACCTTTGGCAACAGATATGTGGCTATTTCCAAATTACA   | 5163 |
| Db | 5071 | GATGACAGTTCACATTTTGAGACCTTTGGCAACAGATATGTGGCTATTTCCAAATTACA   | 5130 |
| 0Y | 5164 | ACCTTGTGCTGGCTGGAGATGATTTGCTAGCACCCATCTCAACAGTAAAGCACCCGACTGT | 5223 |
| Db | 5131 | ACCTTGTGCTGGCTGGAGATGATTTGCTAGCACCCATCTCAACAGTAAAGCACCCGACTGT | 5190 |
| 0Y | 5224 | GACCCATAATTAAGTTAAACCTCGAAGCTCATTTAAGGAGACTGTGGGAACCATCTGTT   | 5283 |
| Db | 5191 | GACCCATAATTAAGTTAAACCTCGAAGCTCATTTAAGGAGACTGTGGGAACCATCTGTT   | 5250 |
| 0Y | 5284 | GGAATTTTCTTTTGTGCAGTTTAAATCATATATATCTTCTGGTGTGGTGAACATGTAC    | 5343 |
| Db | 5251 | GGAATTTTCTTTTGTGCAGTTTAAATCATATATATCTTCTGGTGTGGTGAACATGTAC    | 5310 |
| 0Y | 5344 | ATTCGGGTCATCCGAGAACTTCAGTGTGTCTACTGAGAAAGTCAAGAGCTCTGAGT      | 5403 |
| Db | 5311 | ATTCGGGTCATCCGAGAACTTCAGTGTGTGTCTACTGAGAAAGTCAAGAGCTCTGAGT    | 5370 |
| 0Y | 5404 | GAGGATGACTTTGAGATGTTCTATGAGTGTGGAGAAATTTGATCCGATCAACTCAG      | 5463 |

| DB       | Accession | LOCUS   | DEFINITION | ACCESSION | VERSION | KEYWORDS   | SOURCE | ORGANISM | REFERENCE | AUTHORS | TITLE | JOURNAL | FEATURES | BASE COUNT | ORIGIN | Query Match | Best Local Similarity | Matches 3874; | Conservative | 0; | Mismatches | 0; | Indels | 0; | Gaps | 0; |
|----------|-----------|---|------------|-----------|---------|------------|--------|----------|-----------|---------|-------|---------|----------|------------|--------|-------------|-----------------------|---------------|--------------|----|------------|----|--------|----|------|----|
| Db       | 5371      | GAGGATGACTTGGATGATGCTTATGAGGTTGGGAGAGGTTGATCCGATGCAAGCAG    |            |           |         |            |        |          |           |         |       |         |          |            |        |             |                       |               |              |    |            |    |        |    |      |    |
| Qy       | 5464      | TTCATGGAATTTGAAAAATATCTCAGTTTGACGTGCGCTTGAAACCGCTTCATCTG    |            |           |         |            |        |          |           |         |       |         |          |            |        |             |                       |               |              |    |            |    |        |    |      |    |
| Db       | 5431      | TTTCATGGAATTTGAAAAATATCTCAGTTTGAGCTGCGCTTGAAACCGCTTCATCTG   |            |           |         |            |        |          |           |         |       |         |          |            |        |             |                       |               |              |    |            |    |        |    |      |    |
| Qy       | 5524      | CCACACCAACCAAAACTCCAGTCTATTTCGCCATGATTTGGCCCATGATGATGGGACCG |            |           |         |            |        |          |           |         |       |         |          |            |        |             |                       |               |              |    |            |    |        |    |      |    |
| Db       | 5491      | CCACACCAACCAAAACTCCAGTCTATTTCGCCATGATTTGGCCCATGATGATGGGACCG |            |           |         |            |        |          |           |         |       |         |          |            |        |             |                       |               |              |    |            |    |        |    |      |    |
| Qy       | 5584      | ATCCACTGCTCTGATATCTATTTCCTTTTACAAAGCGGTTCTAGAGAGATGAGAG     |            |           |         |            |        |          |           |         |       |         |          |            |        |             |                       |               |              |    |            |    |        |    |      |    |
| Db       | 5551      | ATCCACTGCTCTGATATCTATTTCCTTTTACAAAGCGGTTCTAGAGAGATGAGAG     |            |           |         |            |        |          |           |         |       |         |          |            |        |             |                       |               |              |    |            |    |        |    |      |    |
| Qy       | 5644      | ATGGATGCTCTACGATACAGATGAGAGAGGATTCATGGCTCCATCTTCCAGGTC      |            |           |         |            |        |          |           |         |       |         |          |            |        |             |                       |               |              |    |            |    |        |    |      |    |
| Db       | 5611      | ATGGATGCTCTACGATACAGATGAGAGAGGATTCATGGCTCCATCTTCCAGGTC      |            |           |         |            |        |          |           |         |       |         |          |            |        |             |                       |               |              |    |            |    |        |    |      |    |
| Qy       | 5704      | TCCATACACCCCAATCAGCTCTACTTTTAAACGAAACAAAGAGAGATTCGCTGAT     |            |           |         |            |        |          |           |         |       |         |          |            |        |             |                       |               |              |    |            |    |        |    |      |    |
| Db       | 5671      | TCCATACACCCCAATCAGCTCTACTTTTAAACGAAACAAAGAGAGATTCGCTGAT     |            |           |         |            |        |          |           |         |       |         |          |            |        |             |                       |               |              |    |            |    |        |    |      |    |
| Qy       | 5764      | ATTACACGGCTTACAGAGACGACCTTTTAAAGCAATGTAAACAGCTTCCCTTACG     |            |           |         |            |        |          |           |         |       |         |          |            |        |             |                       |               |              |    |            |    |        |    |      |    |
| Db       | 5731      | ATTACACGGCTTACAGAGACGACCTTTTAAAGCAATGTAAACAGCTTCCCTTACG     |            |           |         |            |        |          |           |         |       |         |          |            |        |             |                       |               |              |    |            |    |        |    |      |    |
| Qy       | 5824      | TTCATTAACCAAAATCAAAAGTGAGGCTTAATCTTCTTAAAGAGAGATGATTAAT     |            |           |         |            |        |          |           |         |       |         |          |            |        |             |                       |               |              |    |            |    |        |    |      |    |
| Db       | 5791      | TTCATTAACCAAAATCAAAAGTGAGGCTTAATCTTCTTAAAGAGAGATGATTAAT     |            |           |         |            |        |          |           |         |       |         |          |            |        |             |                       |               |              |    |            |    |        |    |      |    |
| Qy       | 5884      | GACAGATTAATGAAACCTCTTATACAGAAAAAACTGATCTGACCATCTCCATCTGACT  |            |           |         |            |        |          |           |         |       |         |          |            |        |             |                       |               |              |    |            |    |        |    |      |    |
| Db       | 5851      | GACAGATTAATGAAACCTCTTATACAGAAAAAACTGATCTGACCATCTCCATCTGACT  |            |           |         |            |        |          |           |         |       |         |          |            |        |             |                       |               |              |    |            |    |        |    |      |    |
| Qy       | 5944      | TGTCCACCTTCCATGACCGGGGTGACAAAGCCCAATTTGGAAAAACATGAGCAAGAGC  |            |           |         |            |        |          |           |         |       |         |          |            |        |             |                       |               |              |    |            |    |        |    |      |    |
| Db       | 5911      | TGTCCACCTTCCATGACCGGGGTGACAAAGCCCAATTTGGAAAAACATGAGCAAGAGC  |            |           |         |            |        |          |           |         |       |         |          |            |        |             |                       |               |              |    |            |    |        |    |      |    |
| Qy       | 6004      | AAAGATGAAAAAGCCCAAGGGAATTA 6030                             |            |           |         |            |        |          |           |         |       |         |          |            |        |             |                       |               |              |    |            |    |        |    |      |    |
| Db       | 5971      | AAAGATGAAAAAGCCCAAGGGAATTA 5997                             |            |           |         |            |        |          |           |         |       |         |          |            |        |             |                       |               |              |    |            |    |        |    |      |    |
| RESULT 9 |           |   |            |           |         |            |        |          |           |         |       |         |          |            |        |             |                       |               |              |    |            |    |        |    |      |    |
| LOCUS    | AX391132  |   | 5889 bp.   | DNA       | linear  | PAT 19-MAR |        |          |           |         |       |         |          |            |        |             |                       |               |              |    |            |    |        |    |      |    |

|    |      |  |      |
|----|------|--|------|
| Db | 2011 | GGAAACAACCTGAACTGAAATGAAAGAAAGATGTAAGTCTTTCACGTTTCATG          | 2070 |
| Oy | 2104 | GACTTTCTAGAAATCCTTCCCAAAGCAAGCAATGATATAGCAGATTCCTAACA          | 2163 |
| Db | 2071 | GACTTCTAGAAAGTCTCTTCCCAAAGCAACGCAATGATATAGCAGATTCCTAACA        | 2130 |
| Oy | 2164 | AATACATAGAAACACTTGAAAGATCCAGGCGAAGAAATGCCACCTCTGTGGTATTAATTT   | 2223 |
| Db | 2131 | AATACATAGAAAGAACTTGAAAGATCCAGGCGAAGAAATGCCACCTGTGGTATTAATTT    | 2190 |
| Oy | 2224 | TCCAACTATTCCTAATCTGGAGCTCTCCCATATGTGGTTAAAGTGAACATATGTC        | 2283 |
| Db | 2191 | TCCAACTATTCCTAATCTGGAGCTCTCCCATATGTGGTTAAAGTGAACATATGTC        | 2250 |
| Oy | 2284 | AACCTGGTGTGATGAGACCAATTTGTTGACCTGGCCATCACCATCTGATTTGTCTTAAT    | 2343 |
| Db | 2251 | AACCTGGTGTGATGAGACCAATTTGTTGACCTGGCCATCACCATCTGATTTGTCTTAAT    | 2310 |
| Oy | 2344 | ACTCTTTTCATGCGCATGAGACACTATCCAAATAGCGGACCATTTCAATATGTGCTTACA   | 2403 |
| Db | 2311 | ACTCTTTTCATGCGCATGAGACACTATCCAAATAGCGGACCATTTCAATATGTGCTTACA   | 2370 |
| Oy | 2404 | GTAGAGAACTTGTTTCACTGGGATCTTTACAGCAAGAAATGTTTCTGAATATATGTCC     | 2463 |
| Db | 2371 | GTAGAGAACTTGTTTCACTGGGATCTTTACAGCAAGAAATGTTTCTGAATATATGTCC     | 2430 |
| Oy | 2464 | ATGAGATCCTTACTATATATATATCCAAAGAGCGTGGAATATCTTTGACGGTTTTATGTGAC | 2523 |
| Db | 2431 | ATGAGATCCTTACTATATATATATCCAAAGAGCGTGGAATATCTTTGACGGTTTTATGTGAC | 2480 |
| Oy | 2524 | CTTAGCTGGTAGAACTTGGACTGGCCAAATGTGGAAGATATCTGTTCTCCGTCATTT      | 2583 |
| Db | 2491 | CTTAGCTGGTAGAACTTGGACTGGCCAAATGTGGAAGATATCTGTTCTCCGTCATTT      | 2550 |
| Oy | 2584 | CGATTTGCTGGAGTTTTCAGTTGGGCAAAATCTTGGCCAACTTAATATGTCTAATAAG     | 2643 |
| Db | 2551 | CGATTTGCTGGAGTTTTCAGTTGGGCAAAATCTTGGCCAACTTAATATGTCTAATAAG     | 2610 |
| Oy | 2644 | ATCATCGGCAATTCCTGGGGGCGCTGCGGCAAAATTTAAACCTGTCTWGGCCATCATCTGC  | 2703 |
| Db | 2611 | ATCATCGGCAATTCCTGGGGGCGCTGCGGCAAAATTTAAACCTGTCTTGGCCATCATCTGC  | 2670 |
| Oy | 2704 | TTTCATTTTGGCGGTGTCGGCATGCAACTCTTGTGTAAGACTACAAAGATTTGTCTGC     | 2763 |
| Db | 2671 | TTTCATTTTGGCGGTGTCGGCATGCAACTCTTGTGTAAGACTACAAAGATTTGTCTGC     | 2730 |
| Oy | 2764 | AAGATGCCAGATGATTTCTCAACCTCCACGCTGGCAATGAATGACTTCTCCACTCCCTC    | 2823 |
| Db | 2731 | AAGATGCCAGATGATTTCTCAACCTCCACGCTGGCAATGAATGACTTCTCCACTCCCTC    | 2790 |
| Oy | 2824 | CTGATGTGTTCCCGCTGCTGTGGGGAGATGATAGAACCATGTGGGCACTGTATGAG       | 2883 |
| Db | 2791 | CTGATGTGTTCCCGCTGCTGTGGGGAGATGATAGAACCATGTGGGCACTGTATGAG       | 2850 |
| Oy | 2884 | GTTCGTGCTCAAGCATGTGCTTACTGTCTTCATGATGTCATGTGATTTGGAACCTA       | 2943 |
| Db | 2851 | GTTCGTGCTCAAGCATGTGCTTACTGTCTTCATGATGTCATGTGATTTGGAACCTA       | 2910 |
| Oy | 2944 | GTGCTCTGGAATCTCTTTGCGCTTGCTTTGAGCTCATTTAGTGCAGACAACCTTGCA      | 3003 |
| Db | 2911 | GTGCTCTGGAATCTCTTTGCGCTTGCTTTGAGCTCATTTAGTGCAGACAACCTTGCA      | 2970 |
| Oy | 3004 | GCCACTGATGATATGTAAGAAATGAATATCTCCAAATTCGTGTGGATAGATGCACAAA     | 3063 |
| Db | 2971 | GCCACTGATGATATGTAAGAAATGAATATCTCCAAATTCGTGTGTGATAGATGCACAAA    | 3030 |
| Oy | 3064 | GGAGTAGCTTATGTGAAAGAAAAATATATGAATTTATTCACACAGCTCTTATTAGAAA     | 3123 |
| Db | 3031 | GGAGTAGCTTATGTGAAAGAAAAATATATGAATTTATTCACACAGCTCTTATTAGAAA     | 3090 |
| Oy | 3124 | CAAAAGATTTAGATGAATTTAAACCACTTGATGATCTAAACAAAGAAAGACGTGT        | 3183 |

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|---|------|--|------|
| D | 3091 | CAAAAGATTAGTGAATAAACCAGCTGATGATCTAAACAACAAGAAAGACAGTTGT        | 3150 |
| Q | 3184 | ATGTCCATCATACACARCAAAATTGGGAAAAGATCTTGACTATCTTAAAGATCTAAATGGA  | 3243 |
| D | 3151 | ATGTCCATCATACACARCAAAATTGGGAAAAGATCTTGACTATCTTAAAGATCTAAATGGA  | 3210 |
| Q | 3244 | ACTCAAGTGGTATAGGAACCTGGCAGCAGTGTGAAAAATACATTATATGATGAAGAATGAT  | 3303 |
| D | 3211 | ACTCAAGTGGTATAGGAACCTGGCAGCAGTGTGAAAAATACATTATATGATGAAGAATGAT  | 3270 |
| Q | 3304 | TACATGTCAATTCATAAACAACCCCACTCTTACGTGACTGTACCAATTCGCTAGAGCAA    | 3363 |
| D | 3271 | TACATGTCAATTCATAAACAACCCCACTCTTACGTGACTGTACCAATTCGCTAGAGCAA    | 3350 |
| Q | 3364 | TCGTACCTTTGAAAAATTTTAAACACGAGAACCTTTAGTAGTAATCGGATCTGGAAACAAGC | 3423 |
| D | 3331 | TCGTACCTTTGAAAAATTTTAAACACGAGAACCTTTAGTAGTAATCGGATCTGGAAACAAGC | 3390 |
| Q | 3424 | AAAAGAAACCTGATGAAACCACTACTCATACGAAGGTAGACACTGTGGACATCGCGCGCA   | 3483 |
| D | 3391 | AAAAGAAACCTGATGAAACCACTACTCATACGAAGGTAGACACTGTGGACATCGCGCGCA   | 3450 |
| Q | 3484 | CCTGAGAAAGAACGCCCGAGTGGAAACCGGAAAGAACTCTTGAACCAAGAGCTGTTTC     | 3543 |
| D | 3451 | CCTGAGAAAGAACGCCCGAGTGGAAACCGGAAAGAACTCTTGAACCAAGAGCTGTTTC     | 3510 |
| Q | 3544 | ACTGAAAGCTGTGTACAAAGATTCGAAGTGTGTCAATCAATGTGAAGAAAGCAGAGGA     | 3603 |
| D | 3511 | ACTGAAAGCTGTGTACAAAGATTCGAAGTGTGTCAATCAATGTGAAGAAAGCAGAGGA     | 3570 |
| Q | 3604 | AAACATGTGTGAACCTGAGAGAGACGTCTTTCCGAAATGTTGAACATPACTGTTTGAG     | 3663 |
| D | 3571 | AAACATGTGTGAACCTGAGAGAGACGTCTTTCCGAAATGTTGAACATPACTGTTTGAG     | 3630 |
| Q | 3664 | ACCTTCATGTTTTCATGATTCCTCCCTTAGAGGGGGCTCGGCACTTTGAAGATATATAT    | 3723 |
| D | 3631 | ACCTTCATGTTTTCATGATTCCTCCCTTAGAGGGGGCTCGGCACTTTGAAGATATATAT    | 3690 |
| Q | 3724 | ATTGATCAGCGAAAGACGATTAAAGACATGTGGAAATATGCTGACAGAGTTTCACTTAC    | 3783 |
| D | 3691 | ATTGATCAGCGAAAGACGATTAAAGACATGTGGAAATATGCTGACAGAGTTTCACTTAC    | 3750 |
| Q | 3784 | ATTTTCATTTCTGGAAATGCTTTCTAAAAATGGGTGGCATATGCTATCAACAATATTTACC  | 3843 |
| D | 3751 | ATTTTCATTTCTGGAAATGCTTTCTAAAAATGGGTGGCATATGCTATCAACAATATTTACC  | 3810 |
| Q | 3844 | AATGCGCTGGTGTGGCGAGCTTCTAAATGTTGATCTTCAATGCTGACGTTTAAACACA     | 3903 |
| D | 3811 | AATGCGCTGGTGTGGCGAGCTTCTAAATGTTGATCTTCAATGCTGACGTTTAAACACA     | 3870 |
| Q | 3904 | AATGCTTTGGGTTACTCAGAACTTGGAGCCATCAATCTCAGAGCACTAAGAGCTCTG      | 3963 |
| D | 3871 | AATGCTTTGGGTTACTCAGAACTTGGAGCCATCAATCTCAGAGCACTAAGAGCTCTG      | 3930 |
| Q | 3964 | AGACCTCTAAGAGCTTATCTGCATTTGAAGGAGTGGGTGTGTGAATGCCCTTTTA        | 4033 |
| D | 3931 | AGACCTCTAAGAGCTTATCTGCATTTGAAGGAGTGGGTGTGTGAATGCCCTTTTA        | 3990 |
| Q | 4024 | GGAGCAATTCATCAATCAATGAAATGTGCTTCGCTTGTCTAATATTCGCGTAAATTTTC    | 4083 |
| D | 3991 | GGAGCAATTCATCAATCAATGAAATGTGCTTCGCTTGTCTAATATTCGCGTAAATTTTC    | 4050 |
| Q | 4084 | AGCATCATGGGCGTAATATTTGTTGGCGGCAATTTACACCTGTAATTAACACCAACT      | 4143 |
| D | 4051 | AGCATCATGGGCGTAATATTTGTTGGCGGCAATTTACACCTGTAATTAACACCAACT      | 4110 |
| Q | 4144 | GGTGACAGTTTGACATCGAAGACGTGAATATCATCTAGTATGCTTAAACTAATAGAA      | 4203 |
| D | 4111 | GGTGACAGTTTGACATCGAAGACGTGAATATCATCTAGTATGCTTAAACTAATAGAA      | 4170 |
| Q | 4204 | AGAAATGAGCTGTGATGGAAGAAATGTGAAGTAACTTTGATATATGTAGGATTTTGG      | 4263 |
| D | 4171 | AGAAATGAGCTGTGATGGAAGAAATGTGAAGTAACTTTGATATATGTAGGATTTTGG      | 4230 |

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|----|------|---|------|
| OY | 4284 | TATCTCTTTGCTTCAGAGTTCACATTCGAAGAGTGTAGTAAATGATGACGA           | 4323 |
| Db | 4231 | TATCTCTTTGCTTCAGAGTTCACATTCGAAGAGTGTAGTAAATGATGACGA           | 4290 |
| OY | 4324 | GTTGATTCAGAAAAGTGGAACTCCAGCCCTAGTAAAGAAAAGTCTGATATCTT         | 4383 |
| Db | 4291 | GTTGATTCAGAAAAGTGGAACTCCAGCCCTAGTAAAGAAAAGTCTGATATCTT         | 4350 |
| OY | 4384 | TACTTTGTTATTTTCATCATCTTTGGGTCCTTCACCTTGAACTGTTATTTGGTGC       | 4443 |
| Db | 4351 | TACTTTGTTATTTTCATCATCTTTGGGTCCTTCACCTTGAACTGTTATTTGGTGC       | 4410 |
| OY | 4444 | ATCATAGATTAATTTCAACACGAGAAAAGAAAGTTGGAGGTCAACATCTTTATGACA     | 4503 |
| Db | 4411 | ATCATAGATTAATTTCAACACGAGAAAAGAAAGTTGGAGGTCAACATCTTTATGACA     | 4470 |
| OY | 4504 | GAAAGAACAGAAATATCATATATGCAATGAAAATTTAGGATCGAAAAACCGCAAAAG     | 4563 |
| Db | 4471 | GAAAGAACAGAAATATCATATATGCAATGAAAATTTAGGATCGAAAAACCGCAAAAG     | 4530 |
| OY | 4564 | CCATATACCTCGACACAGAAAACAAATTTCAAGAAATGTCCTTTGACTTCGTAACAGACAA | 4623 |
| Db | 4531 | CCATATACCTCGACACAGAAAACAAATTTCAAGAAATGTCCTTTGACTTCGTAACAGACAA | 4590 |
| OY | 4624 | GTTTTTGACATTAAGCATCATGATTCATCTGCTTAACATGGTGCACAAATGATGGTGGAA  | 4683 |
| Db | 4591 | GTTTTTGACATTAAGCATCATGATTCATCTGCTTAACATGGTGCACAAATGATGGTGGAA  | 4650 |
| OY | 4684 | ACAGATGACCAAGTGAATGATGATGATACCATTTTGACGACATCATCGAGTTCATT      | 4743 |
| Db | 4651 | ACAGATGACCAAGTGAATGATGATGATGATACCATTTTGACGACATCATCGAGTTCATT   | 4710 |
| OY | 4744 | GTCGTAATTTACTGAGAGAGTGTGACTGAAACATCATCTCTCTACGCCATTTATTTTAAAC | 4803 |
| Db | 4711 | GTCGTAATTTACTGAGAGAGTGTGACTGAAACATCATCTCTCTACGCCATTTATTTTAAAC | 4770 |
| OY | 4804 | ATTGATGGAATATTTTGTGATTTTGTGTGTCATTCCTCCATTTGTAGTATGTTTCTT     | 4863 |
| Db | 4771 | ATTGATGGAATATTTTGTGATTTTGTGTGTCATTCCTCCATTTGTAGTATGTTTCTT     | 4830 |
| OY | 4864 | GCCGAGCTATGAAAAGTATTCGGTCCCTACACCCTGTTCCGAGATCCGGCTTCTGT      | 4923 |
| Db | 4831 | GCCGAGCTATGAAAAGTATTCGGTCCCTACACCCTGTTCCGAGATCCGGCTTCTGT      | 4890 |
| OY | 4924 | AGGATTTGGCCGAATCCTACGCTCGATCAAAAGAGCAAAAGGGATCCGACAGCTGCTTT   | 4983 |
| Db | 4891 | AGGATTTGGCCGAATCCTACGCTCGATCAAAAGAGCAAAAGGGATCCGACAGCTGCTTT   | 4950 |
| OY | 4984 | GCTTTGATGATGTCCCTCTCCGCTGTGTTTAAACATGCGGCTCCTACTCTTCTATGTCATG | 5043 |
| Db | 4951 | GCTTTGATGATGTCCCTCTCCGCTGTGTTTAAACATGCGGCTCCTACTCTTCTATGTCATG | 5010 |
| OY | 5044 | TTTCATCTAAGCCATCTTTGGGAATGCCAACTTTGGCCATCTTAAAGAGAAAGTTGGGATC | 5103 |
| Db | 5011 | TTTCATCTAAGCCATCTTTGGGAATGCCAACTTTGGCCATCTTAAAGAGAAAGTTGGGATC | 5070 |
| OY | 5104 | GATGACATGTCAACCTTTGAGACCTTTGGCAACAGATGATCTGCCATTTCCAAATTTACA  | 5163 |
| Db | 5071 | GATGACATGTTCACACTTTGAGACCTTTGGCAACAGATGATCTGCCATTTCCAAATTTACA | 5130 |
| OY | 5164 | ACCTCTGCTGGCTGGAGTGGATTGTCAGCAACCAATTTCTCAACAGTAAGCCACCGACTGT | 5223 |
| Db | 5131 | ACCTCTGCTGGCTGGAGTGGATTGTCAGCAACCAATTTCTCAACAGTAAGCCACCGACTGT | 5190 |
| OY | 5224 | GACCCCTAATTAAGTTAAACCTGGAACTCAGTTAAGGAGACTGTGGAAACCATCTGTT    | 5283 |
| Db | 5191 | GACCCCTAATTAAGTTAAACCTGGAACTCAGTTAAGGAGACTGTGGAAACCATCTGTT    | 5250 |
| OY | 5284 | GGAATTTCTTTTTTGTGCACTTCAACATCATATATCCCTCCGCTGTGGTGAACATGTAC   | 5343 |
| Db | 5251 | GGAATTTCTTTTTTGTGCACTTCAACATCATATATCCCTCCGCTGTGGTGAACATGTAC   | 5310 |

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|----|------|--|------|
| OY | 5344 | ATGCGGGCATCCCGGAGAACTTGTAGTGTCTCTACTGAAAGAAATGAGACCTCTAGT      | 5403 |
| Db | 5311 | ATCGGGGCACTCCGGAGAACTTCAAGTGTCTACTGAAGAAATGCGAGCCTCTAGT        | 5370 |
| OY | 5404 | GAGCATGACTTTGGAGATCTTATAGAGGTTTGGGGAAGTTTGAATCCGATGCAACTGAG    | 5463 |
| Db | 5371 | GAGATGACTTTGAGATTTCTATAGAGTTTGGGGAAGTTTGAATCCGATGCAACTGAG      | 5430 |
| OY | 5464 | TTTCATGGAATTTGAAAAATTTATCTGAGTTTGGAGCTGCGCTTGAACCGCTCTCAATCTG  | 5523 |
| Db | 5431 | TTTCATGGAATTTGAAAAATTTATCTGAGTTTGGAGCTGCGCTTGAACCGCTCTCAATCTG  | 5490 |
| OY | 5524 | CCACAAACCAAAACAACTCCAGCTCATTTCCCAATGGATTTGGCCATAGTGTAGGTGACCGG | 5583 |
| Db | 5491 | CCACAAACCAAAACAACTCCAGCTCATTTCCCAATGGATTTGGCCATAGTGTAGGTGACCGG | 5550 |
| OY | 5584 | ATCCACTGCTCTGATATCTTATTTGCTTTTCAAAAGCGGTTCTAGSAGAGTGGAGAG      | 5643 |
| Db | 5551 | ATCCACTGCTCTGATATCTTATTTGCTTTTCAAAAGCGGTTCTAGSAGAGTGGAGAG      | 5610 |
| OY | 5644 | ATGGAATGCTTACGAAATACAGATGGAGAGAGGATTCATGGCTTCCATCTTCCAAAGTC    | 5703 |
| Db | 5611 | ATGGAATGCTTACGAAATACAGATGGAGAGAGGATTCATGGCTTCCATCTTCCAAAGTC    | 5670 |
| OY | 5704 | TCCATTCAGCCAAATACGACTACTTAAAGGAAACAAAGGAAGTATCGTGTCAAT         | 5763 |
| Db | 5671 | TCCATTCAGCCAAATACGACTACTTAAAGGAAACAAAGGAAGTATCGTGTCTCAAT       | 5730 |
| OY | 5764 | ATTGACGCTGCTTACAGAGCGCACCTTTTAAAGCAACGTGTAAACCAAGCTTCTTACG     | 5823 |
| Db | 5731 | ATTGACGCTGCTTACAGAGCGCACCTTTTAAAGCAACGTGTAAACCAAGCTTCTTACG     | 5790 |
| OY | 5824 | TACCAATAAAAACAATCAAGAGTGGGCTAATCTTCTATTAAGGAAGACATGATTAAT      | 5883 |
| Db | 5791 | TACCAATAAAAACAATCAAGAGTGGGCTAATCTTCTATTAAGGAAGACATGATTAAT      | 5850 |
| OY | 5884 | GACAGATTAATGAAAACTCTTTACAGAAAAA 5917                           |      |
| Db | 5851 | GACAGATTAATGAAAACTCTTTACAGAAAAA 5884                           |      |

|            |   |  |
|------------|---|--|
|            | RESULT 10   |  |
| AY043484   | LOCUS   |  |
| DEFINITION | 6046 bp   | mRNA linear PRI 24-APR-2002  |
| ACCESSION  | AY043484  | Homo sapiens voltage-gated sodium channel type I mRNA, complete cds. |
| VERSION    | AY043484  |  |
| KEYWORDS   | AY043484.1  | GI:15421161  |
| SOURCE     | Homo sapiens.   |  |
| ORGANISM   | Homo sapiens  |  |
| REFERENCE  | Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eumariola; Eutheria; Primates; Catarrhini; Homnidae; Homo. |  |
| AUTHORS    | 1 (bases 1 to 6046)   |  |
| TITLE      | Sugawara,T., Mazaki-Miyazaki,E., Fukushima,K., Shimomura,J., Fujiwara,T., Hamano,S., Inoue,Y. and Yamakawa,K.               |  |
| JOURNAL    | Frequent mutations of SCN1A in severe myoclonic epilepsy in infancy   |  |
| MEDLINE    | Neurology 58 (7), 1122-1124 (2002)  |  |
| PUBMED     | 21938587  |  |
| REFERENCE  | 2 (bases 1 to 6046)   |  |
| AUTHORS    | Sugawara,T., Mazaki,E.M. and Yamakawa,K.  |  |
| TITLE      | Homo sapiens neuronal voltage-gated sodium channel type I (Nav1.1) mRNA   |  |
| JOURNAL    | Unpublished   |  |
| REFERENCE  | 3 (bases 1 to 6046)   |  |
| AUTHORS    | Sugawara,T., Mazaki,E.M. and Yamakawa,K.  |  |
| TITLE      | Direct Submission   |  |
| JOURNAL    | Submitted (03-JUL-2001) Neurogenetics, BSI, RIKEN, 2-1 Hirosawa,  |  |
| FEATURES   | Wako, Saitama 351-0198, Japan   |  |
| source     | Location/Qualifiers   |  |
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BASE COUNT 1808 a 1188 c 1345 g 1704 t 1 others  
 ORIGIN

Query Match 60.2%; Score 3628; DB 9; Length 6046;  
 Best local similarity 99.8%; Pred. No. 0;  
 Matches 3978; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 2044 GGAACAACACGAACTGAAATGAGAAAGAGTCAAGTCTTCCACGTTCCATG 2103  
 DB 2011 GGAACAACACGAACTGAAATGAGAAAGAGTCAAGTCTTCCACGTTCCATG 2070  
 OY 2104 GACTTCTAAGATCTCTCCAAAGCAACGCAATGATATACCGACATTCACCA 2163  
 DB 2071 GACTTCTAAGATCTCTCCAAAGCAACGCAATGATATACCGACATTCACCA 2130  
 OY 2164 AATACAGTAGAAGACTTGAAGATCCAGCAAGAAATGCCACCTGGTGGTAAATTT 2223  
 DB 2131 AATACAGTAGAAGACTTGAAGATCCAGCAAGAAATGCCACCTGGTGGTAAATTT 2190  
 OY 2224 TCCACATATATCTTAATCTGGAGCTGTTCCATATGTTAAAGTGAACAATGTTGTC 2283  
 DB 2191 TCCACATATATCTTAATCTGGAGCTGTTCCATATGTTAAAGTGAACAATGTTGTC 2250  
 OY 2284 AACCTGCTGAGTGAAGCCATGTTGACCTGGCATGACCAATGCTATGCTTAAT 2343  
 DB 2251 AACCTGCTGAGTGAAGCCATGTTGACCTGGCATGACCAATGCTATGCTTAAT 2310  
 OY 2344 ACTCTTTATGCGCATGAGCACTATCAATGACGACATTCATATATGCTTACA 2403

DB 2311 ACTCTTTATGCGCATGAGCACTATCAATGACGACATTCATATATGCTTACA 2370  
 OY 2404 GTAGGAACCTGTTTTCATCTGGGATCTTACAGCAGAAATGTTTGAAGATATGCCC 2463  
 DB 2371 GTAGGAACCTGTTTTCATCTGGGATCTTACAGCAGAAATGTTTGAAGATATGCCC 2430  
 OY 2464 ATGATACCTTACTATATATTTCCAAAGAGCTGGAATCTTGAAGGTTTATATGAGC 2523  
 DB 2431 ATGATACCTTACTATATATTTCCAAAGAGCTGGAATCTTGAAGGTTTATATGAGC 2490  
 OY 2524 CTAGGCTGTAGAACCTTGAGACGCCAATGTGGAAGATATCTGTTCCGTTCAAT 2583  
 DB 2491 CTAGGCTGTAGAACCTTGAGACGCCAATGTGGAAGATATCTGTTCCGTTCAAT 2550  
 OY 2584 CGATTGCTGCGAGTTTTCAGATTGGCAAAATCTTGGCCAACTTAATATGCTAAT 2643  
 DB 2551 CGATTGCTGCGAGTTTTCAGATTGGCAAAATCTTGGCCAACTTAATATGCTAAT 2610  
 OY 2644 ATCATGGCAATTCGCGGGGGGCTGAGAAATTTAACCTCGTGGCATCATGCTC 2703  
 DB 2611 ATCATGGCAATTCGCGGGGGGCTGAGAAATTTAACCTCGTGGCATCATGCTC 2670  
 OY 2704 TTCAATTTTCCGCTGGTGGCATGACGCTTGTGTAAGACTACAAAGATTTGCTGTC 2763  
 DB 2671 TTCAATTTTCCGCTGGTGGCATGACGCTTGTGTAAGACTACAAAGATTTGCTGTC 2730  
 OY 2764 AACATGCCAGTATGTCTCAACTGCCAGCTGGCAATGATGATCTTCCACTCTTC 2823  
 DB 2731 AACATGCCAGTATGTCTCAACTGCCAGCTGGCAATGATGATCTTCCACTCTTC 2790  
 OY 2824 CTGATTTGCTGCGCGGCTGCTGGGGGATGATATAGACCAATGAGGACTGATGAG 2883  
 DB 2791 CTGATTTGCTGCGCGGCTGCTGGGGGATGATATAGACCAATGAGGACTGATGAG 2850  
 OY 2884 GTTCTGCTGATGAGCATGCTTACTGCTTCAATGATGCTATGATGATGAGTGAACCTA 2943  
 DB 2851 GTTCTGCTGATGAGCATGCTTACTGCTTCAATGATGCTATGATGATGAGTGAACCTA 2910  
 OY 2944 GTGCTGCTGATGCTTCTTCTGCGCTTCTTMTAGGCTATTTAGTGAACACTTGA 3003  
 DB 2911 GTGCTGCTGATGCTTCTTCTGCGCTTCTTMTAGGCTATTTAGTGAACACTTGA 2970  
 OY 3004 GCCACTGATGATGATGATGAAATGAAATGAAATGCTCCAAATGCTGGATGAGTACACAA 3063  
 DB 2971 GCCACTGATGATGATGATGAAATGAAATGAAATGCTCCAAATGCTGGATGAGTACACAA 3030  
 OY 3064 GGAATGCTTATGTAAGAAAGAAATATGATTAATTCACAGTCTTCATTAGGAA 3123  
 DB 3031 GGAATGCTTATGTAAGAAAGAAATATGATTAATTCACAGTCTTCATTAGGAA 3090  
 OY 3124 CAAGAATTTTATGTAAGAAATTAACCACTTGATGATGTAAGCAAGAAAGACATGTT 3183  
 DB 3091 CAAGAATTTTATGTAAGAAATTAACCACTTGATGATGTAAGCAAGAAAGACATGTT 3150  
 OY 3184 ATGTCCATATACACAGAAATGGAAGATTTGACTATCTTAAGATGTAAGTGA 3243  
 DB 3151 ATGTCCATATACACAGAAATGGAAGATTTGACTATCTTAAGATGTAAGTGA 3210  
 OY 3244 ACTACAGTGTATGAGAACTGCGACAGTGTGAAAAATACATATATGTAAGTGA 3303  
 DB 3211 ACTACAGTGTATGAGAACTGCGACAGTGTGAAAAATACATATATGTAAGTGA 3270  
 OY 3304 TACATGCTATTCATTAACAACCCAGCTTACTGCTGATGACCAATGCTGTAGGAA 3363  
 DB 3271 TACATGCTATTCATTAACAACCCAGCTTACTGCTGATGACCAATGCTGTAGGAA 3330  
 OY 3364 TCTGACTTTGAAATTTAAACAGGAGACTTGTGATGATGATGATGATGATGATGAT 3423  
 DB 3331 TCTGACTTTGAAATTTAAACAGGAGACTTGTGATGATGATGATGATGATGATGAT 3390  
 OY 3424 AAGAGAACTGATGAAAGACAGTACTCATGAAAGTACGATGATGATGATGATGATGAT 3483



Db 3391 AAAGAAAGTGAATGAAGAGTACCTCATCAGAAAGTAGACAGTGTGACATCGGCGCA 3450  
OY 3484 CCTGTGAAGAAACAGCCCTAGTGAACCTGAAGAACTGTGAACAGAGCTGTTC 3543  
Db 3451 CCTGTGAAGAAACAGCCCTAGTGAACCTGAAGAACTGTGAACAGAGCTGTTC 3510  
OY 3544 ACTGAAGCTGTGTACAAAGATTCAGTGTGTCAATCAATGTGAGAGAGCAGAGCA 3603  
Db 3511 ACTGAAGCTGTGTACAAAGATTCAGTGTGTCAATCAATGTGAGAGAGCAGAGCA 3570  
OY 3604 AAACAATGTGAACTGTGAAGAGAGCTGTTCGAAATAGTGAACATTAACGTGTGAG 3663  
Db 3571 AAACAATGTGAACTGTGAAGAGAGCTGTTCGAAATAGTGAACATTAACGTGTGAG 3630  
OY 3664 ACCTTATTTGTTCATGATTCCTCTAGAGAGTGTGCTGTGAGATTTGAAGATATAT 3723  
Db 3631 ACCTTATTTGTTCATGATTCCTCTAGAGAGTGTGCTGTGAGATTTGAAGATATAT 3690  
OY 3724 ATTGATCAGAGAAAGAGATTAAGAGATGTGAATATGCTGACAAAGTTCACCTTAC 3783  
Db 3691 ATTGATCAGAGAAAGAGATTAAGAGATGTGAATATGCTGACAAAGTTCACCTTAC 3750  
OY 3784 ATTTTCATTCGTGAATGCTTCTTAATGAGGTGAGCATATGCTATCAACATATTCACC 3843  
Db 3751 ATTTTCATTCGTGAATGCTTCTTAATGAGGTGAGCATATGCTATCAACATATTCACC 3810  
OY 3844 AATGCTGTGTGTGCTGAGCACTTCTTAATGTGTGATGTTCATTTGGCATTTAACAGCA 3903  
Db 3811 AATGCTGTGTGTGCTGAGCACTTCTTAATGTGTGATGTTCATTTGGCATTTAACAGCA 3870  
OY 3904 AATGCTGTGTGTGCTGAGCACTTCTTAATGTGTGATGTTCATTTGGCATTTAACAGCA 3963  
Db 3871 AATGCTGTGTGTGCTGAGCACTTCTTAATGTGTGATGTTCATTTGGCATTTAACAGCA 3930  
OY 3964 AGACCTCTAGAGCCTTATCTCATTTGAAGAGGATGAGGTGTGTGAATGCTTGA 4023  
Db 3931 AGACCTCTAGAGCCTTATCTCATTTGAAGAGGATGAGGTGTGTGAATGCTTGA 3990  
OY 4024 GAGCAATTCATCATCATGATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4083  
Db 3991 GAGCAATTCATCATCATGATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4050  
OY 4084 AGCATATGAGGCGTAATTTGTTGCTGGCAAAATTCACACGTATTTAACACACAACT 4143  
Db 4051 AGCATATGAGGCGTAATTTGTTGCTGGCAAAATTCACACGTATTTAACACACAACT 4110  
OY 4144 GGTGACAGTGTTCATCATCATGATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4203  
Db 4111 GGTGACAGTGTTCATCATCATGATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4170  
OY 4204 AGAATGAGACTGCTCGATGAGAAATGTGAAGTAACTTTGATATGTGATTTGGG 4263  
Db 4171 AGAATGAGACTGCTCGATGAGAAATGTGAAGTAACTTTGATATGTGATTTGGG 4230  
OY 4264 TATCTCTCTTGTGCTCAAGTGTGCAATTCAGAGATGATGATATATATGATGAGCA 4323  
Db 4231 TATCTCTCTTGTGCTCAAGTGTGCAATTCAGAGATGATGATATATATGATGAGCA 4290  
OY 4324 GTTGATTCAGAAATGTGAAGTGTGCAAGTGTGCAAGTGTGCAAGTGTGCAAGTGTGCA 4383  
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Db 4411 ATCATGATATTTTTCAGACCGAGAGAAAGATTTGAGAGTCAAGCATTTATGACA 4470  
OY 4504 GAAGAAGAGAGAAATCTATATGATGATGATGATGATGATGATGATGATGATGATGATG 4563  
Db 4471 GAAGAAGAGAGAAATCTATATGATGATGATGATGATGATGATGATGATGATGATGATG 4530

OY 4564 CCTATACCTGACCGAGAGAAATTTCAAGGATGTGCTTTGACTGTACACAGACA 4623  
Db 4531 CCTATACCTGACCGAGAGAAATTTCAAGGATGTGCTTTGACTGTACACAGACA 4590  
OY 4624 GTTTTGAATTAAGCATCATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4683  
Db 4591 GTTTTGAATTAAGCATCATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4650  
OY 4684 ACAGATACCGAGAGTAAATGTGATACCATTTTGTGAGAGATGATGATGATGATGATG 4743  
Db 4651 ACAGATACCGAGAGTAAATGTGATACCATTTTGTGAGAGATGATGATGATGATGATG 4710  
OY 4744 GTGCTATTTACTGAGAGT 4803  
Db 4711 GTGCTATTTACTGAGAGT 4770  
OY 4804 ATTGATGAGATATTTTGTGATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4863  
Db 4771 ATTGATGAGATATTTTGTGATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4830  
OY 4864 GCCAGCTGATAGAAAGTATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4923  
Db 4831 GCCAGCTGATAGAAAGTATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4890  
OY 4924 AGAATGAGCGATCTACGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 4983  
Db 4891 AGAATGAGCGATCTACGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 4950  
OY 4984 GCTTGTGATGATGCT 5043  
Db 4951 GCTTGTGATGATGCT 5010  
OY 5044 TTGATCTACGCACTTTGGGATGTGCAACTTTGCTATGTGATGAGAGAGTGTGGATC 5103  
Db 5011 TTGATCTACGCACTTTGGGATGTGCAACTTTGCTATGTGATGAGAGAGTGTGGATC 5070  
OY 5104 GATGACATGTTCAACTTTGAGACCTTTGGCAAGAGCATGCTGCTATTCATTAATTA 5163  
Db 5071 GATGACATGTTCAACTTTGAGACCTTTGGCAAGAGCATGCTGCTATTCATTAATTA 5130  
OY 5164 ACCTGTGCTGCTGGAGTGTGCTGACACCATTTCTCAACAGTAAACCCAGCAGT 5223  
Db 5131 ACCTGTGCTGCTGGAGTGTGCTGACACCATTTCTCAACAGTAAACCCAGCAGT 5190  
OY 5224 GACCTTAATTAAGTAAACCTGGAAGCTCACTTAAGGAGACTGTGGAAACCATCTGTT 5283  
Db 5191 GACCTTAATTAAGTAAACCTGGAAGCTCACTTAAGGAGACTGTGGAAACCATCTGTT 5250  
OY 5284 GGAATTTCTTTTGTGAGTATCATCATATCCCTTCCGTTGTGAGATGATGATGATGATG 5343  
Db 5251 GGAATTTCTTTTGTGAGTATCATCATATCCCTTCCGTTGTGAGATGATGATGATGATGATG 5310  
OY 5344 ATGCGGTGATCTGAGAGACTGAGTGTGCTGATGAGAAAGTGTGAGAGCTCTGAGT 5403  
Db 5311 ATGCGGTGATCTGAGAGACTGAGTGTGCTGATGAGAAAGTGTGAGAGCTCTGAGT 5370  
OY 5404 GAGATGACTTTGAGATGTCTATGAGTGTGGAGAACTTTGATCCGATGCACTGAG 5463  
Db 5371 GAGATGACTTTGAGATGTCTATGAGTGTGGAGAACTTTGATCCGATGCACTGAG 5430  
OY 5464 TTGATGAGATTTGAGAAATTTATCTCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 5523  
Db 5431 TTGATGAGATTTGAGAAATTTATCTCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 5490  
OY 5524 CCACAGCAAAACCACTCAGCTCATGATGATGATGATGATGATGATGATGATGATGATGATG 5583  
Db 5491 CCACAGCAAAACCACTCAGCTCATGATGATGATGATGATGATGATGATGATGATGATGATG 5550  
OY 5584 ATTCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5643  
Db 5551 ATTCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5610

|            |  |   |      |
|------------|--|---|------|
| OY         | 5644   | ATGATGCTTACGAATACAGATGGAAGGAGGATTCATGCTTCACATCTTCCAAAGTTC | 5703 |
| Db         | 5611   | ATGATGCTTACGAATACAGATGGAAGGAGGATTCATGCTTCACATCTTCCAAAGTTC | 5670 |
| OY         | 5704   | TCCATACGCAATCACTACTACTTAAACGAAACAAAGAGAGATATCTGCTGCTCAT   | 5763 |
| Db         | 5671   | TCCATACGCAATCACTACTACTTAAACGAAACAAAGAGAGATATCTGCTGCTCAT   | 5730 |
| OY         | 5764   | ATTACGCTGCTTACAGAGCCGACCTTTAAAGGCACTGTAAACAAAGCTTCTTACG   | 5823 |
| Db         | 5731   | ATTACGCTGCTTACAGAGCCGACCTTTAAAGGCACTGTAAACAAAGCTTCTTACG   | 5790 |
| OY         | 5824   | TACATATAAAACAAATCAAGAGTGGGCTATCTTATATAAAGAGACATGATTAAT    | 5883 |
| Db         | 5791   | TACATATAAAACAAATCAAGAGTGGGCTATCTTATATAAAGAGACATGATTAAT    | 5850 |
| OY         | 5884   | GACGAATTAATGAATACTCTATTACAGAAAAAACTGATGACCATGTCCACTGACGT  | 5943 |
| Db         | 5851   | GACGAATTAATGAATACTCTATTACAGAAAAAACTGATGACCATGTCCACTGACGT  | 5910 |
| OY         | 5944   | TGTCACCTTCTTATGACCGGGGTGACAAAGCCATTTGGAAGAAACATGACGAAGGC  | 6003 |
| Db         | 5911   | TGTCACCTTCTTATGACCGGGGTGACAAAGCCATTTGGAAGAAACATGACGAAGGC  | 5970 |
| OY         | 6004   | AAAGTGAAGAAAGCAAGGAAAT 6028                               |      |
| Db         | 5971   | AAAGTGAAGAAAGCAAGGAAAT 5995                               |      |
| RESULT 11  | AF225985   | 8131 bp mRNA linear PRI 01-FEB-2001                       |      |
| LOCUS      | AF225985   |   |      |
| DEFINITION | Homo sapiens voltage-gated sodium channel alpha subunit SCN1A  |   |      |
| ACCESSION  | AF225985   |   |      |
| VERSION    | AF225985.1   | GI:12642269   |      |
| KEYWORDS   |  |   |      |
| SOURCE     | Homo sapiens.  |   |      |
| ORGANISM   | Homo sapiens.  |   |      |
| REFERENCE  | 1 (bases 1 to 8131)  |   |      |
| AUTHORS    | Jeong,S.-Y., Goto,J., and Kanazawa,I.  |   |      |
| TITLE      | Cloning of cDNA for human voltage-gated sodium channel alpha subunit, SCN1A  |   |      |
| JOURNAL    | Unpublished  |   |      |
| REFERENCE  | 2 (bases 1 to 8131)  |   |      |
| AUTHORS    | Jeong,S.-Y., Goto,J., and Kanazawa,I.  |   |      |
| TITLE      | Direct Submision   |   |      |
| JOURNAL    | Submitted (14-JAN-2000) Department of Neurology, University of Tokyo, Graduate School of Medicine, 7-3-1 Hongo, Bunkyo-ku, Tokyo 113-8655, Japan |   |      |
| FEATURES   | Location/Qualifiers  |   |      |
| source     | 1. 8131  |   |      |
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|            | SAISALYILFENPLKAIKILVHSLKILNCTILNCFMNSNPDKNVEY   |   |      |
|            | FTGYTESLKIILARGCELEDFLRDPMWMLDFVTFAVEFVLEIGVNSALRTP  |   |      |
|            | RVIALKTIIVIPGLKIVGALIOSVKLSIDVMLIVFGLISVFALIGQLMGNLRNK   |   |      |
|            | CIDMPPTNALSLEHSIEKNTIVNNTLINTEVEPDKRSTIQSRHYHFLGFLDAL  |   |      |

|    |      |  |      |
|----|------|--|------|
| OY | 2044 | GGACAACACCTGAAGACGTAATGGAAGAGAGGTCAGTCTTCCAGCTTCCAG      | 2103 |
| Db | 2029 | GGACAACACCTGAAGACGTAATGGAAGAGAGGTCAGTCTTCCAGCTTCCAG      | 2088 |
| OY | 2104 | GACTTCTAGAAATCTCTCCCAAGGCAAGCAAGTATGATGACGACATTCAC       | 2163 |
| Db | 2089 | GACTTCTAGAAATCTCTCCCAAGGCAAGCAAGTATGATGACGACATTCAC       | 2148 |
| OY | 2164 | AATACAGTGAAGACCTTAAGATTCAGGCAAGAAATGCCACCTGTTGATTAAT     | 2223 |
| Db | 2149 | AATACAGTGAAGACCTTAAGATTCAGGCAAGAAATGCCACCTGTTGATTAAT     | 2208 |
| OY | 2224 | TCCAACTATCTCTTAATGCGGAGCTGCTCCATATGTTGTTAAAGTGAAGATG     | 2283 |
| Db | 2209 | TCCAACTATCTCTTAATGCGGAGCTGCTCCATATGTTGTTAAAGTGAAGATG     | 2268 |
| OY | 2284 | AACCTGCTGATGAGACCATTTGTTGACCTGACCATACCATCTGATCTCTTAAT    | 2343 |
| Db | 2269 | AACCTGCTGATGAGACCATTTGTTGACCTGACCATACCATCTGATCTCTTAAT    | 2328 |
| OY | 2344 | ACTCTTTTATGCGCATGAGACATATCCATGAGGACCATTTCAATATGCTTACA    | 2403 |
| Db | 2329 | ACTCTTTTATGCGCATGAGACATATCCATGAGGACCATTTCAATATGCTTACA    | 2388 |
| OY | 2404 | GTAGGAAACTGTTGTTTCACTGGGATCTTACAGCAAGAAATTTCTGAAATTAAT   | 2463 |
| Db | 2389 | GTAGGAAACTGTTGTTTCACTGGGATCTTACAGCAAGAAATTTCTGAAATTAAT   | 2448 |
| OY | 2464 | ATGATCTCTTACTATTTTCCAAAGAGCTGGAATATCTTACAGGTTTATGACG     | 2523 |
| Db | 2449 | ATGATCTCTTACTATTTTCCAAAGAGCTGGAATATCTTACAGGTTTATGACG     | 2508 |
| OY | 2524 | CTTACCTGCTGAGAACTTGGCACTGGCAATGTGAAGATTAATCTGCTCCGTTCAAT | 2583 |
| Db | 2509 | CTTACCTGCTGAGAACTTGGCACTGGCAATGTGAAGATTAATCTGCTCCGTTCAAT | 2568 |
| OY | 2584 | CGATTGCTGCGAGTTTCAAGTTGGCAAAATCTTGGCCAACTTAAATATGTAATAAG | 2643 |

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RKOEVSVAIIORAYRRHLKRTYKQASFTYNNKRIKGNALIKEDMIIDRIENNS  
ITERKDTLMTSTACPPSYDRYTKRPIVEKHEDEGDEKXKG\*

BASE COUNT 2453 a 1530 c 1719 g 2422 t  
ORIGIN  
Query Match 54.8% Score 3302; DB 9; Length 8131;  
Best Local Similarity 99.8% Pred. No. 0;  
Matches 3982; Conservative 0; Mismatches 4; Indels 5; Gaps 3;

|    |      |  |      |
|----|------|--|------|
| Db | 2559 | CGATTGCTGGAGATTTCACAGTTGGCAAAATCTTGGCCACGTTAAATATGCTAATAAG   | 2628 |
| Oy | 2644 | ATCATCGGCAATTCCTGGGGGCTCGGGAAATTTAAACCTCGCTTGGCCATCATCTC     | 2703 |
| Db | 2629 | ATCATCGGCAATTCCTGGGGGCTCGGGAAATTTAAACCTCGCTTGGCCATCATCTC     | 2688 |
| Oy | 2704 | TTCAATTTTGGCGGTGGCGGACATGACGCTCTTGGTAAAGGTACAAAGATTGTCTGCG   | 2763 |
| Db | 2689 | TTCAATTTTGGCGGTGGCGGACATGACGCTCTTGGTAAAGGTACAAAGATTGTCTGCG   | 2748 |
| Oy | 2764 | AAGATGCCACGATATGTGTCAACGCC--ACGTGGCAATGAAGACTCTTCACACC       | 2820 |
| Db | 2749 | AAGATGCCACGATATGTGTCAACGCCACCAACGCTGGCAATGAAGACTCTTCACACC    | 2808 |
| Oy | 2821 | TTCCGATGATGTTCCCGCGCTGTGGGAGATGATGAGACCATGCTGGACATGTATG      | 2880 |
| Db | 2809 | TTCCGATGATGTTCCCGCGCTGTGGGAGATGATGAGACCATGCTGGACATGTATG      | 2868 |
| Oy | 2881 | GAGGTGCTGGTCAAGCCATGCTCTTACTGTCTTCATGATGTCATGGTATGGTGAAC     | 2940 |
| Db | 2869 | GAGGTGCTGGTCAAGCCATGCTCTTACTGTCTTCATGATGTCATGGTATGGTGAAC     | 2928 |
| Oy | 2941 | CTAGTGTCTGTAATCTCTTTCTGGCCCTGTGTGAGTCACTTTAGTGCACACCTT       | 3000 |
| Db | 2929 | CTAGTGTCTGTAATCTCTTTCTGGCCCTGTGTGAGTCACTTTAGTGCACACCTT       | 2988 |
| Oy | 3001 | GCACGCACTGATGATGATGATGAAGAATATCTCCAAATGCTGGATATGGATGAC       | 3060 |
| Db | 2989 | GCACGCACTGATGATGATGATGAAGAATATCTCCAAATGCTGGATATGGATGAC       | 3048 |
| Oy | 3061 | AAAGAGTAGCTTATGTGAAGAAAAATATATGATTTATTCACAGTCTCTATTAGG       | 3120 |
| Db | 3049 | AAAGAGTAGCTTATGTGAAGAAAAATATATGATTTATTCACAGTCTCTATTAGG       | 3108 |
| Oy | 3121 | AAACAAAGATTTTATGATGAATTTAAACCACTGATGATCTAAACAACAAGAACAGT     | 3180 |
| Db | 3109 | AAACAAAGATTTTATGATGAATTTAAACCACTGATGATCTAAACAACAAGAACAGT     | 3168 |
| Oy | 3181 | TGTATGTCATCATCATACARAGAAATTTGGAAAGATCTTGACATCTTTAAAGTATAAT   | 3240 |
| Db | 3169 | TGTATGTCATCATCATACARAGAAATTTGGAAAGATCTTGACATCTTTAAAGTATAAT   | 3228 |
| Oy | 3241 | GGAACTACAAGTGTATAGAACTGGCAGCAGTGTGAAAAATACATTATGATGAAGT      | 3300 |
| Db | 3229 | GGAACTACAAGTGTATAGAACTGGCAGCAGTGTGAAAAATACATTATGATGAAGT      | 3288 |
| Oy | 3301 | GATTACATGTCATCATTAACAAACCCAGTCTTACTGTACTGTACCAATGCTGTAGGA    | 3360 |
| Db | 3289 | GATTACATGTCATCATTAACAAACCCAGTCTTACTGTACTGTACCAATGCTGTAGGA    | 3348 |
| Oy | 3361 | GAACTGACTTTGAAAAATTTAAACAGSAAAGATTTAGTAGGAATCGGATGTGSAAGAA   | 3420 |
| Db | 3349 | GAACTGACTTTGAAAAATTTAAACAGSAAAGATTTAGTAGGAATCGGATGTGSAAGAA   | 3408 |
| Oy | 3421 | AGCAAAAGAAATCGAATGGAAGCAGTAGCTCATCAAGAGTAGACACTGT--GGACATCGG | 3479 |
| Db | 3409 | AGCAAAAGAAATCGAATGGAAGCAGTAGCTCATCAAGAGTAGACACTGTGGCAATTCGGG | 3468 |
| Oy | 3480 | CGCACTGTAGAGACACGCCCGTAGTGGAACTGAAGAACTCTTGAACAGAAAGCTTG     | 3539 |
| Db | 3469 | CGC--CTGTAGAAACAGCCCGTAGTGGAACTGAAGAACTCTTGAACAGAAAGCTTG     | 3527 |
| Oy | 3540 | TTTACAGGAAGCGGTCTACAAGAAATTCAAAGTGTGTCCAAATCAATGTGGAAAGGAG   | 3599 |
| Db | 3528 | TTTACAGGAAGCGGTCTACAAGAAATTCAAAGTGTGTCCAAATCAATGTGGAAAGGAG   | 3587 |
| Oy | 3600 | AGGAAACAAATGTGGAACCTGGAAGAGAGTGTTCACAAATAGTTGAACATATCGTT     | 3659 |
| Db | 3588 | AGGAAACAAATGTGGAACCTGGAAGAGAGTGTTCGCAATATGTTGAACATATCGTT     | 3647 |
| Oy | 3660 | TGAGACTTATTGTTTTATGATTTCTCTTAAGTAGTGTCTCTGGCATTGGAAGATAT     | 3719 |

|    |      |  |      |
|----|------|--|------|
| Db | 3648 | TGAAACCTTAATGCTTTTTCATGATATGTCCTTAATAGAGGAGCGTCGGCATTTGAAGANAT | 3707 |
| QY | 3720 | ATATATGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAGGTTTTCAC     | 3779 |
| Db | 3708 | ATATATGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAGGTTTTCAC     | 3767 |
| QY | 3780 | TTACATTTTCATCTCTGGAATATGCTCTGAAAATGGGTGGCATATAGGCTATCAAACTATT  | 3839 |
| Db | 3768 | TTACATTTTCATCTCTGGAATATGCTCTGAAAATGGGTGGCATATAGGCTATCAAACTATT  | 3827 |
| QY | 3840 | CACCAATGCCGAGTGTGGCGAGACTCTAAATGTTGATGTTTCATTTGTCAGTTTAA       | 3899 |
| Db | 3828 | CACCAATGCCGAGTGTGGCGAGACTCTTAATGTTGATGTTTCATTTGTCAGTTTAA       | 3887 |
| QY | 3900 | AGCAAAATGCCCTTGGGTACTCAGAACTTGGAGGCATCAATCTCTCAGACACTAAGAC     | 3959 |
| Db | 3888 | AGCAAAATGCCCTTGGGTACTCAGAACTTGGAGGCATCAATCTCTCAGACACTAAGAC     | 3947 |
| QY | 3960 | TCCTGACCTCTTAAGACCTTATCTCGATTGAAAGGATGAGGGTGGTTGTAATGCCCT      | 4019 |
| Db | 3948 | TCCTGACCTCTTAAGACCTTATCTCGATTGAAAGGATGAGGGTGGTTGTAATGCCCT      | 4007 |
| QY | 4020 | TTTAGGACCAATTCACATCCATCCATGAAATGAGCTGCTGGCTTGTGCTAATTTCTGGCTAT | 4079 |
| Db | 4008 | TTTAGGACCAATTCACATCCATCCATGAAATGAGCTGCTGGCTTGTGCTAATTTCTGGCTAT | 4067 |
| QY | 4080 | TTTTCAGATCATGAGGCGCTAAATTTGTTGCTGGCAAAATCTACACTGATTAACACAC     | 4139 |
| Db | 4068 | TTTTCAGATCATGAGGCGCTAAATTTGTTGCTGGCAAAATCTACACTGATTAACACAC     | 4127 |
| QY | 4140 | AACTGTGACAGGTTTGCATCGAAGACGTGAATTAATCACTGATTTGCTAAACTAAT       | 4199 |
| Db | 4128 | AACTGTGACAGGTTTGCATCGAAGACGTGAATTAATCACTGATTTGCTAAACTAAT       | 4187 |
| QY | 4200 | AGAAAGAAATGAGACTGCTGATGAGAAATATGAAAGTAAACTTGTGAATATGAGANT      | 4255 |
| Db | 4188 | AGAAAGAAATGAGACTGCTGATGAGAAATATGAAAGTAAACTTGTGAATATGAGANT      | 4247 |
| QY | 4260 | TGGGATATCTCTTTCGCTTCAAGTTGGCCATTTCAAGGATGAGATATATGATATGC       | 4319 |
| Db | 4248 | TGGGATATCTCTTTCGCTTCAAGTTGGCCATTTCAAGGATGAGATATATGATATGC       | 4307 |
| QY | 4320 | AGCAGTTGATTCGAAATATGTCGAACTTCGACCTTAAGTATGAAGAAAGTCTGTACATGTA  | 4379 |
| Db | 4308 | AGCAGTTGATTCGAAATATGTCGAACTTCGACCTTAAGTATGAAGAAAGTCTGTACATGTA  | 4367 |
| QY | 4380 | TCTTACTTCTTTATTTTTCATCACTTTGGGTGCTTCTTCACCTTGAACCTGTATATGG     | 4439 |
| Db | 4368 | TCTTACTTCTTTATTTTTCATCACTTTGGGTGCTTCTTCTTCACCTGTATATGG         | 4427 |
| QY | 4440 | TCTCATCTATATATTAATTTTCAACGACGAGAAAAGAAAGTTGGAGGTCAAGACATCTTAT  | 4499 |
| Db | 4428 | TCTCATCTATATATTAATTTTCAACGACGAGAAAAGAAAGTTGGAGGTCAAGACATCTTAT  | 4487 |
| QY | 4500 | GACAGAGACAGAGAAGAAATCTATTAATGCAATGAAAAAATTTAGATCGAAAAAACCGCA   | 4555 |
| Db | 4488 | GACAGAGACAGAGAAGAAATCTATTAATGCAATGAAAAAATTTAGATCGAAAAAACCGCA   | 4547 |
| QY | 4560 | AAAGCCTTACTCTGACACGAGAAACAATTTCAAGGAATGCTTTGACTTGTGTAACAG      | 4615 |
| Db | 4548 | AAAGCCTTACTCTGACACGAGAAACAATTTCAAGGAATGCTTTGACTTGTGTAACAG      | 4607 |
| QY | 4620 | ACAAGTTTTTGACATTAAGCATCATGATTCATCTGCTTAACATGCTCACAAATGAGGT     | 4679 |
| Db | 4608 | ACAAGTTTTTGACATTAAGCATCATGATTCATCTGCTTAACATGCTCACAAATGAGGT     | 4667 |
| QY | 4680 | GGAAACAGATGACAGAGTGAATATGTGACTACATTTTGTCAACGATCAATCTGGTGT      | 4739 |
| Db | 4668 | GGAAACAGATGACAGAGTGAATATGTGACTACATTTTGTCAACGATCAATCTGGTGT      | 4727 |
| QY | 4740 | CATTGTGCTATTTACTGAGAGTGTGTACTGGAATTCATCTCTACAGCCATTAATATT      | 4799 |
| Db | 4728 | CATTGTGCTATTTACTGAGAGTGTGTACTGGAATTCATCTCTACAGCCATTAATATT      | 4787 |

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DEFINITION Sequence 5 from Patent WO214498.  
ACCESSION AX391134  
VERSION AX391134.1 GI:19584234  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1  
AUTHORS Turner C.A., Mathur B. and Mathur D.  
TITLE Novel human ion channel proteins and polynucleotides encoding the same  
JOURNAL Patent: WO 0214498-A 5 21-FEB-2002;  
LEXICON Genetics Incorporated (US)  
FEATURES  
source 1. 4329  
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BASE COUNT 1287 a 840 c 988 g 1211 t 3 others  
ORIGIN

Query Match 38.1%; Score 2295; DB 6; Length 4329;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2044 GGAACAACCACTGAACTGAAATGAGAAAGAGTCAAGTCTTCCAGTTTCATG 2103  
2011 GGAACAACCACTGAACTGAAATGAGAAAGAGTCAAGTCTTCCAGTTTCATG 2070  
2104 GACTTCTAGAGATCTTCCCAAGCAAGCAATGATATAGCCATTCATACA 2163  
2071 GACTTCTAGAGATCTTCCCAAGCAAGCAATGATATAGCCATTCATACA 2130  
2164 AATACATGATGAACTGAAATGAGAAATGAGAAAGAGTCAAGTCTTCCAGTTTCATG 2223  
2131 AATACATGATGAACTGAAATGAGAAATGAGAAAGAGTCAAGTCTTCCAGTTTCATG 2190  
2224 TCCAACTATCTTAACTGAGACTGTTCCATATGTTTAAAGTGAATGTTGTC 2283  
2191 TCCAACTATCTTAACTGAGACTGTTCCATATGTTTAAAGTGAATGTTGTC 2250  
2284 AACCTGTTGATGAGCAACCAATTTGATGACCTGACATCCATCTGTTAAT 2343  
2251 AACCTGTTGATGAGCAACCAATTTGATGACCTGACATCCATCTGTTAAT 2310  
2344 AACCTGTTGATGAGCAACCAATTTGATGACCTGACATCCATCTGTTAAT 2403  
2311 AACCTGTTGATGAGCAACCAATTTGATGACCTGACATCCATCTGTTAAT 2370  
2404 GTAGAAACTGTTGTTTCACTGGGATCTTACAGCAAAATGTTTGTGAAAAATTTATG 2463  
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2464 ATGATCTTATGATG 2523  
2431 ATGATCTTATGATG 2490

|    |      |   |      |
|----|------|---|------|
| QY | 2524 | CTTGGCCCTGGTAAACCTGGACACGCGCATGGTGGAAAGGTTATCTGCTTCGCTGCATTT    | 2583 |
| Db | 2491 | CTTGGCCCTGGTAAACCTGGACACGCGCAATGGGAAGGTTATCTGCTTCGCTGCATTT      | 2550 |
| QY | 2584 | CGATGCTGGGAATTTTTCAAAGTTGGCAAAATCTGTGGCCACGTTTAAATNTCTATAAAG    | 2643 |
| Db | 2551 | CGATGCTGGGAATTTTTCAAAGTTGGCAAAATCTGTGGCCACGTTTAAATNTCTATAAAG    | 2610 |
| QY | 2644 | ATCATCGGCAATTCGCGGGGGGCTGTGGGAAATTTAACCTCGTGTGGCCATCATGTC       | 2703 |
| Db | 2611 | ATCATCGGCAATTCGCGGGGGGCTGTGGGAAATTTAACCTCGTGTGTGGCCATCATGTC     | 2670 |
| QY | 2704 | TTTCATTTTTCGCCGTGGCGGACATGCAAGCTCTTGTGTAAGAAAGCTAATAAGATTGTGTGC | 2763 |
| Db | 2671 | TTTCATTTTTCGCCGTGGCGGACATGCAAGCTCTTGTGTAAGAAAGCTAATAAGATTGTGTGC | 2730 |
| QY | 2764 | AAAGTCCGCAAGTATTTGTCAACTCCCAAGCTGGACATGAATGACTTCTCCACCTCTC      | 2823 |
| Db | 2731 | AAAGTCCGCAAGTATTTGTCAACTCCCAAGCTGGACATGAATGACTTCTCCACCTCTC      | 2790 |
| QY | 2824 | CTGATTTGTTCGCGTCTGTGTGGGGAGTGGAATAGACACATGTGGGACTGTATGGAG       | 2883 |
| Db | 2791 | CTGATTTGTTCGCGTCTGTGTGGGGAGTGGAATAGACACATGTGGGACTGTATGGAG       | 2850 |
| QY | 2884 | GTTCTCTGTCAAGCACTGTGCTTACTGTCTTCTATGATGTGTATGGTAATTTGGAAACCTA   | 2943 |
| Db | 2851 | GTTCTCTGTCAAGCACTGTGCTTACTGTCTTCTATGATGTGTATGGTAATTTGGAAACCTA   | 2910 |
| QY | 2944 | GTTGCTCTGTAATCTTTCGCGCCTGCTTMMTGAGCTCATTTAGTGAAGACACCTTGCA      | 3003 |
| Db | 2911 | GTTGCTCTGTAATCTTTCGCGCCTGCTTMMTGAGCTCATTTAGTGAAGACACCTTGCA      | 2970 |
| QY | 3004 | GCCACTGATGATGATTAATGAATGAATTAATCTCCAAATTCGTGGATAGATGACAAA       | 3063 |
| Db | 2971 | GCCACTGATGATGATTAATGAATGAATTAATCTCCAAATTCGTGGATAGATGACAAA       | 3030 |
| QY | 3064 | GGATGACTTATGTGAAAAAATAATATATGAAATTTATCAACACTCTCTCATTAAGAAA      | 3123 |
| Db | 3031 | GGATGACTTATGTGAAAAAATAATATATGAAATTTATCAACACTCTCTCATTAAGAAA      | 3090 |
| QY | 3124 | CAAAAGATTTTATGATGAATAATTAACCACTGTGATCTAAACAAAGAAAGACAGTTGT      | 3183 |
| Db | 3091 | CAAAAGATTTTATGATGAATAATTAACCACTGTGATCTAAACAAAGAAAGACAGTTGT      | 3150 |
| QY | 3184 | ATGTCCATCATACACAGAAATTTGGGAAAGATCTTGACTATCTTAAAGATGATAATGGA     | 3243 |
| Db | 3151 | ATGTCCATCATACACAGAAATTTGGGAAAGATCTTGACTATCTTAAAGATGATAATGGA     | 3210 |
| QY | 3244 | ACTACAAAGTGGTATATAGAACTGGCAGCAGCTTGGAATAATACATTTATGATGAAGAATAT  | 3303 |
| Db | 3211 | ACTACAAAGTGGTATATAGAACTGGCAGCAGCTTGGAATAATACATTTATGATGAAGAATAT  | 3270 |
| QY | 3304 | TACATGTCATTCATPAACCAACCCAGCTTACTGTGACTGTACCAATTTGCTGTAGAGAA     | 3363 |
| Db | 3271 | TACATGTCATTCATPAACCAACCCAGCTTACTGTGACTGTACCAATTTGCTGTAGAGAA     | 3330 |
| QY | 3364 | TCTGACTTTGAAAAATTTAAACAGGAAAGACTTTAGTAGTAATCGGATCTGGAGAAAGC     | 3423 |
| Db | 3331 | TCTGACTTTGAAAAATTTAAACAGGAAAGACTTTAGTAGTAATCGGATCTGGAGAAAGC     | 3390 |
| QY | 3424 | AAAGAGAACTGAATGAAGCACTAGCTCATCAAGAAAGTATGACACTGTGACACTCGGCGCA   | 3483 |
| Db | 3391 | AAAGAGAACTGAATGAAGCACTAGCTCATCAAGAAAGTATGACACTGTGACACTCGGCGCA   | 3450 |
| QY | 3484 | CTGTGAGAAAGCAAGCCGATAGTGAACCTGGAAGAACTCTTGAACCGAAGACTTGTTTC     | 3543 |
| Db | 3451 | CTGTGAGAAAGCAAGCCGATAGTGAACCTGGAAGAACTCTTGAACCGAAGACTTGTTTC     | 3510 |
| QY | 3544 | ACTGAAGGCTGTGTACAAAGATTCAGTGTGTCAATCAATATGTGGAAAGAGCAGAGGA      | 3603 |
| Db | 3511 | ACTGAAGGCTGTGTACAAAGATTCAGTGTGTGTCAATCAATATGTGGAAAGAGCAGAGGA    | 3570 |
| QY | 3604 | AAACATGTGTGAACCTGTGACAGAGAGCTGTTTCCGAATAGTTGAACATATACGTGTTTGAAG | 3666 |



BASE COUNT 1226 a 810 c 951 g 1156 t 3 others  
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 DB 2131 AATACGATGAGAGATCTTGAAGATCCAGCAGAAATGCCACCCCTGTTGATTAATTT 2190  
 OY 2224 TCCACATATTTCTTAATCTGGGACCTGTCATATTTGGTTAAAGTGAAGACATGTTGTC 2283  
 DB 2191 TCCACATATTTCTTAATCTGGGACCTGTCATATTTGGTTAAAGTGAAGACATGTTGTC 2250  
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 RESULT 14  
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 DEFINITION Sequence 9 from Patent WO0214498.  
 ACCESSION AX391138  
 VERSION AX391138.1 GI:19584236  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1  
 AUTHORS Turner, C.A., Mathur, B. and Mathur, D.  
 TITLE Novel human ion channel proteins and polynucleotides encoding the  
 same  
 JOURNAL Patent: WO 0214498-A 9 21-FEB-2002;  
 FEATURES Lexicon Genetics Incorporated (US)  
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Copyright (c) 1993 - 2003 Compugen Ltd.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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| 17 | 1157 | 19.2 | 1194 | 22 ABA48040 | Human breast cell  |
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| 39 | 358  | 5.9  | 1425 | 22 AAS84262 | DNA encoding novel |
| 40 | 353  | 5.9  | 909  | 22 AAH55782 | Human SCN1A genom  |
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| 44 | 274  | 4.5  | 409  | 22 AAH55772 | Human SCN1A genom  |
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#### ALIGNMENTS

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| XX       |   |
| DT       | 01-JUL-2002 (first entry)                                       |
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| KW       | gene therapy; bioreactor; mental disorder; biological disorder; |
| KW       | gene; medical disorder; ss.                                     |
| XX       |   |
| OS       | Homo sapiens.   |
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PA (LEXI-) LEXICON GENETICS INC.

PI Turner CA, Mathur B, Mathur D;

DR WPI; 2002-280757/32.

DR P-PSDB; AAE20515.

PT Novel polynucleotides encoding human sodium channel proteins,

PT particularly voltage-gated sodium channel proteins useful for drug

PS screening, diagnosis and in gene therapy of biological disorders

PS Claim 2; Page 55-57; 83pp; English.

XX The present sequence is a cDNA encoding novel human protein (NHP), ion  
CC channel protein. NHP share structural similarity with mammalian sodium  
CC channel proteins particularly voltage-gated sodium channel proteins.  
CC NHP oligonucleotides are useful as hybridisation probes for screening  
CC libraries and assessing gene expression patterns. Sequences derived  
CC from regions adjacent to the intron/exon boundaries of NHP gene can be  
CC used to design primers for use in amplification assays to detect  
CC mutations within the exons, splice sites, introns that can be used in  
CC diagnostics and pharmacogenomics. NHP nucleotide sequences are useful  
CC for drug screening effective in the treatment of symptomatic or  
CC phenotypic manifestations of perturbing the normal function of NHP in  
CC the body, and nucleotide constructs encoding NHP products are useful to  
CC genetically engineer host cells to express NHP products in vivo. These  
CC cells deliver a continuous supply of a NHP, a NHP peptide, or a NHP fusion  
CC protein to the body. Nucleotide construct encoding NHP products are  
CC also useful in gene therapy for modulating NHP expression and to  
CC produce genetically engineered host cells to express NHP products in  
CC vivo. NHP nucleotide sequences may also be used as part of ribozyme  
CC and/or triple helix sequences that are useful for NHP gene regulation.  
CC The NHP polypeptides are useful for generating antibodies, as  
CC reagents in diagnostic assays, for identifying other cellular gene  
CC products related to NHP and as reagents in assays for screening for  
CC compounds that are useful in the treatment of mental, biological or  
CC medical disorders and diseases.

XX Sequence 6030 BP; 1786 A; 1190 C; 1345 G; 1706 T; 3 other;

Query Match 100.0%; Score 6030; DB 24; Length 6030;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 6030; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 901 AATGCTACACTATTAATATGAAATCTGCTGATTTGAGTGAAGTCAATATATGATATG 960  
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DB 961 TCAATATATCATTTATTTCTGTGAGAGGTTTATGATGACATCTATGAGAAATAGCT 1020  
QY 1021 GATGAGGCAATATGTCACAGAGAGATATATGATGAGAAAGCTGTAAGAAATCCCAAT 1080  
DB 1021 GATGAGGCAATATGTCACAGAGAGATATATGATGAGAAAGCTGTAAGAAATCCCAAT 1080  
QY 1081 GGTACACAAAGCTTTGATACCTTCAAGTGGGCTTTTGTCTGTCGATTAATGACT 1140  
DB 1081 GGTACACAAAGCTTTGATACCTTCAAGTGGGCTTTTGTCTGTCGATTAATGACT 1140  
QY 1141 CAGGACTTCTGGGAAATCTTTATATCACTGATATGATGCTGCTGAGGAAAGCTATG 1200  
DB 1141 CAGGACTTCTGGGAAATCTTTATATCACTGATATGATGCTGCTGAGGAAAGCTATG 1200  
QY 1201 AATATTTTGTGTTGCTATTTTCTGAGCTCATTTCACTTAATTAATTTGATCTGCT 1260  
DB 1201 AATATTTTGTGTTGCTATTTTCTGAGCTCATTTCACTTAATTAATTTGATCTGCT 1260  
QY 1261 GTGTGGCCATGCGCTACAGAGAGAGAGATGAGGCACTTTGGAAGAGAGAGAGAA 1320  
DB 1261 GTGTGGCCATGCGCTACAGAGAGAGAGATGAGGCACTTTGGAAGAGAGAGAGAA 1320  
QY 1321 GAGGCGGAATTTACAGCATGATTTGAGAGCTTAATAAAGCAACAGAGAGAGAGAG 1380  
DB 1321 GAGGCGGAATTTACAGCATGATTTGAGAGCTTAATAAAGCAACAGAGAGAGAGAG 1380  
QY 1381 GAGGCAAGGCAAGTGCCTACAGATTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440  
DB 1381 GAGGCAAGGCAAGTGCCTACAGATTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440  
QY 1441 GACAGCTATCTGAAGCTCTTAAGTTGAGTTCAAGAGAGTGTCTAAGAGAGAGAGAG 1500  
DB 1441 GACAGCTATCTGAAGCTCTTAAGTTGAGTTCAAGAGAGTGTCTAAGAGAGAGAGAG 1500  
QY 1501 AGGAG 1560



1501 AGAAGAAAAAGAAAGAGAGAGCTGGGGGAGAGAAAGATGAGATGTAATTC 1560  
1561 CAAAAATCTGAATCTGAGAGACACATCAGAGAGAAAGTTTGGCTTCTCATTTGAAGG 1620  
1561 CAAAAATCTGAATCTGAGAGACACATCAGAGAGAAAGTTTGGCTTCTCATTTGAAGG 1620  
1621 AACCGATTGACATATGAAAAAGAGTCTCTCCACACACAGTCTTTGTTGATGATCCGT 1680  
1621 AACCGATTGACATATGAAAAAGAGTCTCTCTCCACACACAGTCTTTGTTGATGATCCGT 1680  
1621 AACCGATTGACATATGAAAAAGAGTCTCTCTCCACACACAGTCTTTGTTGATGATCCGT 1680  
1681 GAGTCCCTATTTTACCAAGGCGAAAAATAGCAGAAACGCTTTTCAGCTTTAGAGGCGA 1740  
1681 GAGTCCCTATTTTACCAAGGCGAAAAATAGCAGAAACGCTTTTCAGCTTTAGAGGCGA 1740  
1741 GCAGAGAGTGTGGATCTGAGAAAGACATTCGCGAGATGATGACACAGCCTTTGAGGAT 1800  
1741 GCAGAGAGTGTGGATCTGAGAAAGACATTCGCGAGATGATGACACAGCCTTTGAGGAT 1800  
1801 AACGAGAGCGGTAGAGATTCCTGTTTGTGCCGAGACAGGAGAGAGACGACACAGC 1860  
1801 AACGAGAGCGGTAGAGATTCCTGTTTGTGCCGAGACAGGAGAGAGACGACACAGC 1860  
1861 AACCTGAGTCAGACAGTATGATCCGAGATCTGGCAGTCTTTCCAGCGAAATGGAG 1920  
1861 AACCTGAGTCAGACAGTATGATCCGAGATCTGGCAGTCTTTCCAGCGAAATGGAG 1920  
1921 ATGACAGACAGCTGTGATTCGAAATGATGTTGTTCTTGGTGGTGGACCTTCAGTTCCT 1980  
1921 ATGACAGACAGCTGTGATTCGAAATGATGTTGTTCTTGGTGGTGGACCTTCAGTTCCT 1980  
1981 ACATGCGCTGTGGAGAGCTTCCGAGAGGTATATATAGCAGATGATGATGAC 2040  
1981 ACATGCGCTGTGGAGAGCTTCCGAGAGGTATATATAGCAGATGATGATGAC 2040  
2041 AATGGAACAACAGCTGAAATGAGAAAGAGAAAGAGTCTTTCCAGCTTCC 2100  
2041 AATGGAACAACAGCTGAAATGAGAAAGAGAAAGAGTCTTTCCAGCTTCC 2100  
2101 ATGACCTTCTAGAGAGCTTCCCAAGGCAAGACAGCAATGATGACCAATTCCTA 2160  
2101 ATGACCTTCTAGAGAGCTTCCCAAGGCAAGACAGCAATGATGACCAATTCCTA 2160  
2161 ACAGAGTGTAGAGAGCTTCCCAAGGCAAGACAGCAATGATGACCAATTCCTA 2220  
2161 ACAGAGTGTAGAGAGCTTCCCAAGGCAAGACAGCAATGATGACCAATTCCTA 2220  
2221 TTTTCAACATATTTCTTAATCTGGAGCTTCTCAGATATGTTTAAAGTGAAGATGTT 2280  
2221 TTTTCAACATATTTCTTAATCTGGAGCTTCTCAGATATGTTTAAAGTGAAGATGTT 2280  
2281 GTGACCTGTGTGATGAGACCAATTTGTGACCTGGCCATCAGCATCTGATTTCTTA 2340  
2281 GTGACCTGTGTGATGAGACCAATTTGTGACCTGGCCATCAGCATCTGATTTCTTA 2340  
2341 AATACCTTTTCAATGAGAGAGAGAGCTATCCATGAGAGAGATTTGATATGATGCTT 2400  
2341 AATACCTTTTCAATGAGAGAGAGAGCTATCCATGAGAGAGATTTGATATGATGCTT 2400  
2401 ACAGTGAAGAACTGGTTTCACTGGAGCTTTACAGCAGAAATGTTTCTGAAAATTAAT 2460  
2401 ACAGTGAAGAACTGGTTTCACTGGAGCTTTACAGCAGAAATGTTTCTGAAAATTAAT 2460  
2461 GCCATGATCCTTACTATATTTTCCAGAGAGGCTGGAATATCTTTGACGGTTTATGCTG 2520  
2461 GCCATGATCCTTACTATATTTTCCAGAGAGGCTGGAATATCTTTGACGGTTTATGCTG 2520  
2521 ACAGTGAAGAACTGGTTTCACTGGAGCTTTACAGCAGAAATGTTTCTGAAAATTAAT 2580  
2521 ACAGTGAAGAACTGGTTTCACTGGAGCTTTACAGCAGAAATGTTTCTGAAAATTAAT 2580  
2581 TTTGATGCTGTGAGAGTTTCAAGTTGGCAAAATCTTGGCAAGCTTAAATATGCTATA 2640  
2581 TTTGATGCTGTGAGAGTTTCAAGTTGGCAAAATCTTGGCAAGCTTAAATATGCTATA 2640

2581 TTTGATGCTGTGAGAGTTTCAAGTTGGCAAAATCTTGGCAAGCTTAAATATGCTATA 2640  
2641 AAGATCATGGGCAATTCCTGGGGGCGCTGGGAAATTAACCTGCTGGCCATCATC 2700  
2641 AAGATCATGGGCAATTCCTGGGGGCGCTGGGAAATTAACCTGCTGGCCATCATC 2700  
2701 GTCTCATATTTTCCCGTGTGGGATGACAGCTCTTTGGTAAAGCTTCAAAAGATGCTC 2760  
2701 GTCTCATATTTTCCCGTGTGGGATGACAGCTCTTTGGTAAAGCTTCAAAAGATGCTC 2760  
2761 TGCAGATGCGCAGTATGATCTCACTCCAGCTGGCAGCATGAAATGCTTCTCCACTCC 2820  
2761 TGCAGATGCGCAGTATGATCTCACTCCAGCTGGCAGCATGAAATGCTTCTCCACTCC 2820  
2821 TTTCTGATGTTGTGTTCCGCGCTGTGGGAGATGATTAAGACCATGTTGGAGTATG 2880  
2821 TTTCTGATGTTGTGTTCCGCGCTGTGGGAGATGATTAAGACCATGTTGGAGTATG 2880  
2881 GAGGTTGCTGTGAGAGCATGCTCTTACTGTCTTCAATGATGATGATGATGAAAC 2940  
2881 GAGGTTGCTGTGAGAGCATGCTCTTACTGTCTTCAATGATGATGATGATGAAAC 2940  
2941 CTAGTGTCTGTGAATCTCTTCTGCGCTTCTTGTGAGCTCATTTAGTGAAGAACCTT 3000  
2941 CTAGTGTCTGTGAATCTCTTCTGCGCTTCTTGTGAGCTCATTTAGTGAAGAACCTT 3000  
3001 GCAGCCAGTATGATGATTAATGAATGAATTAATCTCCAAATGCTGTGATGATGATC 3060  
3001 GCAGCCAGTATGATGATTAATGAATGAATTAATCTCCAAATGCTGTGATGATGATC 3060  
3061 AAGGATGATCTATGAGAAAGAAATTAATGAATTTTCAAGCTGCTTCAATAGG 3120  
3061 AAGGATGATCTATGAGAAAGAAATTAATGAATTTTCAAGCTGCTTCAATAGG 3120  
3121 AAGCAAAAGATTTAGATGAATTAACCACTGATGATGATTAACCAAGAAAGACAGT 3180  
3121 AAGCAAAAGATTTAGATGAATTAACCACTGATGATGATTAACCAAGAAAGACAGT 3180  
3181 TGTATGCTCAATCATATCAGAGAAATTTGGAAAGATCTTCAATGATGATGATGAT 3240  
3181 TGTATGCTCAATCATATCAGAGAAATTTGGAAAGATCTTCAATGATGATGATGAT 3240  
3241 GGAAGTCAAGTGTATGAGAGAGTGGCAGAGTGTGAAATTAATGATGATGATGAT 3300  
3241 GGAAGTCAAGTGTATGAGAGAGTGGCAGAGTGTGAAATTAATGATGATGATGAT 3300  
3301 GATTACATGCTATTAATTAACCAAGCTTACTGTGATGATGATGATGATGATGATGAT 3360  
3301 GATTACATGCTATTAATTAACCAAGCTTACTGTGATGATGATGATGATGATGATGAT 3360  
3361 GAATCTGATTTGAAATTTAAACAGGAGAGCTTATGATGATGATGATGATGATGAT 3420  
3361 GAATCTGATTTGAAATTTAAACAGGAGAGCTTATGATGATGATGATGATGATGAT 3420  
3421 AGCAAGAGAGAGTGAATGAAGAGAGAGTGAATGAAGAGAGAGAGAGAGAGAGAGAG 3480  
3421 AGCAAGAGAGAGTGAATGAAGAGAGAGTGAATGAAGAGAGAGAGAGAGAGAGAGAG 3480  
3481 GCAAGTGTAG 3540  
3481 GCAAGTGTAG 3540  
3541 TTTCACTGAG 3600  
3541 TTTCACTGAG 3600  
3601 GGAAG 3660  
3601 GGAAG 3660  
3661 GAGAGCTTCAATGTTTCAATGATTTCTTCAATGATTTCTTCAATGATTTCTTCAAT 3720  
3661 GAGAGCTTCAATGTTTCAATGATTTCTTCAATGATTTCTTCAATGATTTCTTCAAT 3720  
3720 GAGAGCTTCAATGTTTCAATGATTTCTTCAATGATTTCTTCAATGATTTCTTCAAT 3780

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|----|------|---|------|
| Oy | 3721 | TATATTGATCAGGAAAGACGATTAAAGACATGTTGGAAATAGCTGACAAAGTTTCACT    | 3780 |
| Db | 3721 | TATATTGATCAGGAAAGACGATTAAAGACATGTTGGAAATAGCTGACAAAGTTTCACT    | 3780 |
| Oy | 3781 | TACATTTTCATCTCGAAATAGCTTCCTAAATAGGGGCGCATATAGGCTATCAACAATATTC | 3840 |
| Db | 3781 | TACATTTTCATCTCGAAATAGCTTCCTAAATAGGGGCGCATATAGGCTATCAACAATATTC | 3840 |
| Oy | 3841 | ACCAATGCCGTGTGGCTGACCTTAAATGTTGATGTTTCATTTGGTCAAGTTTAA        | 3900 |
| Db | 3841 | ACCAATGCCGTGTGGCTGACCTTAAATGTTGATGTTTCATTTGGTCAAGTTTAA        | 3900 |
| Oy | 3901 | GCAATGCCCTGGGTACTCTAGAACTTGAAGCATCAAAATCTCTAGACACTAAGACT      | 3960 |
| Db | 3901 | GCAATGCCCTGGGTACTCTAGAACTTGAAGCATCAAAATCTCTAGACACTAAGACT      | 3960 |
| Oy | 3961 | CTAGACCTCTAAGAGCCTATCTCATATTTGAAGGATAGGGTGGTTGTAAGCCCT        | 4020 |
| Db | 3961 | CTAGACCTCTAAGAGCCTATCTCATATTTGAAGGATAGGGTGGTTGTAAGCCCT        | 4020 |
| Oy | 4021 | TTAGGCAATTCATCCATCATGAAATGTGCTCTGCTTATATCTGGCTAAT             | 4080 |
| Db | 4021 | TTAGGCAATTCATCCATCATGAAATGTGCTCTGCTTATATCTGGCTAAT             | 4080 |
| Oy | 4081 | TTGACGCAATGGGCGTAATTTGTTGGCGCAATCTACCATGTATTAACACCA           | 4140 |
| Db | 4081 | TTGACGCAATGGGCGTAATTTGTTGGCGCAATCTACCATGTATTAACACCA           | 4140 |
| Oy | 4141 | ACTGGTACAGGTTTGACATCGAAGACGTAAATATCATATCATGATGGCTTAAACTATA    | 4200 |
| Db | 4141 | ACTGGTACAGGTTTGACATCGAAGACGTAAATATCATATCATGATGGCTTAAACTATA    | 4200 |
| Oy | 4201 | GAAGAATATGAGCTGCTGATGGAATAATGCAAAAGTAAATTTGATATATAGATAT       | 4260 |
| Db | 4201 | GAAGAATATGAGCTGCTGATGGAATAATGCAAAAGTAAATTTGATATATAGATAT       | 4260 |
| Oy | 4261 | GGGATCTCTCTTGGCTTCAAGTTGGCACATTCAAAGATGATGATATATGATCA         | 4320 |
| Db | 4261 | GGGATCTCTCTTGGCTTCAAGTTGGCACATTCAAAGATGATGATATATGATCA         | 4320 |
| Oy | 4321 | GCAATGATTCAGAAATGTGGAATCTCAGCCTAAGTATGAAGAAATCTGTACATGAT      | 4380 |
| Db | 4321 | GCAATGATTCAGAAATGTGGAATCTCAGCCTAAGTATGAAGAAATCTGTACATGAT      | 4380 |
| Oy | 4381 | CTTACCTTGTATTTTTCATCATCTTGGGCTCTTACCTTGACCTGTAATATGGT         | 4440 |
| Db | 4381 | CTTACCTTGTATTTTTCATCATCTTGGGCTCTTACCTTGACCTGTAATATGGT         | 4440 |
| Oy | 4441 | GTCATCATAGATAATTTCAACACGACGAAAAAGAAATTTGAGGCTCAAGACATCTTATG   | 4500 |
| Db | 4441 | GTCATCATAGATAATTTCAACACGACGAAAAAGAAATTTGAGGCTCAAGACATCTTATG   | 4500 |
| Oy | 4501 | ACAGAGAAGAGAAATCTATATGCAATGAAAAATTTAGATGCAAAAAAACCGCA         | 4560 |
| Db | 4501 | ACAGAGAAGAGAAATCTATATGCAATGAAAAATTTAGATGCAAAAAAACCGCA         | 4560 |
| Oy | 4561 | AAGCCTATACCTGCAGACGAAACAAATTTCAAGAAATGCTCTTGACTTGTAACAGA      | 4620 |
| Db | 4561 | AAGCCTATACCTGCAGACGAAACAAATTTCAAGAAATGCTCTTGACTTGTAACAGA      | 4620 |
| Oy | 4621 | CAAGTTTTCACATTAAGCAATCATGATCTGCATCTTAAATGGTCAACATATGGTG       | 4680 |
| Db | 4621 | CAAGTTTTCACATTAAGCAATCATGATCTGCATCTTAAATGGTCAACATATGGTG       | 4680 |
| Oy | 4681 | GAAACAGTACAGAGTGAATATGTACATATTTGTCACGATCAATCTGGTGTG           | 4740 |
| Db | 4681 | GAAACAGTACAGAGTGAATATGTACATATTTGTCACGATCAATCTGGTGTG           | 4740 |
| Oy | 4741 | ATTGCTGATTTTACTGAGAGGTGTACTGAAATCTCATCTCTACGCCATTTATATTT      | 4800 |
| Db | 4741 | ATTGCTGATTTTACTGAGAGGTGTACTGAAATCTCATCTCTACGCCATTTATATTT      | 4800 |

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|----|------|---|------|
| QY | 4801 | ACCAATGGATGGAAATATTTTGGATTTGGGGTGTGATCTCTCCATGTAGATGTTT       | 4860 |
| Db | 4801 | ACCAATGGATGGAAATATTTTGGATTTGGGGTGTGATCTCTCCATGTAGATGTTT       | 4860 |
| QY | 4861 | CTTGCGAGCGATGATGAGAAAGATATTCGTCGCCACCTGTGCGAGTATCCGCTCT       | 4920 |
| Db | 4861 | CTTGCGAGCGATGATGAGAAAGATATTCGTCGCCACCTGTGCGAGTATCCGCTCT       | 4920 |
| QY | 4921 | GCTAGGATTTGGCCGAATCTACGTCGTGATCCAAAGAGCAAAAGGGATCCGACGCTGC    | 4980 |
| Db | 4921 | GCTAGGATTTGGCCGAATCTACGTCGTGATCCAAAGAGCAAAAGGGATCCGACGCTGC    | 4980 |
| QY | 4981 | TTTGCTTTGGATGATGATCCCTTCTCGGTGTTTAACATGCGCTCTACTCTTCTAGTC     | 5040 |
| Db | 4981 | TTTGCTTTGGATGATGATCCCTTCTCGGTGTTTAACATGCGCTCTACTCTTCTAGTC     | 5040 |
| QY | 5041 | ATGTTCACTACGGCAATCTTTGGGATGTCCAACTTTGCTATGTTAAAGGAAATTTGGG    | 5100 |
| Db | 5041 | ATGTTCACTACGGCAATCTTTGGGATGTCCAACTTTGCTATGTTAAAGGAAATTTGGG    | 5100 |
| QY | 5101 | ATCGATGACATGTTCAACTTTTGAGACCTTTGGGCAAGCATGATCGCTATTTCCAAAT    | 5160 |
| Db | 5101 | ATCGATGACATGTTCAACTTTTGAGACCTTTGGGCAAGCATGATGCTATTTCCAAAT     | 5160 |
| QY | 5161 | ACAACCTTCTGCTGGCTGGGATGATGTCAGACCACTTCTCAAGATGAAGCACCCGAC     | 5220 |
| Db | 5161 | ACAACCTTCTGCTGGCTGGGATGATGTCAGACCACTTCTCAAGATGAAGCACCCGAC     | 5220 |
| QY | 5221 | TGTGACCTTAATTAAGTTTAACCTCGGAAGCTCAGTTAAAGGAGACTGTGGAAACCATCT  | 5280 |
| Db | 5221 | TGTGACCTTAATTAAGTTTAACCTCGGAAGCTCAGTTAAAGGAGACTGTGGAAACCATCT  | 5280 |
| QY | 5281 | GTGTGAAATTTTCTTTTGTGACGTACATCATATATCTCTCGTGTGTGTGAAACAG       | 5340 |
| Db | 5281 | GTGTGAAATTTTCTTTTGTGACGTACATCATATATCTCTCGTGTGTGTGAAACAG       | 5340 |
| QY | 5341 | TACATCGCGGTCATCTGAGAACTTCAAGTGTGCTACTAGAAAGAAATGACAGGCTCTG    | 5400 |
| Db | 5341 | TACATCGCGGTCATCTGAGAACTTCAAGTGTGCTACTAGAAAGAAATGACAGGCTCTG    | 5400 |
| QY | 5401 | ACTGAGATGACTTTGAGATGTCTATGAGGTTTGGGAGAAAGTTTGTATCCGATGCAACT   | 5460 |
| Db | 5401 | ACTGAGATGACTTTGAGATGTCTATGAGGTTTGGGAGAAAGTTTGTATCCGATGCAACT   | 5460 |
| QY | 5461 | CAGTTCAGGAAATTTGAAAAATATCATGATTTGGACGTCGCGCTGGAACCGCTCTCAT    | 5520 |
| Db | 5461 | CAGTTCAGGAAATTTGAAAAATATCATGATTTGGACGTCGCGCTGGAACCGCTCTCAT    | 5520 |
| QY | 5521 | CTTGCCACAACCAAAACAACTCCAGCTCATTTGCCATGATTTGCCATGATGTGATGTAC   | 5580 |
| Db | 5521 | CTTGCCACAACCAAAACAACTCCAGCTCATTTGCCATGATTTGCCATGATGTGATGTAC   | 5580 |
| QY | 5581 | CGGATCCACTGTTGATATCTTATTTGCTTTTACAACGCGGGTCTTAGAGAGATGTGA     | 5640 |
| Db | 5581 | CGGATCCACTGTTGATATCTTATTTGCTTTTACAACGCGGGTCTTAGAGAGATGTGA     | 5640 |
| QY | 5641 | GAGATGATGTGCTACGAAATACAGATGGAAGACGATTCATGGCTTCCAAATCCCTTCAG   | 5700 |
| Db | 5641 | GAGATGATGTGCTCTACGAAATACAGATGGAAGACGATTCATGGCTTCCAAATCCCTTCAG | 5700 |
| QY | 5701 | GTCCTCATACGCAATCACTACTATTAAACGAAAAACAAGAGAAATATCTGCTGTC       | 5760 |
| Db | 5701 | GTCCTCATACGCAATCACTACTATTAAACGAAAAACAAGAGAAATATCTGCTGTC       | 5760 |
| QY | 5761 | ATTATTCAGCGTCTTACAGACGCGCACTTTTAAACGAACTGTAAACAGCTTCCTT       | 5820 |
| Db | 5761 | ATTATTCAGCGTCTTACAGACGCGCACTTTTAAACGAACTGTAAACAGCTTCCTT       | 5820 |
| QY | 5821 | ACGTACATTAATAACAAATCAAAAGGTGGGGCTTAATCTTATTAATAAGAAACATGATA   | 5880 |
| Db | 5821 | ACGTACATTAATAACAAATCAAAAGGTGGGGCTTAATCTTATTAATAAGAAACATGATA   | 5880 |
| QY | 5881 | ATTGACAAATTAATGAAAACTATTTACAGAAAAAACTGATCTACACATGCTCCACTGCA   | 5940 |

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Db 5881 ATGACAGATATATGAAACCTATATACGAAAAACATGATCGACCATGTCACATGCA 5940
QY 5941 GCTTGTCCACCTTCCTATGACCGGGTGACAAACCATTTGTGAAAAACATGACAGAA 6000
Db 5941 GCTTGTCCACCTTCCTATGACCGGGTGACAAACCATTTGTGAAAAACATGACAGAA 6000
QY 6001 GCGCAAGATGAAAAAGCCAAAGGAATAA 6030
Db 6001 GCGCAAGATGAAAAAGCCAAAGGAATAA 6030

RESULT 2
AAD32845
ID AAD32845 standard; cDNA; 5922 BP.
XX AAD32845;
XX 01-JUL-2002 (first entry)
DE Human ion channel cDNA #7.
XX Human; novel human protein; NHP: voltage-gated sodium channel;
XX gene therapy; bio reactor; mental disorder; biological disorder;
XX gene; medical disorder; ss.
OS Homo sapiens.
XX Key Location/Qualifiers
XX CDS 1..5922
XX /tag- a
XX /product- "Human ion channel protein #7"
XX /transl_except- (pos:2874..2876, aa:Xaa)
XX /transl_except- (pos:3199..3201, aa:Xaa)
XX /note- "Xaa = any amino acid"
XX PN WO200214498-A2.
XX PD 21-FEB-2002.
XX PF 15-AUG-2001; 2001WO-US25650.
XX PR 16-AUG-2000; 2000US-225989P.
XX PA (LEXI-) LEXICON GENETICS INC.
XX PI Turner CA, Mathur B, Mathur D;
XX MPI: 2002-280757/32.
XX P-PSDB; AAE20516.
XX PT Novel polynucleotides encoding human sodium channel proteins,
XX particularly voltage-gated sodium channel proteins useful for drug
XX screening, diagnosis and in gene therapy of biological disorders
XX PS Claim 1; Page 62-64; 83pp; English.
XX
XX The present sequence is a cDNA encoding novel human protein (NHP), ion
XX channel protein. NHP share structural similarity with mammalian sodium
XX channel proteins particularly voltage-gated sodium channel proteins.
XX NHP oligonucleotides are useful as hybridisation probes for screening
XX libraries and assessing gene expression patterns. Sequences derived
XX from regions adjacent to the intron/exon boundaries of NHP gene can be
XX used to design primers for use in amplification assays to detect
XX mutations within the exons, splice sites, introns that can be used in
XX diagnostics and pharmacogenomics. NHP nucleotide sequences are useful
XX for drug screening effective in the treatment of symptomatic or
XX phenotypic manifestations of perturbing the normal function of NHP in
XX the body, and nucleotide constructs encoding NHP products are useful to
XX genetically engineer host cells to express NHP products in vivo. These
XX genetically engineered cells function as bio reactors in the body
XX delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion
XX protein to the body. Nucleotide construct encoding NHP products are

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CC also useful in gene therapy for modulating NHP expression and to
CC produce genetically engineered host cells to express NHP products in
CC vivo. NHP nucleotide sequences may also be used as part of ribozyme
CC and/or triple helix sequences that are useful for NHP gene regulation.
CC The NHP polypeptides are useful for generating antibodies, as
CC reagents in diagnostic assays, for identifying other cellular gene
CC products related to NHP and as reagents in assays for screening for
CC compounds that are useful in the treatment of mental, biological or
CC medical disorders and diseases.
XX
XX Sequence 5922 BP; 1746 A; 1166 C; 1320 G; 1687 T; 3 other;
SQ
Query Match 98.1%; Score 5917; DB 24; Length 5922;
Best local similarity 100.0%; Pred. No. 0;
Matches 5917; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGCAAAACAGTCTTGTACCAACGACGTGACAGCTTCACATCTTCACACAGAA 60
Db 1 ATGAGCAAAACAGTCTTGTACCAACGACGTGACAGCTTCACATCTTCACACAGAA 60
QY 61 TCTCTGGGGCTATGAAAGCCATTCAGAAAGAAAGGCAAAAGATCCCAACACAGAC 120
Db 61 TCTCTGGGGCTATGAAAGCCATTCAGAAAGAAAGGCAAAAGATCCCAACACAGAC 120
QY 121 AAAAAAGATGACGAGAAATGGGCCAAAGCCAAATGTGACTTGAAGCTGAAAGAAC 180
Db 121 AAAAAAGATGACGAGAAATGGGCCAAAGCCAAATGTGACTTGAAGCTGAAAGAAC 180
QY 181 CTTCATTTATTTATGAGACATTCCTCCAGAGATGGTGTGACAGCCCTGAGAGACTG 240
Db 181 CTTCATTTATTTATGAGACATTCCTCCAGAGATGGTGTGACAGCCCTGAGAGACTG 240
QY 241 GACCCCTACTATATCATTAAGAAACCTTTATAGTATGAAATTAAGGAAGCCATCTTC 300
Db 241 GACCCCTACTATATCATTAAGAAACCTTTATAGTATGAAATTAAGGAAGCCATCTTC 300
QY 301 CGGTTAGTGCACACCTGCTGCCCTGTACATTTTAACTCCCTCAATCCCTTAGAATAA 360
Db 301 CGGTTAGTGCACACCTGCTGCCCTGTACATTTTAACTCCCTCAATCCCTTAGAATAA 360
QY 361 GCTATTAAGATTTGTGATCATTCATTTATGACAGATGCTAATTTATGTCACATTTTGA 420
Db 361 GCTATTAAGATTTGTGATCATTCATTTATGACAGATGCTAATTTATGTCACATTTTGA 420
QY 421 AACGTGTGTTATGAGAAAGAGTAACCCCTCTATGAGCAAAAGATGTAATACACC 480
Db 421 AACGTGTGTTATGAGAAAGAGTAACCCCTCTATGAGCAAAAGATGTAATACACC 480
QY 481 TTCACAGAAATATATCTTTTGAATCACTTATAAATATGCAAGGGGATTCGTGTTA 540
Db 481 TTCACAGAAATATATCTTTTGAATCACTTATAAATATGCAAGGGGATTCGTGTTA 540
QY 541 GAAGATTTTACTTCTCTGGGATCATGAACTGCTCGATTTCACTGTCATTAATTT 600
Db 541 GAAGATTTTACTTCTCTGGGATCATGAACTGCTCGATTTCACTGTCATTAATTT 600
QY 601 GCGTAGCTCACAGAGTTGTGAGACCTGGCAATGTCTCGGATGAGAAACATTAGAGTT 660
Db 601 GCGTAGCTCACAGAGTTGTGAGACCTGGCAATGTCTCGGATGAGAAACATTAGAGTT 660
QY 661 CTCGAGCATTTGAAGAGATTTGAGTTCAGTCCAGAGCCGTAACATTTGGAGCCCTG 720
Db 661 CTCGAGCATTTGAAGAGATTTGAGTTCAGTCCAGAGCCGTAACATTTGGAGCCCTG 720
QY 721 ATCCAGTCTGTGAAGAGCTCTCAGATGATATGATCTGACTGTCTGTCTAGAGGTA 780
Db 721 ATCCAGTCTGTGAAGAGCTCTCAGATGATATGATCTGACTGTCTGTCTAGAGGTA 780
QY 781 TTTCCTTAATTTGGGCTGACCTTTATGAGGCAACCTGAGAGTAATATATATATG 840
Db 781 TTTCCTTAATTTGGGCTGACCTTTATGAGGCAACCTGAGAGTAATATATATATG 840
QY 841 CCTCCACCAATGCTTCTCTGGAGGAGATAGTATAGAAAAAGATATATATATATAT 900

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Db 841 CCTCCACCAATGCTTCTTGAGAGACATATAGAAAAGAAATATCTGATATAT 900  
 Oy 901 AATGATACCTTAAATATGAATGCTCTTGAGTTGATGAGAGTCAATATTCACAT 960  
 Db 901 AATGATACCTTAAATATGAATGCTCTTGAGTTGATGAGAGTCAATATTCACAT 960  
 Oy 961 TCAGATATCATATATATCTTGAGAGGTTTTTATGACATATATGGAATAGCTCT 1020  
 Db 961 TCAGATATCATATATATCTTGAGAGGTTTTTATGACATATATGGAATAGCTCT 1020  
 Oy 1021 GATGACGCGCAATGCTCCAGAGGATATATGCTGGAAGCTGATGAATCCCATATAT 1080  
 Db 1021 GATGACGCGCAATGCTCCAGAGGATATATGCTGGAAGCTGATGAATCCCATATAT 1080  
 Oy 1081 GCGTACACACCTTATGATACCTGATGAGGCTTTTGTCTGCTGTTGATGATGACT 1140  
 Db 1081 GCGTACACACCTTATGATACCTGATGAGGCTTTTGTCTGCTGTTGATGATGACT 1140  
 Oy 1141 CAGGACCTTCTGGGAAATCTTTATCATCTGACATTCGCTGCTGGGAAACGTACATG 1200  
 Db 1141 CAGGACCTTCTGGGAAATCTTTATCATCTGACATTCGCTGCTGGGAAACGTACATG 1200  
 Oy 1201 AATATTTTGTGCTGCTATTTCTTGAGGCTCATCTACATATATATATGATCTGCT 1260  
 Db 1201 AATATTTTGTGCTGCTATTTCTTGAGGCTCATCTACATATATATATGATCTGCT 1260  
 Oy 1261 GTGGGGGCGCATGGCTTACAGAGAAACAGATGAGGCGCCTTGAGAGAGAGAGAGAA 1320  
 Db 1261 GTGGGGGCGCATGGCTTACAGAGAAACAGATGAGGCGCCTTGAGAGAGAGAGAGAA 1320  
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 Db 1321 GAGGCGGAAATTTAGACAGATATGAAACAGCTTAAAGAACAGAGAGAGAGAGAG 1380  
 Oy 1381 GCAGCAGCGCACTGCTCAGAACATTCAGAGAGCCGAGCTGAGAGAGAGAGAGAG 1440  
 Db 1381 GCAGCAGCGCACTGCTCAGAACATTCAGAGAGCCGAGCTGAGAGAGAGAGAGAG 1440  
 Oy 1441 GACAGCTATCTGAAGCTTCTGAGTTGAGTTGCAAGAGTGTGCAAGAGAGAGAGAG 1500  
 Db 1441 GACAGCTATCTGAAGCTTCTGAGTTGAGTTGCAAGAGTGTGCAAGAGAGAGAGAG 1500  
 Oy 1501 AGGAG 1560  
 Db 1501 AGGAG 1560  
 Oy 1561 CAAAATCTGATCTGAG 1620  
 Db 1561 CAAAATCTGATCTGAG 1620  
 Oy 1621 AACGATGATGATGAG 1680  
 Db 1621 AACGATGATGATGAG 1680  
 Oy 1681 GCGTCTCTATTTTACAG 1740  
 Db 1681 GCGTCTCTATTTTACAG 1740  
 Oy 1741 GCAAAGAGATGAT 1800  
 Db 1741 GCAAAGAGATGAT 1800  
 Oy 1801 AAG 1860  
 Db 1801 AAG 1860  
 Oy 1861 AACGAG 1920  
 Db 1861 AACGAG 1920  
 Oy 1921 ATGACAG 1980  
 Db 1921 ATGACAG 1980

Db 1921 ATGACAG 1980  
 Oy 1981 ACATGCGCTGTTGAG 2040  
 Db 1981 ACATGCGCTGTTGAG 2040  
 Oy 2041 AATGAG 2100  
 Db 2041 AATGAG 2100  
 Oy 2101 ATGAGCTTCTAG 2160  
 Db 2101 ATGAGCTTCTAG 2160  
 Oy 2161 ACAATATGATGAT 2220  
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 Oy 2221 TTTTCCACATATCTTATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 2280  
 Db 2221 TTTTCCACATATCTTATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 2280  
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 Db 2281 GTCAACCTGCTGATGAG 2340  
 Oy 2341 AATATCTTCTATGAG 2400  
 Db 2341 AATATCTTCTATGAG 2400  
 Oy 2401 ACAGTAG 2460  
 Db 2401 ACAGTAG 2460  
 Oy 2461 GCGATGATCTTATCTATATATTTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2520  
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 Db 2521 ACAGTAG 2580  
 Oy 2581 TTTGATGATGAT 2640  
 Db 2581 TTTGATGATGAT 2640  
 Oy 2641 AAGATCATGAT 2700  
 Db 2641 AAGATCATGAT 2700  
 Oy 2701 GCTTCTATTTTGGCGAG 2760  
 Db 2701 GCTTCTATTTTGGCGAG 2760  
 Oy 2761 TGCAG 2820  
 Db 2761 TGCAG 2820  
 Oy 2821 TTTCTGATGATGAG 2880  
 Db 2821 TTTCTGATGATGAG 2880  
 Oy 2881 GAGGTCGTCGAT 2940  
 Db 2881 GAGGTCGTCGAT 2940  
 Oy 2941 CTAGTGTCTGAT 3000  
 Db 2941 CTAGTGTCTGAT 3000  
 Oy 3001 GCAGCAG 3060  
 Db 3001 GCAGCAG 3060

QY 3061 AAAGAGTACCTATGTAAGAAAGAAATATATGATTTATTCACAGCTTCATTAGG 3120  
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DB 3121 AAACAAAGATTTAGATGAATTAACCACTTGATGATCTAACAACAGAAAGACAGT 3180  
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DB 3181 TGTATGTCACATACACACAGAAATTTGGAAAGATCTTGACTATCTTAAGATGTAAT 3240  
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DB 3301 GATTACATGATGATGATGAAAGCTGGACAGCTGTGAAATTAATATATGATGAAGT 3360  
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DB 3361 GAATCTGACTTTGAAATTTTAAACACGAGACCTTACTAGTGAATCGGATCTGGAAGA 3420  
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DB 3421 AGCAAAAGAAACCTGAATGAAGAGAGCTACCTACAGAAAGCTGAGACCTGAGACG 3480  
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DB 3481 GCACCTGATGAGAAACACGCTGATGAGACCTGAGAAACCTGAGAAACCTGAGAAAC 3540  
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QY 3601 GGAAGAAACATGATGAGAAACCTGAGAAAGCTGAGAAACCTGAGAAACCTGAGAA 3660  
DB 3601 GGAAGAAACATGATGAGAAACCTGAGAAAGCTGAGAAACCTGAGAAACCTGAGAA 3660  
QY 3661 GAGACCTGATGAGAAACCTGAGAAAGCTGAGAAACCTGAGAAACCTGAGAAACCT 3720  
DB 3661 GAGACCTGATGAGAAACCTGAGAAAGCTGAGAAACCTGAGAAACCTGAGAAACCT 3720  
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DB 3721 TATATGATGAGAAACCTGAGAAAGCTGAGAAACCTGAGAAACCTGAGAAACCT 3780  
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DB 3781 TACATTTGATGAGAAACCTGAGAAAGCTGAGAAACCTGAGAAACCTGAGAAACCT 3840  
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DB 3841 ACCAATGCTGATGAGAAACCTGAGAAAGCTGAGAAACCTGAGAAACCTGAGAAACCT 3900  
QY 3901 GCAAAATGCTGATGAGAAACCTGAGAAAGCTGAGAAACCTGAGAAACCTGAGAAACCT 3960  
DB 3901 GCAAAATGCTGATGAGAAACCTGAGAAAGCTGAGAAACCTGAGAAACCTGAGAAACCT 3960  
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QY 4081 TTACAGCAATTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 4140  
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QY 4201 GAAAGAAATGACAGCTGATGAGAAAGCTGAGAAAGCTGAGAAAGCTGAGAAAGCT 4260  
DB 4201 GAAAGAAATGACAGCTGATGAGAAAGCTGAGAAAGCTGAGAAAGCTGAGAAAGCT 4260  
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DB 4261 GGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4320  
QY 4321 GCAGTTGATTCAGAAATGAGAAAGCTGAGAAAGCTGAGAAAGCTGAGAAAGCT 4380  
DB 4321 GCAGTTGATTCAGAAATGAGAAAGCTGAGAAAGCTGAGAAAGCTGAGAAAGCT 4380  
QY 4381 CTTTACTTTGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 4440  
DB 4381 CTTTACTTTGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 4440  
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DB 4441 GTCATCATGATTAATTTTACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4500  
QY 4501 ACAGAAAGACAG 4560  
DB 4501 ACAGAAAGACAG 4560  
QY 4561 AAGCTATACCTGACAG 4620  
DB 4561 AAGCTATACCTGACAG 4620  
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DB 4621 CAAGTTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4680  
QY 4681 GAAACAGATGACAG 4740  
DB 4681 GAAACAGATGACAG 4740  
QY 4741 ATTGTCATTTACTGAG 4800  
DB 4741 ATTGTCATTTACTGAG 4800  
QY 4801 ACCATGATGAG 4860  
DB 4801 ACCATGATGAG 4860  
QY 4861 CTTGCGACCTGATGAG 4920  
DB 4861 CTTGCGACCTGATGAG 4920  
QY 4921 GCTAGATGAG 4980  
DB 4921 GCTAGATGAG 4980  
QY 4981 TTGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5040  
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DB 5041 ATGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5100  
QY 5101 ATGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5160  
DB 5101 ATGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5160  
QY 5161 ACAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5220  
DB 5161 ACAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5220  
QY 5221 TGTGACCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 5280



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Db 5221 TGTGACCTTAATAAGTAACCTGGAAGCTGATTAAGGAGAGACTGGAGAACCATCTP 5280
OY 5281 GTTGAATTTCTTTTCTTGTCACTTACATCATATCTCTCTGTTGGTGAACATG 5340
Db 5281 GTTGAATTTCTTTTCTTGTCACTTACATCATATCTCTCTGTTGGTGAACATG 5340
OY 5341 TACATGCGGTCACTCTGAGAACTTCACTGTTGCTACTGAAGAAGTGAAGCTCTG 5400
Db 5341 TACATGCGGTCACTCTGAGAACTTCACTGTTGCTACTGAAGAAGTGAAGCTCTG 5400
OY 5401 AGTGAAGATGACTTGTGAGATGTTCTATGAGGTTGGAGAAAGTTGATCCGATCACT 5460
Db 5401 AGTGAAGATGACTTGTGAGATGTTCTATGAGGTTGGAGAAAGTTGATCCGATCACT 5460
OY 5461 CAGTTATGGAATTTGAAAAATTTATCTCACTTGTGAGCTGCGCTTGAACCGCTTCAAT 5520
Db 5461 CAGTTATGGAATTTGAAAAATTTATCTCACTTGTGAGCTGCGCTTGAACCGCTTCAAT 5520
OY 5521 CTGCGCAACCAACAACTCCAGCTCATTTGCCATGATTTGCCATGCTGATGCTGAC 5580
Db 5521 CTGCGCAACCAACAACTCCAGCTCATTTGCCATGATTTGCCATGCTGATGCTGAC 5580
OY 5581 CGGATCCACTGCTGCTGATATCTTATTTGCTTTACAAAGCGGCTTCTAGAGAGATGGA 5640
Db 5581 CGGATCCACTGCTGCTGATATCTTATTTGCTTTACAAAGCGGCTTCTAGAGAGATGGA 5640
OY 5641 GAGATGATGCTCTACGAATPACAGATGAGAAGCGATTCATGCTTCCAACTCTTCCAA 5700
Db 5641 GAGATGATGCTCTACGAATPACAGATGAGAAGCGATTCATGCTTCCAACTCTTCCAA 5700
OY 5701 GTCCTCTACAGCAATCACTCTACTTTAAAGCAAAACAAAGAGATGCTGTC 5760
Db 5701 GTCCTCTACAGCAATCACTCTACTTTAAAGCAAAACAAAGAGATGCTGTC 5760
OY 5761 ATTATTCAGCTGCTTACAGAGCCGACCTTTTAAAGCACTTAAACAGCTTCTCTT 5820
Db 5761 ATTATTCAGCTGCTTACAGAGCCGACCTTTTAAAGCACTTAAACAGCTTCTCTT 5820
OY 5821 ACCTACATTAATAAATAAATAAAGTGGGCTTAATCTTCTTAAAGAGACATGATA 5880
Db 5821 ACCTACATTAATAAATAAATAAAGTGGGCTTAATCTTCTTAAAGAGACATGATA 5880
OY 5881 ATTGACAGATTAATAAATAAATAAAGTGGGCTTAAAGAGACATGATA 5917
Db 5881 ATTGACAGATTAATAAATAAATAAAGTGGGCTTAAAGAGACATGATA 5917

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XX PI Rouleau GA, LaFreniere RG, Rochefort D, Cossette P, Ragsdale D;
XX DR WPI: 2001-355945/37.
XX DR P-PSDB: AAB9674.
XX PT Determining a predisposition to epilepsy and/or development of epilepsy
XX PT comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a
XX PT DNA variant, equivalent, or mutation which shows a linkage
XX PT disequilibrium.
XX PS disclosure; Page 90-93; 26pp; English.
XX CC The present invention describes a method (M1) of determining an
XX CC individual's predisposition to epilepsy and/or development of epilepsy,
XX CC as well as predicting the individual's response to medication. The
XX CC method comprises determining the genotype of at least one gene selected
XX CC from SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating
XX CC which shows a linkage disequilibrium. SCN1A, SCN2A and SCN3A are all
XX CC sodium channel genes located on chromosome 2. The idiopathic generalised
XX CC epilepsy (IGE) gene is more specifically localised on chromosome
XX CC 2q23-q31. Compounds identified as modulators of the biological activity
XX CC of SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating
XX CC epilepsy or other neurological disorders. They have anticonvulsant and
XX CC neuroprotective activities. AAB5763 to AAB56164 and AAB9674 to
XX CC AAB9679 represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR
XX CC primers, oligonucleotides and proteins given in the exemplification of
XX CC the present invention.
XX SQ Sequence 8378 BP; 2496 A; 1575 C; 1782 G; 2525 T; 0 other;

Query Match 94.6%; Score 5705; DB 22; Length 8378;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 6025; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

OY 1 ATGAGCAACAGAGTCTGTACACAGAGCTGACAGCTTCACTTCTTACAGAGAA 60
Db 266 ATGAGCAACAGAGTCTGTACACAGAGCTGACAGCTTCACTTCTTACAGAGAA 325
OY 61 TCTCTGCGCTATTTGAAGAGCATTGACAGAGAAAGCAAGAAATCCAAACAGAC 120
Db 326 TCTCTGCGCTATTTGAAGAGCATTGACAGAGAAAGCAAGAAATCCAAACAGAC 385
OY 121 AAAAAATATGACGAGAAATGCGCCAAAGCCAAATGTGATCTGAGAGTGAAGAAAC 180
Db 386 AAAAAATATGACGAGAAATGCGCCAAAGCCAAATGTGATCTGAGAGTGAAGAAAC 445
OY 181 CTTCATTTATTTATGAGAGATTCCTCCAGAGATGCTGACAGAGCCCTGAGAGACTG 240
Db 446 CTTCATTTATTTATGAGAGATTCCTCCAGAGATGCTGACAGAGCCCTGAGAGACTG 505
OY 241 GACCCCTACTATATCAATTAAGAAATCTTTATATGATTAATAAAGGAGCCATCTTC 300
Db 506 GACCCCTACTATATCAATTAAGAAATCTTTATATGATTAATAAAGGAGCCATCTTC 365
OY 301 CGGTTCAGTGCACCCCTGCTGCTGATTTAACTTAACTCCCTTCAATCTCTTGAAGAAATA 360
Db 566 CGGTTCAGTGCACCCCTGCTGCTGATTTAACTTAACTCCCTTCAATCTCTTGAAGAAATA 625
OY 361 GCTATTAAGATTTGATACATTCATTTATGAGAGTGTATTAATGTCACATTTTGAACA 420
Db 626 GCTATTAAGATTTGATACATTCATTTATGAGAGTGTATTAATGTCACATTTTGAACA 685
OY 421 AACTGTGTTTATGACATGATTAACCTCTGATTTGAACAAAGATGTAATACACC 480
Db 686 AACTGTGTTTATGACATGATTAACCTCTGATTTGAACAAAGATGTAATACACC 745
OY 481 TTGACAGAGATTAATTAATTTGAAATCACTTATTAATAAATTTGAGAGGATTTGTTTA 540
Db 746 TTGACAGAGATTAATTAATTTGAAATCACTTATTAATAAATTTGAGAGGATTTGTTTA 805
OY 541 GAAGATTTACTTCTTCCGAGATCCAGAGAGCTGCTGATTTCACTGATTTACATTTT 600

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Dh 806 GAAGATTTTACCTTCCTCGGGATCCATGAACTGGCTCGATGTCATCTGATTTACATTT 865  
Qy 601 GGTACGTCACAGAGTTGTGGACCTGGGCATGTCGGATGAGAAATTCAGACTT 660  
Dh 866 GCGTAGCGACAGAGTTGTGGACCTGGGCATGTCGGATGAGAAATTCAGACTT 925  
Qy 661 CTCGAGCATTAAGAGACGATTTGATCCAGGCTGGAAGAACATTTGGGACCCCTG 720  
Dh 926 CTCGAGCATTAAGAGACGATTTGATCCAGGCTGGAAGAACATTTGGGACCCCTG 985  
Qy 721 ATCCAGCTGTGAAGAACCTCTCAGATGTAATGATCTGACTGTCTGTCTGAGCGTA 780  
Dh 986 ATCCAGCTGTGAAGAACCTCTCAGATGTAATGATCTGACTGTCTGTCTGAGCGTA 1045  
Qy 781 TTTGCTCAATTTGGCTGACCTGTTCATGAGGCAACCTGAGGAATTAATGTAATGAG 840  
Dh 1046 TTTGCTCAATTTGGCTGACCTGTTCATGAGGCAACCTGAGGAATTAATGTAATGAG 1105  
Qy 841 CCTCCACCAATGCTTCCTTGAGAGACATAGTATAGAAAGAAATATACGTGAAATTA 900  
Dh 1106 CCTCCACCAATGCTTCCTTGAGAGACATAGTATAGAAAGAAATATACGTGAAATTA 1165  
Qy 901 AATGATACATTAATTAATGAATGCTCTTGAATTTGACTGGAAGTCAATATTCAGAT 960  
Dh 1166 AATGATACATTAATTAATGAATGCTCTTGAATTTGACTGGAAGTCAATATTCAGAT 1225  
Qy 961 TCAAGATATCAATTTCTCTGAGGCTTTTATGATGCACTATGTAATGAAATGCTCT 1020  
Dh 1226 TCAAGATATCAATTTCTCTGAGGCTTTTATGATGCACTATGTAATGAAATGCTCT 1285  
Qy 1021 GATGAGGCAATGTCAGAGGATATATGCTGGAAGCTGAGAAATCCCAATTA 1080  
Dh 1286 GATGAGGCAATGTCAGAGGATATATGCTGGAAGCTGAGAAATCCCAATTA 1345  
Qy 1081 GGTACACAGCTTTGATACCTCTCAGTTGGCTTTTGTCTGCTGTAATGACT 1140  
Dh 1346 GGTACACAGCTTTGATACCTCTCAGTTGGCTTTTGTCTGCTGTAATGACT 1405  
Qy 1141 CAGAGCTCTGGGAAATCTTATACATGACATACCTGCTGGGAAAGCAATGATG 1200  
Dh 1406 CAGAGCTCTGGGAAATCTTATACATGACATACCTGCTGGGAAAGCAATGATG 1465  
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Dh 1466 AATATTTTGTGTTGCTATTTTCTGGGCTCACTTCACTAATAATTTGATCTGCT 1525  
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Dh 1526 GTGTGGCCATGGCTTACAGAGAACAGATCAGGCCACCTTGGAGAAAGCAGACGAAA 1585  
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Dh 1586 GAGGCGCAATTTCCAGCAATGATGTAACAGCTTAATAAAGCAAGAGAGCACTCAGCAG 1645  
Qy 1381 GCAGCAAGGCAACTGCTCAGAAACATTCAGAGAGCCAGTGCAGAGGAGGCTCTCA 1440  
Dh 1646 GCAGCAAGGCAACTGCTCAGAAACATTCAGAGAGCCAGTGCAGAGGAGGCTCTCA 1705  
Qy 1441 GACAGCTCATGGAAGCTCTAAGTTGAGTTCCAAAGAGTCTAAGAGAAAGAAATCGG 1500  
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Dh 1766 AGGAAGAAAGAAAGAAAG 1825  
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Dh 1886 AACCAGTATGATATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1945

Qy 1681 GGTCCCTATTTTACCAAGGCGAATATGACAGAAAGAGCTTTTACGTTAGAGGGCA 1740  
Dh 1946 GGTCCCTATTTTACCAAGGCGAATATGACAGAAAGAGCTTTTACGTTAGAGGGCA 2005  
Qy 1741 GCAAGAGATGTGGATCTGAGAAAGCATTCGAGATGATGAGCAGCAGCTTTGAGAT 1800  
Dh 2006 GCAAGAGATGTGGATCTGAGAAAGCATTCGAGATGATGAGCAGCAGCTTTGAGAT 2065  
Qy 1801 AACGAGAGCGGTAGAGATTTCTTTTGTGCCCCGACAGACAGGAGAGAGAGAGAGAG 1860  
Dh 2066 AACGAGAGCGGTAGAGATTTCTTTTGTGCCCCGACAGACAGGAGAGAGAGAGAGAG 2125  
Qy 1861 AACCTGAGTCAGACAGTGGTGCATCCGGATGCTGGAGTGTTCACAGGAATGGGAAG 1920  
Dh 2126 AACCTGAGTCAGACAGTGGTGCATCCGGATGCTGGAGTGTTCACAGGAATGGGAAG 2185  
Qy 1921 ATGACAGCAGCTGTGATTTGCAATGCTGTGTTCTCTGTTGGTGGAGCTTCAGTTC 1980  
Dh 2186 ATGACAGCAGCTGTGATTTGCAATGCTGTGTTCTCTGTTGGTGGAGCTTCAGTTC 2245  
Qy 1981 ACATGCGCTGTGGAGAGCTTCTCCAGAGTGATTAATGATAGCCAGCTGATGAC 2040  
Dh 2246 ACATGCGCTGTGGAGAGCTTCTCCAGAGTGATTAATGATAGCCAGCTGATGAC 2305  
Qy 2041 AATGGAAACACAGTGAATGAAATGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAG 2100  
Dh 2306 AATGGAAACACAGTGAATGAAATGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAG 2365  
Qy 2101 ATGAGACTTTCTAGAGATCCTTCCAAAGCAAGCAGCAGATGATATACAGCATCTA 2160  
Dh 2366 ATGAGACTTTCTAGAGATCCTTCCAAAGCAAGCAGCAGATGATATACAGCATCTA 2425  
Qy 2161 ACAATACAGTAGAGAGACTTGAAGATCCAGGAGAGAAATGCCAGCTGTGTGTA 2220  
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Qy 2221 TTTTCCAGATATCTTAAATGAGGAGAGCTGTCCCATATTTGTTAAAGAGAAAGT 2280  
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Dh 2546 GTCAACCTGCTGTGATGAGACCATTTGTTGACCTGGCCATCAGATCTGATGCTTA 2605  
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Dh 2606 AATACTCTTTTCAATGAGCAGTACATATCCAAATGAGAGAGAGAGAGAGAGAGAG 2665  
Qy 2401 ACAGTAGAAAGCTGTGTTTCACTGGAGCTTTACAGCAAGATGTTTGGAAATAT 2460  
Dh 2666 ACAGTAGAAAGCTGTGTTTCACTGGAGCTTTACAGCAAGATGTTTGGAAATAT 2725  
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Dh 2786 AGCTTAGCTGTGATGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2845  
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Dh 2846 TTTGATGCTGTGAGATTTTCAAGTTGAGGAAATCTTGGCAAGCTTAAATGCTA 2905  
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Dh 2906 AAGATATGAGCAATTCCTGAGGAGCTGTGGAATTAACCTCTCTTGGCATATC 2965  
Qy 2701 GTCTTCATTTTGGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2760  
Dh 2966 GTCTTCATTTTGGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3025

2761 TGCAGATGCGCAGTATGTCACCTCCACGCTGGCAGATGATGACTTCTTCCACTCC 2820  
3026 TGCAGATGCGCAGTATGTCACCTCCACGCTGGCAGATGATGACTTCTTCCACTCC 3085  
2821 TTCCTGATGTTGTTCCGCGCTGTGTGGGAGTGATAGACACCATGTGGACTGTATG 2880  
3086 TTCCTGATGTTGTTCCGCGCTGTGTGGGAGTGATAGACACCATGTGGACTGTATG 3145  
2881 GAGGTGCGGTGTCAGACCATGTCCTTACTGTCCTTCAATGTCATGATGATGATGGAAC 2940  
3146 GAGGTGCGGTGTCAGACCATGTCCTTACTGTCCTTCAATGTCATGATGATGGAAC 3205  
2941 CTAGTGTCTGATGTCCTTCTTGGCCTTGTGCTTGTGAGCTCATTTAGTGACACACTT 3000  
3206 CTAGTGTCTGATGTCCTTCTTGGCCTTGTGCTTGTGAGCTCATTTAGTGACACACTT 3265  
3001 GCAGCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3060  
3266 GCAGCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3325  
3061 AAGGATGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3120  
3326 AAGGATGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3385  
3121 AAGCAAAAGATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3180  
3386 AAGCAAAAGATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3445  
3181 TGTATGTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 3240  
3446 TGTATGTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 3505  
3241 GGAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3300  
3506 GGAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3565  
3301 GATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3360  
3566 GATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3625  
3361 GATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3420  
3626 GATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3685  
3421 AGCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3480  
3686 AGCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3745  
3481 GCACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3540  
3746 GCACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3805  
3541 TTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3600  
3806 TTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3865  
3601 GGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3660  
3866 GGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3925  
3661 GAGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3720  
3926 GAGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3984  
3721 TATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3780  
3985 TATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4044  
3781 TATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3840  
4045 TATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4104  
3841 ACCAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3900

4105 ACCAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4164  
3901 GCATATGCTTGGTTACTAGAACTTTGAGACATGCAATCTCTAGACACTAAGACT 3960  
4165 GCATATGCTTGGTTACTAGAACTTTGAGACATGCAATCTCTAGACACTAAGACT 4224  
3961 CTGAGACTCTGAGAGCTTATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 4020  
4225 CTGAGACTCTGAGAGCTTATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 4284  
4021 TTAGAGCAATTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 4080  
4285 TTAGAGCAATTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 4344  
4081 TTGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4140  
4345 TTGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4404  
4141 ACTGTCAGAGTTTGCATGCAAGAGCTGAAATGATGATGATGATGATGATGATGATGATG 4200  
4405 ACTGTCAGAGTTTGCATGCAAGAGCTGAAATGATGATGATGATGATGATGATGATGATG 4464  
4201 GAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4260  
4465 GAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4524  
4261 GGGTATCTCTTCTTCTTCAAGTTGCCATCTCAAGATGATGATGATGATGATGATGATG 4320  
4525 GGGTATCTCTTCTTCTTCAAGTTGCCATCTCAAGATGATGATGATGATGATGATGATG 4584  
4321 GCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4380  
4585 GCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4644  
4381 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4440  
4645 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4704  
4441 GTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4500  
4705 GTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4764  
4501 ACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4560  
4765 ACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4824  
4561 AAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4620  
4825 AAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4884  
4621 CAAGTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4680  
4885 CAAGTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4944  
4681 GAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4740  
4945 GAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5004  
4741 ATTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4800  
5005 ATTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5064  
4801 ACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4860  
5065 ACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5124  
4861 CTGCGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4920  
5125 CTGCGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5184  
4921 GCTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4980



CC in biopsied tissues in which TRICH expression may be correlated with a  
 CC disease, to generate hybridization probes for mapping naturally occurring  
 CC genomic sequence, and in drug screening. The present sequence is human  
 CC TRICH-13 cDNA.

XX Sequence 6027 BP; 1785 A; 1189 C; 1348 G; 1705 T; 0 other;

Query Match 87.3%; Score 5262; DB 24; Length 6027;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 6012; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

OY 1 ATGAGCAACAAGTGGCTTGTACACAGACCTGACAGCTTCACTTCTTCCACAGAGAA 60  
 Db 1 ATGAGCAACAAGTGGCTTGTACACAGACCTGACAGCTTCACTTCTTCCACAGAGAA 60  
 OY 61 TCTCTTGGCGCTATTGAAAGAGCATTTGCAAGAAAGAAAGAAAGAAATCCCAACAGAC 120  
 Db 61 TCTCTTGGCGCTATTGAAAGAGCATTTGCAAGAAAGAAAGAAAGAAATCCCAACAGAC 120  
 OY 121 AAAAAAGATGAGAGCAAGAAATGAGCCCAAGCCAAATAGTACTTGGAGCTGGAAGAAAC 180  
 Db 121 AAAAAAGATGAGAGCAAGAAATGAGCCCAAGCCAAATAGTACTTGGAGCTGGAAGAAAC 180  
 OY 181 CTTCATTTATTATGAGACATTTCTCCAGAGATGCTGACAGGCCCTGAGAGACTG 240  
 Db 181 CTTCATTTATTATGAGACATTTCTCCAGAGATGCTGACAGGCCCTGAGAGACTG 240  
 OY 241 GACCCCTACTATATCAATAAGAAACTTTTATATGATGAAAGAAAGAAAGAAAGAAAGAA 300  
 Db 241 GACCCCTACTATATCAATAAGAAACTTTTATATGATGAAAGAAAGAAAGAAAGAAAGAA 300  
 OY 301 CGGTTCAGTCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
 Db 301 CGGTTCAGTCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
 OY 361 GCTATTAAATTTGGTACATTTATTTACAGCATTTATTTATTTATTTATTTATTTATTT 420  
 Db 361 GCTATTAAATTTGGTACATTTATTTACAGCATTTATTTATTTATTTATTTATTTATTT 420  
 OY 421 AACTGCTGTTTATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480  
 Db 421 AACTGCTGTTTATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480  
 OY 481 TTTCACAGAAATATATCTTTTGAATCACTTAAATTAATTTGCAAGGAGATCTGTTT 540  
 Db 481 TTTCACAGAAATATATCTTTTGAATCACTTAAATTAATTTGCAAGGAGATCTGTTT 540  
 OY 541 GAAGATTTTACTTCTGCGGATTCATTTATTTACAGCATTTATTTATTTATTTATTTATTT 600  
 Db 541 GAAGATTTTACTTCTGCGGATTCATTTATTTACAGCATTTATTTATTTATTTATTTATTT 600  
 OY 601 GGTACAGTACAGAGATTTTGTGACCTGGGCAATGCTCGGCAATTTGAAACATTTCAAGTT 660  
 Db 601 GGTACAGTACAGAGATTTTGTGACCTGGGCAATGCTCGGCAATTTGAAACATTTCAAGTT 660  
 OY 661 CTTCGAGCATTTGAAGAGATTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 720  
 Db 661 CTTCGAGCATTTGAAGAGATTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 720  
 OY 721 ATCCAGTCTGTGAAGAGCTCTCAGATGATGATGATGATGATGATGATGATGATGATGAT 780  
 Db 721 ATCCAGTCTGTGAAGAGCTCTCAGATGATGATGATGATGATGATGATGATGATGATGAT 780  
 OY 781 TTTGCTATTTGGGCTGAGCTGCTGATGAGGCAACCTGAGAAATTAATTAATTAATTAATTA 840  
 Db 781 TTTGCTATTTGGGCTGAGCTGCTGATGAGGCAACCTGAGAAATTAATTAATTAATTAATTA 840  
 OY 841 CCTCCACCAATGCTCTCTTGGAGAAATAGATAGAAAGAAATTAATTAATTAATTAATTAAT 900  
 Db 841 CCTCCACCAATGCTCTCTTGGAGAAATAGATAGAAAGAAATTAATTAATTAATTAATTAAT 900  
 OY 901 AATGATCACTTATTAATGAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
 Db 901 AATGATCACTTATTAATGAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960

Db 901 AATGATCACTTATTAATGAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
 OY 961 TCAAGATATCAATTTTCTGAGGGGTTTTAGATGACATATATGGAATAGCTT 1020  
 Db 961 TCAAGATATCAATTTTCTGAGGGGTTTTAGATGACATATATGGAATAGCTT 1020  
 OY 1021 GATGAGGCAATGCTCAGAGGATATATGCTGGAAGCTGTAAGAAATCCCAATTAAT 1080  
 Db 1021 GATGAGGCAATGCTCAGAGGATATATGCTGGAAGCTGTAAGAAATCCCAATTAAT 1080  
 OY 1081 GGTACACAAAGCTTATATACCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 1140  
 Db 1081 GGTACACAAAGCTTATATACCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 1140  
 OY 1141 CAGGACTTGGGAAATTTTATATCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 1200  
 Db 1141 CAGGACTTGGGAAATTTTATATCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 1200  
 OY 1201 AATATTTTGTGTGCTATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260  
 Db 1201 AATATTTTGTGTGCTATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260  
 OY 1261 GTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320  
 Db 1261 GTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320  
 OY 1321 GAGGCGAATTTTACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380  
 Db 1321 GAGGCGAATTTTACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380  
 OY 1381 GCAGCAAGGCAACTGCTCAGACATTTCCAGAGAGCCAGTGCAGAGAGGAGGCTCTCA 1440  
 Db 1381 GCAGCAAGGCAACTGCTCAGACATTTCCAGAGAGCCAGTGCAGAGAGGAGGCTCTCA 1440  
 OY 1441 GACAGCTCATCTGAGAGCTTAAAGTTGAGTTCCAGAGAGTCTTAAGAGAAAGAAATTCG 1500  
 Db 1441 GACAGCTCATCTGAGAGCTTAAAGTTGAGTTCCAGAGAGTCTTAAGAGAAAGAAATTCG 1500  
 OY 1501 AGGAAAGAAAGAAAGAAAG 1560  
 Db 1501 AGGAAAGAAAGAAAGAAAG 1560  
 OY 1561 CAAAAATCTGAATCTGAG 1620  
 Db 1561 CAAAAATCTGAATCTGAG 1620  
 OY 1621 AACCGATGACATATGAAG 1680  
 Db 1621 AACCGATGACATATGAAG 1680  
 OY 1681 GGTGCTGCTATTTTACAG 1740  
 Db 1681 GGTGCTGCTATTTTACAG 1740  
 OY 1741 GCAAGAGATGAGAGATGAG 1800  
 Db 1741 GCAAGAGATGAGAGATGAG 1800  
 OY 1801 AACGAG 1860  
 Db 1801 AACGAG 1860  
 OY 1861 AACCTGAGTACAG 1920  
 Db 1861 AACCTGAGTACAG 1920  
 OY 1921 ATGACAG 1980  
 Db 1921 ATGACAG 1980  
 OY 1981 ACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040  
 Db 1981 ACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040

OY 2041 AATGGAACAACCACTGAAATGAAATGAGAAAGAGTCAAGTCTTCCACGTTTC 2100  
DB 2041 AATGGAACAACCACTGAAATGAAATGAGAAAGAGTCAAGTCTTCCACGTTTC 2100  
OY 2101 AATGGAATCTTCTAGAGATCTCTCCCAAGGCAAGACATGATATAGCAGCATTTCA 2160  
DB 2101 AATGGAATCTTCTAGAGATCTCTCCCAAGGCAAGACATGATATAGCAGCATTTCA 2160  
OY 2161 ACAATACAGTACAGACATCTGAAAGATCCAGCAGAAATGCCACCTGTTGATATA 2220  
DB 2161 ACAATACAGTACAGACATCTGAAAGATCCAGCAGAAATGCCACCTGTTGATATA 2220  
OY 2221 TTTTCCAAATCTTCTTAACTCGGAGCTCTTCCAAATGTTGTTAAAGGAAACATGTT 2280  
DB 2221 TTTTCCAAATCTTCTTAACTCGGAGCTCTTCCAAATGTTGTTAAAGGAAACATGTT 2280  
OY 2281 GTCAACCTGTTGATGAGACCCATTTGTTGACCTGGCCATCAACATCTGATTTCTTA 2340  
DB 2281 GTCAACCTGTTGATGAGACCCATTTGTTGACCTGGCCATCAACATCTGATTTCTTA 2340  
OY 2341 AATACCTTTTCAATGAGCAGACATATCCAAATGAGACCATTTCAATATGTCCTT 2400  
DB 2341 AATACCTTTTCAATGAGCAGACATATCCAAATGAGACCATTTCAATATGTCCTT 2400  
OY 2401 ACAGTAGGAACCTGTTTCACTGGAGTCTTCAAGCAAGAAATGTTTCCGAAATATAT 2460  
DB 2401 ACAGTAGGAACCTGTTTCACTGGAGTCTTCAAGCAAGAAATGTTTCCGAAATATAT 2460  
OY 2461 GCCATGGATCTTACTATTTTCCAAAGAGCTGGAATCTTTCAGGCTTTATTTGTTG 2520  
DB 2461 GCCATGGATCTTACTATTTTCCAAAGAGCTGGAATCTTTCAGGCTTTATTTGTTG 2520  
OY 2521 ACCGTTAGCTGTGAGAACTTGGACCTGCCAATGAGGAAATATCTGTTCCGTTCA 2580  
DB 2521 ACCGTTAGCTGTGAGAACTTGGACCTGCCAATGAGGAAATATCTGTTCCGTTCA 2580  
OY 2581 TTTCCAGTGTGAGAGTTTCAAGTTGGGCAAAATCTGGCAACGTTAAATATGCTATA 2640  
DB 2581 TTTCCAGTGTGAGAGTTTCAAGTTGGGCAAAATCTGGCAACGTTAAATATGCTATA 2640  
OY 2641 AAGATCATGCGCAATTCCTGGGGGGCTCTGGAAATTTAAACCTGCTTGGCCATCATC 2700  
DB 2641 AAGATCATGCGCAATTCCTGGGGGGCTCTGGAAATTTAAACCTGCTTGGCCATCATC 2700  
OY 2701 GTCTTCAATTTTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2760  
DB 2701 GTCTTCAATTTTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2760  
OY 2761 TGCAGATGCGCAGTGTATTTGCAACCTGCCAGGTCGCAATGATGATCTTCCACTCC 2820  
DB 2761 TGCAGATGCGCAGTGTATTTGCAACCTGCCAGGTCGCAATGATGATCTTCCACTCC 2820  
OY 2821 TTCCCTGATTTGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2880  
DB 2821 TTCCCTGATTTGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2880  
OY 2881 GAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2940  
DB 2881 GAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2940  
OY 2941 CTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3000  
DB 2941 CTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3000  
OY 3001 GCAGCCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3060  
DB 3001 GCAGCCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3060  
OY 3061 AAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3120  
DB 3061 AAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3120

OY 3121 AAACAAAGATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3180  
DB 3121 AAACAAAGATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3180  
OY 3181 TGTATGCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3240  
DB 3181 TGTATGCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3240  
OY 3241 GGAACCTACAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3300  
DB 3241 GGAACCTACAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3300  
OY 3301 GATTACATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3360  
DB 3301 GATTACATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3360  
OY 3361 GAATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3420  
DB 3361 GAATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3420  
OY 3421 AGCAAGAGAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3480  
DB 3421 AGCAAGAGAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3480  
OY 3481 GCACCTGTAG 3540  
DB 3481 GCACCTGTAG 3540  
OY 3541 TTCACTGAG 3600  
DB 3541 TTCACTGAG 3600  
OY 3601 GGAAGAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3660  
DB 3601 GGAAGAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3660  
OY 3661 GAGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3720  
DB 3661 GAGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3720  
OY 3721 TATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3780  
DB 3721 TATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3780  
OY 3781 TACATTTTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3840  
DB 3781 TACATTTTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3840  
OY 3841 ACCAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3900  
DB 3841 ACCAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3900  
OY 3901 GCAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3960  
DB 3901 GCAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3960  
OY 3961 CTGAGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4020  
DB 3961 CTGAGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4020  
OY 4021 TTAGAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4080  
DB 4021 TTAGAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4080  
OY 4081 TTGAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4140  
DB 4081 TTGAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4140  
OY 4141 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4200  
DB 4141 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4200  
OY 4201 GAAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4260



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Db 4201 GAAAGAAATGAGACGTGCGAGGAGAAAATGTGAAGTAACCTTGTGATTAAGTATGAGATTT 4260
Oy 4261 GGGATATCTCTCTTGTCTCAAGTGTGCCATTCATAAGGATGGATGATATATATATATGCA 4320
Db 4261 GGGATATCTCTCTTGTCTCAAGTGTGCCATTCATAAGGATGGATGATATATATATGCA 4320
Oy 4321 GCATGTATTCAGAAATGTGGAATCCAGCTCAAGCTTAAGTGAAGAAAGTCTATACATGAT 4380
Db 4321 GCATGTATTCAGAAATGTGGAATCCAGCTCAAGCTTAAGTGAAGAAAGTCTATACATGAT 4380
Oy 4381 CTCTACCTTTGTTATTTTCATCATCTTTGGGCTCTTCCCTTCACTTGAACCTGTTATTTGCT 4440
Db 4381 CTCTACCTTTGTTATTTTCATCATCTTTGGGCTCTTCCCTTCACTTGAACCTGTTATTTGCT 4440
Oy 4441 GTCTATCATAGTATTTTCAACCCAGCAAAAAGTGTGAGAGTCAAGACATCTTTATG 4500
Db 4441 GTCTATCATAGTATTTTCAACCCAGCAAAAAGTGTGAGAGTCAAGACATCTTTATG 4500
Oy 4501 ACAGAGACAGAGAAATATCTATATGCAATGAAAAAATAGATGAAAAAACCGCA 4560
Db 4501 ACAGAGACAGAGAAATATCTATATGCAATGAAAAAATAGATGAAAAAACCGCA 4560
Oy 4561 AAGCTATACCTCGACAGCAAGAAACAAATTTCAAGGAATGCTCTTGAAGTCTGAACGCA 4620
Db 4561 AAGCTATACCTCGACAGCAAGAAACAAATTTCAAGGAATGCTCTTGAAGTCTGAACGCA 4620
Oy 4621 CAATTTTTCATATAGCATATGATTTCTCATCTCTTCAACATGCTGACATATGCTG 4680
Db 4621 CAATTTTTCATATAGCATATGATTTCTCATCTCTTCAACATGCTGACATATGCTG 4680
Oy 4681 GAAACAGATGACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4740
Db 4681 GAAACAGATGACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4740
Oy 4741 ATTTGCTATTTTACTGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 4800
Db 4741 ATTTGCTATTTTACTGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 4800
Oy 4801 ACCATTTGATGAGATATTTTGTGATTTTGTGATGATGATGATGATGATGATGATGATG 4860
Db 4801 ACCATTTGATGAGATATTTTGTGATTTTGTGATGATGATGATGATGATGATGATGATG 4860
Oy 4861 CTTCGCGAGTGAAGAAATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4920
Db 4861 CTTCGCGAGTGAAGAAATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4920
Oy 4921 GCTAGATTTGGCCGATTCCTACGCTCTGATCAAGAGCAAGAGGAGATCCGACGCTGCTC 4980
Db 4921 GCTAGATTTGGCCGATTCCTACGCTCTGATCAAGAGCAAGAGGAGATCCGACGCTGCTC 4980
Oy 4981 TTTGCTTTGATGATGCTCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5040
Db 4981 TTTGCTTTGATGATGCTCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5040
Oy 5041 ATGTTCAATCTAGGCAATCTTTGGGATGCAAACTTTGCTTAAGAGAGGAGGATGGG 5100
Db 5041 ATGTTCAATCTAGGCAATCTTTGGGATGCAAACTTTGCTTAAGAGAGGAGGATGGG 5100
Oy 5101 ATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5160
Db 5101 ATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5160
Oy 5161 ACAACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5220
Db 5161 ACAACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5220
Oy 5221 TGTGACCTTAATAAGTAACTGGAAGCTCAAGTTAAGAGAGAGTGTGGAGACCAATCT 5280
Db 5221 TGTGACCTTAATAAGTAACTGGAAGCTCAAGTTAAGAGAGAGTGTGGAGACCAATCT 5280
Oy 5281 GTTGAATTTTCTTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 5340
Db 5281 GTTGAATTTTCTTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 5340

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Db 5381 GTTGAATTTTCTTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 5340
Oy 5341 TACATCGGGGATCTCGAGAACTGATGATGATGATGATGATGATGATGATGATGATGATG 5400
Db 5341 TACATCGGGGATCTCGAGAACTGATGATGATGATGATGATGATGATGATGATGATGATG 5400
Oy 5401 AGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5460
Db 5401 AGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5460
Oy 5461 CAGTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5520
Db 5461 CAGTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5520
Oy 5521 CTGCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 5580
Db 5521 CTGCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 5580
Oy 5581 CGGATCCACTGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5640
Db 5581 CGGATCCACTGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5640
Oy 5641 GAGATGATGCTCTACGAAATACAGATGAGAGAGGATGATGATGATGATGATGATGATGAT 5700
Db 5641 GAGATGATGCTCTACGAAATACAGATGAGAGAGGATGATGATGATGATGATGATGATGAT 5700
Oy 5701 GTCTCTATACGCAATACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5760
Db 5701 GTCTCTATACGCAATACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5760
Oy 5761 ATTATTCAGGCTGCTTACAGAGGCTGCTTAAAGCAAGTGAAGCAAGTCTGCTT 5820
Db 5761 ATTATTCAGGCTGCTTACAGAGGCTGCTTAAAGCAAGTGAAGCAAGTCTGCTT 5820
Oy 5821 ACATCAATTAACCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 5880
Db 5821 ACATCAATTAACCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 5880
Oy 5881 ATTGACGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 5940
Db 5881 ATTGACGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 5940
Oy 5941 GCTTGTCCACTTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6000
Db 5941 GCTTGTCCACTTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6000
Oy 6001 GGCAGATGAAAAAGCAAGGAAAA 6027
Db 6001 GGCAGATGAAAAAGCAAGGAAAA 6027

RESULT 5
AAH55764
ID AAH55764 standard; cDNA; 8378 BP.
XX
AC AAH55764;
XX
DT 04-SEP-2001 (first entry)
XX
DE Human neonatal form of SCN1A nucleotide sequence SEQ ID NO:2.
XX
KW Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;
KW diagnosis; mutation; chromosome 2q23-q31; neurological disorder;
KW anticonvulsant; neuroprotective; ss.
XX
OS Homo sapiens.
XX
PN NC0200138564-A2.
XX
PD 31-MAY-2001.
XX
PF 24-NOV-2000; 2000MO-CA01404.
XX

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OY 2308 GTTGACCTGGCCATCACCATCTGATGTCTTAATAACTCTTTTCATGCGCATGAGGAC 2367  
|||||  
Db 2572 GTTGACCTGGCCATCACCATCTGATGTCTTAATAACTCTTTTCATGCGCATGAGGAC 2631  
OY 2368 TATCCAAAGAGGAGGACATTTCAATAATGTGCTACAGTAGAGAACTTGGTTTCACTGG 2427  
|||||  
Db 2632 TATCCAAAGAGGAGGACATTTCAATAATGTGCTACAGTAGAGAACTTGGTTTCACTGG 2691  
OY 2428 ATCTTACAGCAGAAATGTTCTGAAATTAATTCAGTAGATCCCTACTATTATTTCGA 2487  
|||||  
Db 2692 ATCTTACAGCAGAAATGTTCTGAAATTAATTCAGTAGATCCCTACTATTATTTCGA 2751  
OY 2488 GAAAGCTGGAATATCTTGAAGGTTTATTCAGCTTACCTGCTAGAACTTGGACTC 2547  
|||||  
Db 2752 GAAAGCTGGAATATCTTGAAGGTTTATTCAGCTTACCTGCTAGAACTTGGACTC 2811  
OY 2548 GCCAATGTGGAAGATTAATCTGTTCTCCGTTTCATTTGCAATTCGCGATTCAGTTG 2607  
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Db 2812 GCCAATGTGGAAGATTAATCTGTTCTCCGTTTCATTTGCAATTCGCGATTCAGTTG 2871  
OY 2608 GCAAAATCTGGCCACAGCTTAATATGCTAATAAGATCATCGCAATTCGCTGGGGCT 2667  
|||||  
Db 2872 GCAAAATCTGGCCACAGCTTAATATGCTAATAAGATCATCGCAATTCGCTGGGGCT 2931  
OY 2668 CTGGGAAATTTAACCTGCTGCTGGCATCATCGCTTCATTTTGGCCGTGGCATG 2727  
|||||  
Db 2932 CTGGGAAATTTAACCTGCTGCTGGCATCATCGCTTCATTTTGGCCGTGGCATG 2991  
OY 2728 CAGCTCTTGTGTAAGAGCTACAAAGATTTGTCTGCAAGATCGCAAGATTTGCACTC 2787  
|||||  
Db 2992 CAGCTCTTGTGTAAGAGCTACAAAGATTTGTCTGCAAGATCGCAAGATTTGCACTC 3051  
OY 2788 CCAGCTGGCCACAGCTTAATATGCTAATAAGATCATCGCAATTCGCTGGGGCT 2847  
|||||  
Db 3052 CCAGCTGGCCACAGCTTAATATGCTAATAAGATCATCGCAATTCGCTGGGGCT 3111  
OY 2848 GGGGAGTGGATAGAGACCATGTGAGCTGTATGAGTGTGCTGCAAGCATGCGCT 2907  
|||||  
Db 3112 GGGGAGTGGATAGAGACCATGTGAGCTGTATGAGTGTGCTGCAAGCATGCGCT 3171  
OY 2908 ACTGCTTCATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 2967  
|||||  
Db 3172 ACTGCTTCATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 3231  
OY 2968 TTGCTTTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3027  
|||||  
Db 3232 TTGCTTTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3291  
OY 3028 AATAATCTCCAAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3087  
|||||  
Db 3292 AATAATCTCCAAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3351  
OY 3088 ATATATGATTTATTCACACAGCTCTTCATTAAGAAACAAAAGATTTAGATGAATTA 3147  
|||||  
Db 3352 ATATATGATTTATTCACACAGCTCTTCATTAAGAAACAAAAGATTTAGATGAATTA 3411  
OY 3148 CCAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3207  
|||||  
Db 3412 CCAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3471  
OY 3208 GGGGAAAGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3267  
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Db 3472 GGGGAAAGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3531  
OY 3268 AGCAGTGTGAAAAATACATTAATGATGAAGATTAACATGCTCATTAACAAACCC 3327  
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Db 3532 AGCAGTGTGAAAAATACATTAATGATGAAGATTAACATGCTCATTAACAAACCC 3591  
OY 3328 ACTTTCAGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3387  
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Db 3592 ACTTTCAGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3651  
OY 3388 GAAAGCTTATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3447  
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Db 3652 GAAAGCTTATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3711  
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OY 3448 AGCTATGAGAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3507  
|||||  
Db 3712 AGCTATGAGAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3771  
OY 3508 GAACTGGAAGAACTCTGGAACAGAGCTTTCACAGAGGCTGTACAAAGATTC 3567  
|||||  
Db 3772 GAACTGGAAGAACTCTGGAACAGAGCTTTCACAGAGGCTGTACAAAGATTC 3831  
OY 3568 AAGTGTGCTCAATCATGCTGGAAGAGCAGAGGAAACAAATGCTGAACCTGGAAG 3627  
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Db 3832 AAGTGTGCTCAATCATGCTGGAAGAGCAGAGGAAACAAATGCTGAACCTGGAAG 3891  
OY 3628 AGTGTTCCTGCAATGCTGGAAGATTAACATCTGCTGCTGCTGCTGCTGCTGCTG 3687  
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Db 3892 AGTGTTCCTGCAATGCTGGAAGATTAACATCTGCTGCTGCTGCTGCTGCTGCTG 3951  
OY 3688 CTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3747  
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Db 3952 CTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4011  
OY 3748 AGCATGCTGGAATATGCTGCAAGAGTTCCTACATTTTCATTCGGAATGCTCTA 3807  
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Db 4012 AGCATGCTGGAATATGCTGCAAGAGTTCCTACATTTTCATTCGGAATGCTCTA 4071  
OY 3808 AATGGGTGCGATATGCTATCAAAATTTTCACCAATGCTGCTGCTGCTGCTGCTG 3867  
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Db 4072 AATGGGTGCGATATGCTATCAAAATTTTCACCAATGCTGCTGCTGCTGCTGCTG 4130  
OY 3868 TTAATGTTGATGCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3927  
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Db 4131 TTAATGTTGATGCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4190  
OY 3928 GGAGCATCAATTCCTCAGACACTAGAGCTGAGACTCTPAAGACCTTATCTGCA 3987  
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Db 4191 GGAGCATCAATTCCTCAGACACTAGAGCTGAGACTCTPAAGACCTTATCTGCA 4250  
OY 3988 TTTGAAGGATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4047  
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Db 4251 TTTGAAGGATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4310  
OY 4048 GTGCTTTCGCTTCTTATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4107  
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Db 4311 GTGCTTTCGCTTCTTATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4370  
OY 4108 GCTGCAATTCCTACACACTGATTAACACACACTGCTGACAGGTTGACATGCAAGC 4167  
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Db 4371 GCTGCAATTCCTACACACTGATTAACACACACTGCTGACAGGTTGACATGCAAGC 4430  
OY 4168 GTGAATTAATCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4227  
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Db 4431 GTGAATTAATCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4490  
OY 4228 AATGGAAGTAACTTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 4287  
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Db 4491 AATGGAAGTAACTTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 4550  
OY 4288 ACATTCAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4347  
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Db 4551 ACATTCAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4610  
OY 4348 CAGCTTAAGTGAAGAAAGTCTGATCATGATCTTACTTGTATTTTCATCATCTT 4407  
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Db 4611 CAGCTTAAGTGAAGAAAGTCTGATCATGATCTTACTTGTATTTTCATCATCTT 4670  
OY 4408 GGGCTCTTCTACCTGGAAGCTGTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4467  
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Db 4671 GGGCTCTTCTACCTGGAAGCTGTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4730  
OY 4468 AAAAAGATTTGAGGCTCAAGATCTTTATGACAGAGAACAGAAATCTATAT 4527  
|||||



[illegible]

Db 4731 AAAAAAGTTTGAAGTCAGACATCTTATGACAGAAAGACAGAAATCTATAT 4790  
 QY 4528 GCAATGAAAAATTTAGATCGAAAAAACCAGAAACCTATCTCTGACCCAGAAAAA 4587  
 Db 4731 GCAATGAAAAATTTAGATCGAAAAAACCAGAAACCTATCTCTGACCCAGAAAAA 4850  
 QY 4588 TTTCAAGGAATGCTTTGACTCTGTAACAGACAAGTTTGGACATAAGCATGATT 4647  
 Db 4851 TTTCAAGGAATGCTTTGACTCTGTAACAGACAAGTTTGGACATAAGCATGATT 4910  
 QY 4648 CTCATCTGCTTACATGCTGACATGATGTAAGAAACAGATGACAGATGAATATG 4707  
 Db 4911 CTCATCTGCTTACATGCTGACATGATGTAAGAAACAGATGACAGATGAATATG 4970  
 QY 4708 ACTACATTTTGTACAGCATCAATCTGCTTCTATTTACTGAGAGATGTGA 4767  
 Db 4971 ACTACATTTTGTACAGCATCAATCTGCTTCTATTTACTGAGAGATGTGA 5030  
 QY 4768 CTGAACATCTCTCTACGCAATTTATTTTACATGAGATGAAATTTTGTATTT 4827  
 Db 5031 CTGAACATCTCTCTACGCAATTTATTTTACATGAGATGAAATTTTGTATTT 5090  
 QY 4828 GTGCTGTCATCTCTCTACGCAATTTATTTTCTGAGATGTAAGAAATTTTCT 4887  
 Db 5091 GTGCTGTCATCTCTCTACGCAATTTATTTTCTGAGATGTAAGAAATTTTCT 5150  
 QY 4888 GTGCTGTCATCTCTCTACGCAATTTATTTTCTGAGATGTAAGAAATTTTCT 4947  
 Db 5151 GTGCTGTCATCTCTCTACGCAATTTATTTTCTGAGATGTAAGAAATTTTCT 5210  
 QY 4948 ATCAAAGGAGCAAGAGGATCCGACAGCTGCTTTGCTTATGATGCTCTCTG 5007  
 Db 5211 ATCAAAGGAGCAAGAGGATCCGACAGCTGCTTTGCTTATGATGCTCTCTG 5270  
 QY 5008 TTTGTTAACATGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5067  
 Db 5271 TTTGTTAACATGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5330  
 QY 5068 TCCAACTTTGCT 5127  
 Db 5331 TCCAACTTTGCT 5390  
 QY 5128 TTTGGCAACAGATGATCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5187  
 Db 5391 TTTGGCAACAGATGATCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5450  
 QY 5188 CTAGACCCCATCTCTCAACAGTAAAGCCAGCTGACCCCTATTAAGTTAACCTG 5247  
 Db 5451 CTAGACCCCATCTCTCAACAGTAAAGCCAGCTGACCCCTATTAAGTTAACCTG 5510  
 QY 5248 AGCTCAGTTAAGGAGACATCTGAGAACCCATCTGTTGAATTTCTTTTCTCTCT 5307  
 Db 5511 AGCTCAGTTAAGGAGACATCTGAGAACCCATCTGTTGAATTTCTTTTCTCTCT 5570  
 QY 5308 ATCATATATCT 5367  
 Db 5571 ATCATATATCT 5530  
 QY 5368 AGTGTGCTAGTAAAGAGTGAAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5427  
 Db 5631 AGTGTGCTAGTAAAGAGTGAAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5690  
 QY 5428 GAGTTTGGAGAGATTTGATCCGATGCAACTCAGTTCTGATGAAATTTGAATAT 5487  
 Db 5691 GAGTTTGGAGAGATTTGATCCGATGCAACTCAGTTCTGATGAAATTTGAATAT 5750  
 QY 5488 CAGTTTGAAGTGGCTGTAACCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5547  
 Db 5751 CAGTTTGAAGTGGCTGTAACCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5810  
 QY 5548 ATTGCATGATTTGCGCATGATGATGATGATGATGATGATGATGATGATGATGAT 5607  
 Db 5811 ATTGCATGATTTGCGCATGATGATGATGATGATGATGATGATGATGATGATGAT 5870

QY 5608 GCTTTTCAAGAGCGGCTTCTAGAGAGATGAGAGATGATGATGATGATGATGATG 5667  
 Db 5871 GCTTTTCAAGAGCGGCTTCTAGAGAGATGAGAGATGATGATGATGATGATGATG 5930  
 QY 5668 GAAGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5727  
 Db 5931 GAAGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5990  
 QY 5728 TTTAAACGAAACAGAGAGATGATGATGATGATGATGATGATGATGATGATG 5787  
 Db 5991 TTTAAACGAAACAGAGAGATGATGATGATGATGATGATGATGATGATGATG 6050  
 QY 5788 CTTTAAACGAAACAGAGATGATGATGATGATGATGATGATGATGATGATG 5847  
 Db 6051 CTTTAAACGAAACAGAGATGATGATGATGATGATGATGATGATGATGATG 6110  
 QY 5848 GGGGCTAATCTCTTCTTAAAGAGATGATGATGATGATGATGATGATGATGAT 5907  
 Db 6111 GGGGCTAATCTCTTCTTAAAGAGATGATGATGATGATGATGATGATGATGAT 6170  
 QY 5908 ACAGAAAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5967  
 Db 6171 ACAGAAAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6230  
 QY 5968 ACAGAAAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6027  
 Db 6231 ACAGAAAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6290  
 QY 6028 TAA 6030  
 Db 6291 TAA 6293

RESULT 6  
 ID AAD32846  
 AAD32846 standard; cDNA; 4362 BP.  
 AC AAD32846;  
 DT 01-JUL-2002 (first entry)  
 DE Human ion channel cDNA #8.  
 KW Human; novel human protein; NHE; voltage-gated sodium channel;  
 KW gene therapy; bioreactor; mental disorder; biological disorder;  
 KW gene; medical disorder; ss.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..4362  
 FT /tag- a  
 FT /product- "Human ion channel protein #8"  
 FT /transl\_except- (pos:2974..2976, aa:Xaa)  
 FT /note- "Xaa - any amino acid"  
 PN W0200214498-A2.  
 PD 21-FEB-2002.  
 XX  
 PF 15-AUG-2001; 2001WO-US25650.  
 PR 16-AUG-2000; 2000US-225989P.  
 XX  
 PA (LEXI-) LEXICON GENETICS INC.  
 XX Turner CA, Mathur B, Mathur D;  
 DR WPI; 2002-280757/32.  
 DR P-PDB; AAE20517.  
 XX







QY 1621 AACGATGACATATGAAAGAGGTACTCTCCACACAGCTCTTGTGACATCCGT 1680  
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Db 1621 AACGATGACATATGAAAGAGGTACTCTCCACACAGCTCTTGTGACATCCGT 1680  
QY 1681 GGTCTCCATTTTTCACCAAGCGCAATATGCAAAACAGCTTTTACGTTTAAAGGGCGA 1740  
| | | | |  
Db 1681 GGTCTCCATTTTTCACCAAGCGCAATATGCAAAACAGCTTTTACGTTTAAAGGGCGA 1740  
QY 1741 GCAAAGATGTGGATCTGAGAACAGCTTGGCAATATGATGAGCAACAGCTTTGAGAT 1800  
| | | | |  
Db 1741 GCAAAGATGTGGATCTGAGAACAGCTTGGCAATATGATGAGCAACAGCTTTGAGAT 1800  
QY 1801 AACGAGACCGGTAGATCTCTTGTGTCGCCACGACAGAGAGAGAGAGAGAGAGAGAG 1860  
| | | | |  
Db 1801 AACGAGACCGGTAGATCTCTTGTGTCGCCACGACAGAGAGAGAGAGAGAGAGAGAG 1860  
QY 1861 AACCTGACTGACAGCAGTAGGTGATCCCGAGTCTGCGAGTGTTCAGAGCAATGGGAG 1920  
| | | | |  
Db 1861 AACCTGACTGACAGCAGTAGGTGATCCCGAGTCTGCGAGTGTTCAGAGCAATGGGAG 1920  
QY 1921 ATGCAACACACTGTGTGATGCAATGTGTGTGTCTGTTGTGTGTGTGTGTGTGTGTGT 1980  
| | | | |  
Db 1921 ATGCAACACACTGTGTGATGCAATGTGTGTGTCTGTTGTGTGTGTGTGTGTGTGTGT 1980  
QY 1981 ACATGCGCTGTGTGACAGCTTCTGCGACAGGTGATTAATAGATAGCAGCTACTGATGAC 2040  
| | | | |  
Db 1981 ACATGCGCTGTGTGACAGCTTCTGCGACAGGTGATTAATAGATAGCAGCTACTGATGAC 2040  
QY 2041 AATGAGAACACACTGAAAGACTGAAATGAGAAAGAGAGAGAGAGAGAGAGAGAGAG 2100  
| | | | |  
Db 2041 AATGAGAACACACTGAAAGACTGAAATGAGAAAGAGAGAGAGAGAGAGAGAGAGAG 2100  
QY 2101 ATGCACTTTCTGAGAGATCTCTTCCAAAGGCAAGCAGCAGATGATAGCAGATCTGA 2160  
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Db 2101 ATGCACTTTCTGAGAGATCTCTTCCAAAGGCAAGCAGCAGATGATAGCAGATCTGA 2160  
QY 2161 ACAAAATAGAGTAGAAGAACTGAAAGAAATCCAGACAGAAATGCCAGCTGTGTATATA 2220  
| | | | |  
Db 2161 ACAAAATAGAGTAGAAGAACTGAAAGAAATCCAGACAGAAATGCCAGCTGTGTATATA 2220  
QY 2221 TTTTCAACATATATCTTAATCTGAGACTGTCTCCATATTTGGTTAAAGTGAAGCATGTT 2280  
| | | | |  
Db 2221 TTTTCAACATATATCTTAATCTGAGACTGTCTCCATATTTGGTTAAAGTGAAGCATGTT 2280  
QY 2281 GTCAACCTGTGTGATGAGAGCCATTTGTGTGACCTGTGCAATCTCTATTTGCTTA 2340  
| | | | |  
Db 2281 GTCAACCTGTGTGATGAGAGCCATTTGTGTGACCTGTGCAATCTCTATTTGCTTA 2340  
QY 2341 AATGACTGTTTCATGAGCCATGAGCAGCTATTCATGAGCAGCAGCTTCAATATGCTCT 2400  
| | | | |  
Db 2341 AATGACTGTTTCATGAGCCATGAGCAGCTATTCATGAGCAGCAGCTTCAATATGCTCT 2400  
QY 2401 ACAATGAGAACTGTTGTTTCTGAGATCTTTACAGCAGAAATGTTTCTGAAAATTTAT 2460  
| | | | |  
Db 2401 ACAATGAGAACTGTTGTTTCTGAGATCTTTACAGCAGAAATGTTTCTGAAAATTTAT 2460  
QY 2461 GCAATGAGCTTCTATTTTTCACAGAAAGCGGAAATCTTTGACGCTTTATTTG 2520  
| | | | |  
Db 2461 GCAATGAGCTTCTATTTTTCACAGAAAGCGGAAATCTTTGACGCTTTATTTG 2520  
QY 2521 AGCGTTAGCGGTAGAACTTGTGACAGTGGCAAAATCTTGGCAACGTTAAATATGTAATA 2580  
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Db 2521 AGCGTTAGCGGTAGAACTTGTGACAGTGGCAAAATCTTGGCAACGTTAAATATGTAATA 2580  
QY 2581 TTTGATGCTGTGAGATTTTCAAGTTGCAAAATCTTGGCAACGTTAAATATGTAATA 2640  
| | | | |  
Db 2581 TTTGATGCTGTGAGATTTTCAAGTTGCAAAATCTTGGCAACGTTAAATATGTAATA 2640  
QY 2641 AAGATATGCGGCAATTCGCGGGGCGCTGTGGGAAATTTAAACCTCTGTGGCAGCATCATC 2700  
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Db 2641 AAGATATGCGGCAATTCGCGGGGCGCTGTGGGAAATTTAAACCTCTGTGGCAGCATCATC 2700  
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Db 2701 GTCTTCATTTTTCGCGGTGCGGAGTCTCTTTGTGTAAGTACAAAGATTTGTC 2760  
| | | | |  
QY 2761 TCGAAGATGCGCAATGATGTGCAACTCCAGCTGGCAGCATGAATGACTTCTCCACTCC 2820  
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| | | | |  
Db 2821 TTCTGATTTGTGTTCCCGCTGTGTGTGGAGATGATAGACCATGTGGAGCTGTATG 2880  
QY 2881 GAGTTCTGCGCAAGCATGTGCTTACTGTCTTCAATGATGATGATGATGATGATGATG 2940  
| | | | |  
Db 2881 GAGTTCTGCGCAAGCATGTGCTTACTGTCTTCAATGATGATGATGATGATGATGATG 2940  
QY 2941 CTAGTGTCTGTAATCTCTTCTGCGCTGTGTGTGATGATGATGATGATGATGATGATG 3000  
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Db 2941 CTAGTGTCTGTAATCTCTTCTGCGCTGTGTGTGATGATGATGATGATGATGATGATG 3000  
QY 3001 GCAGCCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3060  
| | | | |  
Db 3001 GCAGCCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3060  
QY 3061 AAGGAGTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3120  
| | | | |  
Db 3061 AAGGAGTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3120  
QY 3121 AAGGAGTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3180  
| | | | |  
Db 3121 AAGGAGTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3180  
QY 3181 TGTATGCTCAATCATATCAGAGAAATTTGGAAAGATCTGACTATTTAAAGATGTAAT 3240  
| | | | |  
Db 3181 TGTATGCTCAATCATATCAGAGAAATTTGGAAAGATCTGACTATTTAAAGATGTAAT 3240  
QY 3241 GGAAGTACAGAGTGTATGAGAACTGCGAGCAGCTTGAAGAAATCATATTTGATGAAAT 3300  
| | | | |  
Db 3241 GGAAGTACAGAGTGTATGAGAACTGCGAGCAGCTTGAAGAAATCATATTTGATGAAAT 3300  
QY 3301 GATTACATGTCATATTAACCAACCCAGCTTACTGTGATGATGATGATGATGATGATGATG 3360  
| | | | |  
Db 3301 GATTACATGTCATATTAACCAACCCAGCTTACTGTGATGATGATGATGATGATGATGATG 3360  
QY 3361 GAATGCTCTTTGAAATTTAAACAGGAGACTTATGATGATGATGATGATGATGATGATG 3420  
| | | | |  
Db 3361 GAATGCTCTTTGAAATTTAAACAGGAGACTTATGATGATGATGATGATGATGATGATG 3420  
QY 3421 AGCAAGAGAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3480  
| | | | |  
Db 3421 AGCAAGAGAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3480  
QY 3481 GCACTGTGAGAAAGACAGCCGCTAGTGAACCTGGAAGAACTTTGAACAGAGCTTGT 3540  
| | | | |  
Db 3481 GCACTGTGAGAAAGACAGCCGCTAGTGAACCTGGAAGAACTTTGAACAGAGCTTGT 3540  
QY 3541 TTTACTGAAAGCTGTGTACAAAGATTCAGTGTTCAAATCAATGTGGAAGAGCAGA 3600  
| | | | |  
Db 3541 TTTACTGAAAGCTGTGTACAAAGATTCAGTGTTCAAATCAATGTGGAAGAGCAGA 3600  
QY 3601 GGAAGAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3660  
| | | | |  
Db 3601 GGAAGAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3660  
QY 3661 GAGACCTTCATTTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3720  
| | | | |  
Db 3661 GAGACCTTCATTTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3720  
QY 3721 TATATGATGACGAGAAAGCATTAAGACAGTGTGGAATATGTCGACAGAGTTTCACT 3780  
| | | | |  
Db 3721 TATATGATGACGAGAAAGCATTAAGACAGTGTGGAATATGTCGACAGAGTTTCACT 3780  
QY 3781 TACATTTCAATCTGGAATGCTTTAAAGAGGCGCATATGCGCTATGCAATATTTTC 3840  
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|         |   |
|---------|---|
| RESULT# | 7   |
| ID      | AADJ32847 standard; cDNA; 4179 BP.                              |
| XX      | AADJ32847;  |
| AC      |   |
| XX      |   |
| DT      | 01-JUL-2002 (first entry)                                       |
| XX      |   |
| DE      | Human ion channel CDNA #9.                                      |
| XX      |   |
| KW      | Human; novel human protein; NHP; voltage-gated sodium channel;  |
| KM      | gene therapy; bioreactor; mental disorder; biological disorder; |
| KW      | gene; medical disorder; ss.                                     |
| XX      |   |
| OS      | Homo sapiens.   |
| XX      |   |
| FH      |   |
| FT      | Location/Qualifiers   |
| FT      | 1..4179   |
| FT      | /*tag= a  |
| FT      | /product= "Human ion channel protein #9"                        |
| FT      | /transl_except= (pos:2974..2976, aa:Xaa)                        |
| FT      | /transl_except= (pos:3199..3201, aa:Xaa)                        |
| FT      | /note= "Xaa = any amino acid"                                   |
| XX      |   |
| PN      | WO200214498-A2.   |
| XX      |   |
| PD      | 21-FEB-2002.  |
| XX      |   |
| PF      | 15-AUG-2001; 2001WO-US25650.                                    |
| XX      |   |
| PR      | 16-AUG-2000; 2000US-225989P.                                    |
| XX      |   |
| PA      | (LEXI-) LEXICON GENETICS INC.                                   |
| XX      |   |

The present sequence is a cDNA encoding novel human protein (NHP), ion channel protein. NHP share structural similarity with mammalian sodium channel proteins particularly voltage-gated sodium channel proteins. NHP oligonucleotides are useful as hybridisation probes for screening libraries and assessing gene expression patterns. Sequences derived from regions adjacent to the intron/exon boundaries of NHP gene can be used to design primers for use in amplification assays to detect mutations within the exons, splice sites, introns that can be used in diagnostics and pharmacogenomics. NHP nucleotide sequences are useful for drug screening effective in the treatment of symptomatic or phenotypic manifestations of perturbing the normal function of NHP in the body, and nucleotide constructs encoding NHP products are useful to genetically engineer host cells to express NHP products *in vivo*. These delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion protein to the body. Nucleotide construct encoding NHP products are also useful in gene therapy for modulating NHP expression and to produce genetically engineered host cells to express NHP products *in vivo*. NHP nucleotide sequences may also be used as part of ribozyme and/or triple helix sequences that are useful for NHP gene regulation. The NHP polypeptides are useful for generating antibodies, as reagents in diagnostic assays, for identifying other cellular gene products related to NHP and as reagents in assays for screening compounds that are useful in the treatment of mental, biological or medical disorders and diseases.

|         |       |              |    |            |    |        |    |      |   |
|---------|-------|--------------|----|------------|----|--------|----|------|---|
| Matches | 4152; | Conservative | 0; | Mismatches | 0; | Indels | 0; | Cons | 0 |
|---------|-------|--------------|----|------------|----|--------|----|------|---|

0' gbps

y 1 ATGAGGCAAAAGAGCTTGTACCAACAGGACCTTCAACCTTCCACCAAGAA 60  
 |||||  
 Db 1 ATGAGCAAAAGAGCTTGTACCAACAGGACCTTCAACCTTCCACCAAGAA 60  
 |||||

[illegible]

|    |     |   |     |
|----|-----|---|-----|
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| Db | 121 | AAAAAAAAATACGACGAAATATGGCGCCCAACCAAAATGTACATTGGAACTGGAAAGAC | 180 |

y7 161 CTTCACATTTATTTATGAGACATTCCTCCAGAAATGCTGCAGAGCCCTCGAGGACCTG 240  
 |||||  
 Db 181 CTTCACATTTATTTATGAGACATTCCTCCAGAAATGCTGCAGAGCCCTCGAGGACCTG 240  
 |||||

| Accession | Sequence   | Length |
|-----------|--|--------|
| U1        | GAACCTACTATTCATTAAGAAACTTTTATAGTTCATTAAGGAAGCCATCTTC | 300    |
| U2        |  |        |
| U3        |  |        |
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| U5        |  |        |
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| U16       |  |        |
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| U18       |  |        |
| U19       |  |        |
| U20       |  |        |
| U21       | GAACCTACTATTCATTAAGAAACTTTTATAGTTCATTAAGGAAGCCATCTTC | 300    |
| U22       |  |        |
| U23       |  |        |
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| U99       |  |        |
| U100      |  |        |

[illegible][illegible]

Db 421 AACTGTTGTTATGACATGATGTAACCTCTGATTTGACAAAGATGTAGAAATCACC 480  
Oy 481 TTCACAGAAATATATACCTTTTGAATCATTATATAAATATATGCAAGGGGATTCGTCTTA 540  
Db 481 TTCACAGAAATATATACCTTTTGAATCATTATATAAATATATGCAAGGGGATTCGTCTTA 540  
Oy 541 GAAGATTTTACTCTCTCTGCGGATTCAGTAACTGGCTGATTTTCACTCTCATTTACATTT 600  
Db 541 GAAGATTTTACTCTCTCTGCGGATTCAGTAACTGGCTGATTTTCACTCTCATTTACATTT 600  
Oy 601 GCGTACGTCACAGAGTTTGTGACCGCGCAATGCTCCGCAATTTGAGAACATTCACAGATT 660  
Db 601 GCGTACGTCACAGAGTTTGTGACCGCGCAATGCTCCGCAATTTGAGAACATTCACAGATT 660  
Oy 661 CTCGAGCAATTTGAGACGATTTCACTCATTTCCAGGCTTGAACCACTTTGTGGAGCCCTG 720  
Db 661 CTCGAGCAATTTGAGACGATTTCACTCATTTCCAGGCTTGAACCACTTTGTGGAGCCCTG 720  
Oy 721 ATCCAGTCTGTGTAAGAAAGCTCTCAGATTTATGATGATGATGATGATGATGATGATGAT 780  
Db 721 ATCCAGTCTGTGTAAGAAAGCTCTCAGATTTATGATGATGATGATGATGATGATGATGAT 780  
Oy 781 TTTGCTATATTTGGCTGACGCTGTTCAATGCGCAACCTGAGAAATATATATACATG 840  
Db 781 TTTGCTATATTTGGCTGACGCTGTTCAATGCGCAACCTGAGAAATATATATACATG 840  
Oy 841 CCTCCACCAATGCTTCTCTTGGAGAACTATATAGAAAGAAATATATCTGATTTAT 900  
Db 841 CCTCCACCAATGCTTCTCTTGGAGAACTATATAGAAAGAAATATATCTGATTTAT 900  
Oy 901 AATGATACCTTATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960  
Db 901 AATGATACCTTATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960  
Oy 961 TCAAGATATCATTTATTTCTGAGAGGTTTTTATGATGATGATGATGATGATGATGATGAT 1020  
Db 961 TCAAGATATCATTTATTTCTGAGAGGTTTTTATGATGATGATGATGATGATGATGATGAT 1020  
Oy 1021 GATGAGGCGCAATGTCACAGAGGATATATGATGATGATGATGATGATGATGATGAT 1080  
Db 1021 GATGAGGCGCAATGTCACAGAGGATATATGATGATGATGATGATGATGATGATGAT 1080  
Oy 1081 GCGTACACAGCTTTGATACCTTCACTGATGATGATGATGATGATGATGATGATGAT 1140  
Db 1081 GCGTACACAGCTTTGATACCTTCACTGATGATGATGATGATGATGATGATGATGAT 1140  
Oy 1141 CAGGACTTCTGGAAGAAATCTTTATCAAGTACATTTAGCTGCTGGAAAAAGTACATG 1200  
Db 1141 CAGGACTTCTGGAAGAAATCTTTATCAAGTACATTTAGCTGCTGGAAAAAGTACATG 1200  
Oy 1201 AATATTTTGTGTGTCATTTTCTTGGGCTCATTTCTACCTAATTAATTTGATCTGCT 1260  
Db 1201 AATATTTTGTGTGTCATTTTCTTGGGCTCATTTCTACCTAATTAATTTGATCTGCT 1260  
Oy 1261 GTGATGCGCATGCGCTTACAGAGAAAGAAATCAGGCGCACTTTGAAAGAGAGAAAGAA 1320  
Db 1261 GTGATGCGCATGCGCTTACAGAGAAAGAAATCAGGCGCACTTTGAAAGAGAGAAAGAA 1320  
Oy 1321 GAGGCGCAATTTTACAGAGATGATTTGAACAGCTTAAAAAGCAAGAGAGAGAGAGAGAG 1380  
Db 1321 GAGGCGCAATTTTACAGAGATGATTTGAACAGCTTAAAAAGCAAGAGAGAGAGAGAGAG 1380  
Oy 1381 GCAGCAAGGCGCACTGCTTACAGAGATTTCCAGAGAGAGAGAGAGAGAGAGAGAGAG 1440  
Db 1381 GCAGCAAGGCGCACTGCTTACAGAGATTTCCAGAGAGAGAGAGAGAGAGAGAGAGAG 1440  
Oy 1441 GACAGTCAATTCAGAGAGCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAA 1500  
Db 1441 GACAGTCAATTCAGAGAGCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAA 1500  
Oy 1501 AGGAAAGAAAGAAAG 1560  
Db 1501 AGGAAAGAAAGAAAG 1560

Oy 1561 CAAAATCTGATCTGAG 1620  
Db 1561 CAAAATCTGATCTGAG 1620  
Oy 1621 AACCGATGATATGAAAG 1680  
Db 1621 AACCGATGATATGAAAG 1680  
Oy 1681 GGCCTCCATTTTTCACCAAGGCGAAATAGCAGAAACAGGCTTTTACGCTTTAGAGGGCGA 1740  
Db 1681 GGCCTCCATTTTTCACCAAGGCGAAATAGCAGAAACAGGCTTTTACGCTTTAGAGGGCGA 1740  
Oy 1741 GCAAG 1800  
Db 1741 GCAAG 1800  
Oy 1801 AACGAG 1860  
Db 1801 AACGAG 1860  
Oy 1861 AACCTGATGACAG 1920  
Db 1861 AACCTGATGACAG 1920  
Oy 1921 ATGCAAG 1980  
Db 1921 ATGCAAG 1980  
Oy 1981 AATGAG 2040  
Db 1981 AATGAG 2040  
Oy 2041 AATGAG 2100  
Db 2041 AATGAG 2100  
Oy 2101 ATGAGATTTCTGAAAGATCTTCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2160  
Db 2101 ATGAGATTTCTGAAAGATCTTCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2160  
Oy 2161 ACNAATACAGATGAG 2220  
Db 2161 ACNAATACAGATGAG 2220  
Oy 2221 TTTTCAACATATTTTAACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2280  
Db 2221 TTTTCAACATATTTTAACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2280  
Oy 2281 GTCAACCTGATGATGAG 2340  
Db 2281 GTCAACCTGATGATGAG 2340  
Oy 2341 AATACCTTTTCAATGAG 2400  
Db 2341 AATACCTTTTCAATGAG 2400  
Oy 2401 ACAGTAG 2460  
Db 2401 ACAGTAG 2460  
Oy 2461 GGCATGATCTTACATTTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAA 2520  
Db 2461 GGCATGATCTTACATTTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAA 2520  
Oy 2521 AACCTTACCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAA 2580  
Db 2521 AACCTTACCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAA 2580  
Oy 2581 TTTGATGCTGAG 2640  
Db 2581 TTTGATGCTGAG 2640

|    |      |  |      |
|----|------|--|------|
| OY | 2641 | AAATCATGTGGCAATTCGGTGGGGGCTGTGGAAATTTAAACCTCGTCTTGCGCATCATC  | 2700 |
|    |      |  |      |
| Db | 2641 | AAATCATGTGGCAATTCGGTGGGGGCTGTGGAAATTTAAACCTCGTCTTGCGCATCATC  | 2700 |
| OY | 2701 | GTCTTCATTTTGGCCGTGGTGGGATCGACATCTTTGGTAAAGCTACAAAGATTTGTGC   | 2760 |
| Db | 2701 | GTCTTCATTTTGGCCGTGGTGGGATCGACATCTTTGGTAAAGCTACAAAGATTTGTGC   | 2760 |
| OY | 2761 | TGCAAGATCGCAGATGTTCACATCCACGCTGGGCACATGATGATCTTTCACATCC      | 2820 |
| Db | 2761 | TGCAAGATCGCAGATGTTCACATCCACGCTGGGCACATGATGATCTTTCACATCC      | 2820 |
| OY | 2821 | TTTCCGATTTGGTCCCGGTGGTCTGTGGGGAGTGGATAGACACATGTGGGACGTATG    | 2880 |
| Db | 2821 | TTTCCGATTTGGTCCCGGTGGTCTGTGGGGAGTGGATAGACACATGTGGGACGTATG    | 2880 |
| OY | 2881 | GAGGTGTGGTGCACAGCCATGTGGCTTACTGTCTCATGTGGTCAATGGTGTATGGAAC   | 2940 |
| Db | 2881 | GAGGTGTGGTGCACAGCCATGTGGCTTACTGTCTCATGTGGTCAATGGTGTATGGAAC   | 2940 |
| OY | 2941 | CTATGTGTCTGGAATCTCTTCTTGGCCCTTGTAGCTCATTTAGTGCAGACAACTT      | 3000 |
| Db | 2941 | CTATGTGTCTGGAATCTCTTCTTGGCCCTTGTAGCTCATTTAGTGCAGACAACTT      | 3000 |
| OY | 3001 | GGAGCCACTGATGATGATTAATGAAATGAAATTAATCTCCAAATTTGTGGATAGATGCAC | 3060 |
| Db | 3001 | GGAGCCACTGATGATGATTAATGAAATGAAATTAATCTCCAAATTTGTGGATAGATGCAC | 3060 |
| OY | 3061 | AAAGAGTAGCTTTATGTGAAAGAAATTTATGATTTATTCACACTCCCTCATTTAGG     | 3120 |
| Db | 3061 | AAAGAGTAGCTTTATGTGAAAGAAATTTATGATTTATTCACACTCCCTCATTTAGG     | 3120 |
| OY | 3121 | AAACAAAGATTTTATGATGAATTTAAACACTGTGATCTTAACACAGAAAGACAGT      | 3180 |
| Db | 3121 | AAACAAAGATTTTATGATGAATTTAAACACTGTGATCTTAACACAGAAAGACAGT      | 3180 |
| OY | 3181 | TGTATGTCCATCTATACARAGAAATTTGGGAAAGATCTTGACTATCTTTAAAGATGTAA  | 3240 |
| Db | 3181 | TGTATGTCCATCTATACARAGAAATTTGGGAAAGATCTTGACTATCTTTAAAGATGTAA  | 3240 |
| OY | 3241 | GGAACTACAACTGGTATATAGCACTGGGAGAGAGTTGAAAAATCATATATGATGAAGT   | 3300 |
| Db | 3241 | GGAACTACAACTGGTATATAGCACTGGGAGAGAGTTGAAAAATCATATATGATGAAGT   | 3300 |
| OY | 3301 | GATTACATGTCAATCATTAACAAACCCAGCTTACTGTGACTGTACCAATTTGCTGTAGA  | 3360 |
| Db | 3301 | GATTACATGTCAATCATTAACAAACCCAGCTTACTGTGACTGTACCAATTTGCTGTAGA  | 3360 |
| OY | 3361 | GAATCTGACTTTGAAAAATTTAAACACGGAAACCTTATAGTGAATCGGATCTGGAGAA   | 3420 |
| Db | 3361 | GAATCTGACTTTGAAAAATTTAAACACGGAAACCTTATAGTGAATCGGATCTGGAGAA   | 3420 |
| OY | 3421 | AGCAAAAGAAACGATGAAAGACAGTACTCATCAGAAAGGATCAGCTGTGGACATCGC    | 3480 |
| Db | 3421 | AGCAAAAGAAACGATGAAAGACAGTACTCATCAGAAAGGATCAGCTGTGGACATCGC    | 3480 |
| OY | 3481 | GCACCTGTAGAAACAGCCCGTAGTGGAACTGGAAGAACTTTGAACACGAGCTGT       | 3540 |
| Db | 3481 | GCACCTGTAGAAACAGCCCGTAGTGGAACTGGAAGAACTTTGAACACGAGCTGT       | 3540 |
| OY | 3541 | TTTCCGATTTGGTCCCGGTGGTCTGTGGGGAGTGGATAGACACATGTGGGACGTATG    | 3600 |
| Db | 3541 | TTTCCGATTTGGTCCCGGTGGTCTGTGGGGAGTGGATAGACACATGTGGGACGTATG    | 3600 |
| OY | 3601 | GGAAACAAATGTGTGAACTCGAAGAGAGAGTGTTCGCAATAGTTGAACATTAATCGTTT  | 3660 |
| Db | 3601 | GGAAACAAATGTGTGAACTCGAAGAGAGAGTGTTCGCAATAGTTGAACATTAATCGTTT  | 3660 |
| OY | 3661 | GAGACCTTCATTTGTTTCATGATTTCTCTTATGATGTGTCTGCGCATTTGAAGATATA   | 3720 |
| Db | 3661 | GAGACCTTCATTTGTTTCATGATTTCTCTTATGATGTGTCTGCGCATTTGAAGATATA   | 3720 |
| OY | 3721 | TATATGTATGAGGAAGACGATTAAGACGATTTTGAATATGTCTGCACAGTTTTTCACT   | 3780 |

| Db       | 3721   | TATATTGATCGACGGAAGACGATTAAAGCATGTGGATATATCTACAAAGTTTCAC    | 3780 |
|----------|--|--|------|
| Oy       | 3781   | TGACATTTTCATTCGGAATGCTTCTAAAAATGGGTGGCATATGCTATCAACATATTTG | 3840 |
| Db       | 3781   | TACATTTTCATTCGGAATGCTTCTAAAAATGGGTGGCATATGCTATCAACATATTTG  | 3840 |
| Oy       | 3841   | ACCAATGCGTGTGGCTGGAGATCTCTTAATGTTGATGTTTCATTTGGTCAAGTTTAA  | 3900 |
| Db       | 3841   | ACCAATGCGTGTGGCTGGAGATCTCTTAATGTTGATGTTTCATTTGGTCAAGTTTAA  | 3900 |
| Oy       | 3901   | GCAAAATGCGTGTGGCTGGAGATCTCTTAATGTTGATGTTTCATTTGGTCAAGTTTAA | 3960 |
| Db       | 3901   | GCAAAATGCGTGTGGCTGGAGATCTCTTAATGTTGATGTTTCATTTGGTCAAGTTTAA | 3960 |
| Oy       | 3961   | CTGAGACTCTTAAGAGCTTATCTCGATTGTAAGAGGATGAGGATGAGTGAATCCCTT  | 4020 |
| Db       | 3961   | CTGAGACTCTTAAGAGCTTATCTCGATTGTAAGAGGATGAGGATGAGTGAATCCCTT  | 4020 |
| Oy       | 4021   | TTAGAGCAATTCATCCATCATGAAATGCTCTGCTGTTGCTTAATATCTGCTAAT     | 4080 |
| Db       | 4021   | TTAGAGCAATTCATCCATCATGAAATGCTCTGCTGTTGCTTAATATCTGCTAAT     | 4080 |
| Oy       | 4081   | TTGAGCATCATGAGGCGTAATTTGTTGCTGCGAAATTTACACTGATTAAACGACA    | 4140 |
| Db       | 4081   | TTGAGCATCATGAGGCGTAATTTGTTGCTGCGAAATTTACACTGATTAAACGACA    | 4140 |
| Oy       | 4141   | ACTGCTGACAGG 4152  |      |
| Db       | 4141   | ACTGCTGACAGG 4152  |      |
| RESULT 8 |  |  |      |
| AD32848  |  |  |      |
| ID       | AD32848  | standard; cDNA; 4197 BP.                                   |      |
| AC       | AD32848;   |  |      |
| XX       |  |  |      |
| DT       | 01-JUL-2002  | (first entry)  |      |
| XX       |  |  |      |
| DE       | Human ion channel cDNA #10.  |  |      |
| KW       | Human; novel human protein; NMP; voltage-gated sodium channel;     |  |      |
| KW       | gene therapy; bioreactor; mental disorder; biological disorder;    |  |      |
| KW       | gene; medical disorder; ss.  |  |      |
| XX       |  |  |      |
| OS       | Homo sapiens.  |  |      |
| XX       |  |  |      |
| Key      |  |  |      |
| FT       | 1..4197  | Location/Qualifiers  |      |
| FT       | CDS  |  |      |
| FT       | /tag= "a   |  |      |
| FT       | /product= "Human ion channel protein #10"                          |  |      |
| FT       | /transl_except= (pos:2974..2976, aa:Xaa)                           |  |      |
| FT       | /transl_except= (pos:3199..3201, aa:Xaa)                           |  |      |
| FT       | /note= "Xaa = any amino acid"                                      |  |      |
| PN       | W0200214498-A2.  |  |      |
| XX       |  |  |      |
| XX       | 21-FEB-2002.   |  |      |
| PD       |  |  |      |
| XX       |  |  |      |
| PF       | 15-AUG-2001; 2001WO-US25650.                                       |  |      |
| XX       |  |  |      |
| PR       | 16-AUG-2000; 2000US-225989P.                                       |  |      |
| XX       |  |  |      |
| PA       | (LEXI-) LEXICON GENETICS INC.                                      |  |      |
| XX       |  |  |      |
| PI       | Turner CA, Mathur B, Mathur D;                                     |  |      |
| XX       |  |  |      |
| DR       | WPI; 2002-280757/32.   |  |      |
| XX       |  |  |      |
| DR       | P-PSDB; AAE20519.  |  |      |
| XX       |  |  |      |
| PT       | Novel polynucleotides encoding human sodium channel proteins,      |  |      |
| PT       | particularly voltage-gated sodium channel proteins useful for drug |  |      |

|    |  |
|----|--|
| PT | screening, diagnosis and in gene therapy of biological disorders |
| XX |  |
| PS | Claim 1; Page 78-79; 83pp; English.                              |

The present sequence is a cDNA encoding novel human protein (NHP). Ion channel protein. NHP share structural similarity with mammalian sodium channel proteins particularly voltage-gated sodium channel proteins. NHP oligonucleotides are useful as hybridisation probes for screening libraries and assessing gene expression patterns. Sequences derived from regions adjacent to the intron/exon boundaries of NHP gene can be used to design primers for use in amplification assays to detect mutations within the exons, splice sites, introns that can be used in diagnostics and pharmacogenomics. NHP nucleotide sequences are useful for drug screening effective in the treatment of symptomatic or phenotypic manifestations of perturbing the normal function of NHP in the body, and nucleotide constructs encoding NHP products are useful to genetically engineer host cells to express NHP products *in vivo*. These genetically engineered cells function as bioreactors in the body delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion protein to the body. Nucleotide construct encoding NHP products are also useful in gene therapy for modulating NHP expression and to produce genetically engineered host cells to express NHP products *in vivo*. NHP nucleotide sequences may also be used as part of ribozyme and/or triple helix sequences that are useful for NHP gene regulation. The NHP polypeptides are useful for generating antibodies, as reagents in diagnostic assays, for identifying other cellular gene products related to NHP and as reagents in assays for screening for compounds that are useful in the treatment of mental, biological or medical disorders and diseases.

SQ Sequence 4197 BP; 1232 A; 821 C; 965 G; 1176 T; 3 other;

| Query Match | Score | DB  | Length |
|-------------|-------|-----|--------|
| 66.48;      | 4003; | 24; | 4197;  |

Matches 4003; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|    |     |   |     |
|----|-----|---|-----|
| OY | 1   | ATNAGGAAAGAGGCTTGTCACACAGGAGCTGCAGCTTCAACTCTTCACACAGAA        | 60  |
| OY | 1   | ATNAGGAAAGAGGCTTGTCACACAGGAGCTGCAGCTTCAACTCTTCACACAGAA        | 60  |
| Db | 1   | ATNGGCAAAAGAGCTTGTCACACAGGAGCTGCAGCTTCAACTCTTCACACAGAA        | 60  |
| OY | 61  | TCTCTGGGCGCTATTGGAAGAGCGATTCGAGAGAAAAAGGCCAAGATTCGCAACGAGAC   | 120 |
| Db | 61  | TCTCTGGGCGCTATTGGAAGAGCGATTCGAGAGAAAAAGGCCAAGATTCGCAACGAGAC   | 120 |
| OY | 121 | AAAAAGATGAGCAGCAAAATGCGCCAAAGCCAAATAGTGACTTGGAGCTGCAAGAAC     | 180 |
| Db | 121 | AAAAAGATGAGCAGCAAAATGCGCCAAAGCCAAATAGTGACTTGGAGCTGCAAGAAC     | 180 |
| OY | 181 | CTTCATTATTATTATGAGAGATTCCTCCAGAGTGGTGCACAGCGCCCTGGAGGACCTG    | 240 |
| Db | 181 | CTTCATTATTATTATGAGAGATTCCTCCAGAGTGGTGCACAGCGCCCTGGAGGACCTG    | 240 |
| OY | 241 | GACCCCTACTATATCAATAAAGAAAACCTTTATAGTAAATTAAGGAGGCATCTTC       | 300 |
| Db | 241 | GACCCCTACTATATCAATAAAGAAAACCTTTATAGTAAATTAAGGAGGCATCTTC       | 300 |
| OY | 301 | CGGTCAGTGCACACTCGCCCTGTACATTTTAACTCCCTCAATCCTTTAGGAAAATA      | 360 |
| Db | 301 | CGGTCAGTGCACACTCGCCCTGTACATTTTAACTCCCTCAATCCTTTAGGAAAATA      | 360 |
| OY | 361 | GCTATTAAAGATTGGTACATTCATATTACAGACGCTAATTATGTGACTATTTTACA      | 420 |
| Db | 361 | GCTATTAAAGATTGGTACATTCATATTACAGACGCTAATTATGTGACTATTTTACA      | 420 |
| OY | 421 | AACCTGTGATTATACAGATGAGTAACTCCATATTGGACAAAAGAAATGTAATTAACC     | 480 |
| Db | 421 | AACCTGTGATTATACAGATGAGTAACTCCATATTGGACAAAAGAAATGTAATTAACC     | 480 |
| OY | 481 | TTCCACAGAAATATACATTTTGAATCACTTTAAAAAATATTCGAAGGGCACTTCGTTTA   | 540 |
| Db | 481 | TTCCACAGAAATATACATTTTGAATCACTTTAAAAAATATATTCGAAGGGCACTTCGTTTA | 540 |
| OY | 541 | GAGATTTTACTTCCTTGGGAGATCATGAACTGGCTCGATTCACCTCATTTACAATT      | 600 |

|    |      |   |      |
|----|------|---|------|
| Db | 541  | GAAGATTTTACTTCCCTGGGATCCATGGAACTGGCTCGAATTCACGTCAATTAATTT     | 600  |
| QY | 601  | GCGTAGCTCAGAGAGTTTGTGGACCTGGGCAATGTCTCGCATTTGAGAACTTCAGATT    | 660  |
| Db | 601  | GCGTAGCTCAGAGAGTTTGTGGACCTGGGCAATGTCTCGCATTTGAGAACTTCAGATT    | 660  |
| QY | 661  | CTCCGACATTTGAAGAGATTCAGATTCAGATTCAGACCTGGAAGAACATTTGGAGCCCTG  | 720  |
| Db | 661  | CTCCGACATTTGAAGAGATTCAGATTCAGATTCAGACCTGGAAGAACATTTGGAGCCCTG  | 720  |
| QY | 721  | ATCCAGCTGTGGAAGAAGCTCTCAGATGTATATGATCCTGACTGTCTGTCTGAGCGTA    | 780  |
| Db | 721  | ATCCAGCTGTGGAAGAAGCTCTCAGATGTATATGATCCTGACTGTCTGTCTGAGCGTA    | 780  |
| QY | 781  | TTTGTCTGTAAATGGGCTGCAGCTGTTCATGGGCCAACCTGAGGAATAAATGTATCAATGC | 840  |
| Db | 781  | TTTGTCTGTAAATGGGCTGCAGCTGTTCATGGGCCAACCTGAGGAATAAATGTATCAATGC | 840  |
| QY | 841  | CCCTCCACACATGCTTCCCTGGAGGAACATTAATATGAAAAGAAATATTAACGTGAATAT  | 900  |
| Db | 841  | CCCTCCACACATGCTTCCCTGGAGGAACATTAATATGAAAAGAAATATTAACGTGAATAT  | 900  |
| QY | 901  | AATGTAACACTTATTAATATGAATCTGCTTGTAGTTGATGAGATCAATATATCAAGAT    | 960  |
| Db | 901  | AATGTAACACTTATTAATATGAATCTGCTTGTAGTTGATGAGATCAATATATCAAGAT    | 960  |
| QY | 961  | TCAAGATATCATATATTTTCCGAGAGGTTTTTTAGATGACACTATGTGGAATAGCTCT    | 1020 |
| Db | 961  | TCAAGATATCATATATTTTCCGAGAGGTTTTTTAGATGACACTATGTGGAATAGCTCT    | 1020 |
| QY | 1021 | GATGACAGCCCAATGCTCCAGAGGATATATGTGTGTAAGACTGGTAGAAATCCCAATAT   | 1080 |
| Db | 1021 | GATGACAGCCCAATGCTCCAGAGGATATATGTGTGTAAGACTGGTAGAAATCCCAATAT   | 1080 |
| QY | 1081 | GGCTACACAACTTGTATACCTCAATGGGCTTTTCTCTGTTCGACTATGACT           | 1140 |
| Db | 1081 | GGCTACACAACTTGTATACCTCAATGGGCTTTTCTCTGTTCGACTATGACT           | 1140 |
| QY | 1141 | CAGGACTTCTGGGAAATCTTTATCAACTGACATTAACGTCTGCTGGGAAAAACGTACATG  | 1200 |
| Db | 1141 | CAGGACTTCTGGGAAATCTTTATCAACTGACATTAACGTCTGCTGGGAAAAACGTACATG  | 1200 |
| QY | 1201 | ATATTTTGTGTGTCATTTCTTGGGCTACTTCTACCTAATTAATTTGATCTGGCT        | 1260 |
| Db | 1201 | ATATTTTGTGTGTCATTTCTTGGGCTACTTCTACCTAATTAATTTGATCTGGCT        | 1260 |
| QY | 1261 | GTGGTGGCATGGGCTTCAGAGGAACGAATCAGGCCACTTGGAGAAAGCAGAACAGAA     | 1320 |
| Db | 1261 | GTGGTGGCATGGGCTTCAGAGGAACGAATCAGGCCACTTGGAGAAAGCAGAACAGAA     | 1320 |
| QY | 1321 | GAGGCGGAATTTACAGAGATGATTTGAACAGCTTAAAAAACACAGAGGACAGCTCAGAG   | 1380 |
| Db | 1321 | GAGGCGGAATTTACAGAGATGATTTGAACAGCTTAAAAAACACAGAGGACAGCTCAGAG   | 1380 |
| QY | 1381 | GCAGCACGCGCACTGCCCTAGAACATTCAGAGACCCAGTGCAGCAGGACGCTCTCA      | 1440 |
| Db | 1381 | GCAGCACGCGCACTGCCCTAGAACATTCAGAGACCCAGTGCAGCAGGACGCTCTCA      | 1440 |
| QY | 1441 | GACACCTCATCGAAGCCTCAAGTTAGTTCAGAGGTCCAGAGGTCAAGGAAAGAAATGCG   | 1500 |
| Db | 1441 | GACACCTCATCGAAGCCTCAAGTTAGTTCAGAGGTCCAGAGGTCAAGGAAAGAAATGCG   | 1500 |
| QY | 1501 | AGGAGAAAGAAAAAGAAAGAGACATCTGTGTGGGGAAGAGAAAGATGAGATGAATTC     | 1560 |
| Db | 1501 | AGGAGAAAGAAAAAGAAAGAGACATCTGTGTGGGGAAGAGAAAGATGAGATGAATTC     | 1560 |
| QY | 1561 | CAAAAATCTGAATCTGAGAGCAGCATCAGAGGAAAGTTTGTGCTTCTCATTTAGAGG     | 1620 |
| Db | 1561 | CAAAAATCTGAATCTGAGAGCAGCATCAGAGGAAAGTTTGTGCTTCTCATTTAGAGG     | 1620 |
| QY | 1621 | AACGATTCACATATGAAAAGAGTACTCTCCGCCACACAGCTTGTGTGACATCGGT       | 1680 |
| Db | 1621 | AACGATTCACATATGAAAAGAGTACTCTCCGCCACACAGCTTGTGTGACATCGGT       | 1680 |



Db 1621 AACGATTCATATGAAAAAGAGTACCTCCGCCACACCACTCTTTGTGACATCCGT 1680  
 QY 1681 GCGTCCCTATTTTCACCAAGCGGAATACAGAACAGCTTTTACGTTTAGAGGGCGA 1740  
 Db 1681 GCGTCCCTATTTTCACCAAGCGGAATACAGAACAGCTTTTACGTTTAGAGGGCGA 1740  
 QY 1741 GCAAGAGATGTGGGATCTGAGAACACTTCGAGATGATGACACACGCTTTGAGAT 1800  
 Db 1741 GCAAGAGATGTGGGATCTGAGAACACTTCGAGATGATGACACACGCTTTGAGAT 1800  
 QY 1801 AACGAGACCGGTAGAGATTCCTTTGTTGTGCCGACGACGAGAGAGAGACCAACG 1860  
 Db 1801 AACGAGACCGGTAGAGATTCCTTTGTTGTGCCGACGACGAGAGAGAGACCAACG 1860  
 QY 1861 AACCTGAGTCAGACAGATGATCCGGATGCTGGCAGTGTTCACGCGAATGGGAAG 1920  
 Db 1861 AACCTGAGTCAGACAGATGATCCGGATGCTGGCAGTGTTCACGCGAATGGGAAG 1920  
 QY 1921 ATGCAACGACGCTGAGATTCGCAATGTGTGTGTCTGTGTGTGTGTGTGTGTGTGT 1980  
 Db 1921 ATGCAACGACGCTGAGATTCGCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1980  
 QY 1981 ACATGCGCTGTGTGACACCTCTGCGCAGAGGTATATGATATGACGCTACTGATGAC 2040  
 Db 1981 ACATGCGCTGTGTGACACCTCTGCGCAGAGGTATATGATATGACGCTACTGATGAC 2040  
 QY 2041 AATGACACACCACTGAAATGTAATGAAAGAGAGAGAGTCTTTCACGCTTCC 2100  
 Db 2041 AATGACACACCACTGAAATGTAATGAAAGAGAGAGAGTCTTTCACGCTTCC 2100  
 QY 2101 ATGACCTTTCTAGAGATTCCTCCCAAGGACAGACGAGATATGACGACCTTCTA 2160  
 Db 2101 ATGACCTTTCTAGAGATTCCTCCCAAGGACAGACGAGATATGACGACCTTCTA 2160  
 QY 2161 ACAATACAGTAGAAGACTGGAAGATCCAGGACGAGAAATGCCCTGTGTGGATATA 2220  
 Db 2161 ACAATACAGTAGAAGACTGGAAGATCCAGGACGAGAAATGCCCTGTGTGGATATA 2220  
 QY 2221 TTTTCCACATATTTCTTATATCTGGACCTGTCTCCATATGTTGTTAAAGTAAACATGT 2280  
 Db 2221 TTTTCCACATATTTCTTATATCTGGACCTGTCTCCATATGTTGTTAAAGTAAACATGT 2280  
 QY 2281 GTCAACCGGTGTGATGAGGACCACTTGTGACCGGCGCACACCATCTGATGTCTTA 2340  
 Db 2281 GTCAACCGGTGTGATGAGGACCACTTGTGACCGGCGCACACCATCTGATGTCTTA 2340  
 QY 2341 AATACCTTTTTCATGAGGACGACATATCAATGACGACCAATTCATATATGTGCTT 2400  
 Db 2341 AATACCTTTTTCATGAGGACGACATATCAATGACGACCAATTCATATATGTGCTT 2400  
 QY 2401 ACAGTAGAAGACTGTGTTTCACTGAGATCTTACAGACGAAATGTTCTGAAATATAT 2460  
 Db 2401 ACAGTAGAAGACTGTGTTTCACTGAGATCTTACAGACGAAATGTTCTGAAATATAT 2460  
 QY 2461 GCCATGATCCTTACTATTTATTTCCAGAAAGGCGTAATATCTTGACGGTTTATGTG 2520  
 Db 2461 GCCATGATCCTTACTATTTATTTCCAGAAAGGCGTAATATCTTGACGGTTTATGTG 2520  
 QY 2521 ACAGTAGAAGACTGTGTTTCACTGAGATCTTACAGACGAAATGTTCTGAAATATAT 2580  
 Db 2521 ACAGTAGAAGACTGTGTTTCACTGAGATCTTACAGACGAAATGTTCTGAAATATAT 2580  
 QY 2581 TTTTGCATTTGCTGAGATTTTCACTGAGATCTTACAGACGAAATGTTCTGAAATATAT 2640  
 Db 2581 TTTTGCATTTGCTGAGATTTTCACTGAGATCTTACAGACGAAATGTTCTGAAATATAT 2640  
 QY 2641 AACATCATCGGCAATTCCTGAGGAGGCTCTGGAATATTAACCTGCTTGCCATATC 2700  
 Db 2641 AACATCATCGGCAATTCCTGAGGAGGCTCTGGAATATTAACCTGCTTGCCATATC 2700  
 QY 2701 GTCTTCATTTTGTGCGGTGTGCGCATGACCTTTTGTGTAAGAGTAAAGATGTGTG 2760  
 Db 2701 GTCTTCATTTTGTGCGGTGTGCGCATGACCTTTTGTGTAAGAGTAAAGATGTGTG 2760

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QY 2761 TGCAGATGCCAGATGATTTGTCACTCCAGCGTGGCACATGATGATCTTCCATCC 2820  
 Db 2761 TGCAGATGCCAGATGATTTGTCACTCCAGCGTGGCACATGATGATCTTCCATCC 2820  
 QY 2821 TTTCTGATTTGTGTTCCGCGTGTGTGTGGGAGTGTAGAGACATGTGGGACTGTATG 2880  
 Db 2821 TTTCTGATTTGTGTTCCGCGTGTGTGTGGGAGTGTAGAGACATGTGGGACTGTATG 2880  
 QY 2881 GAGGTGCTGGTCAAGCAGTGTGCTTACTGTCTTATGATGTCTGTGTGTGTGTGTGT 2940  
 Db 2881 GAGGTGCTGGTCAAGCAGTGTGCTTACTGTCTTATGATGTCTGTGTGTGTGTGTGT 2940  
 QY 2941 CTAGTGTCTGATCTCTTCTGCGCTTGTCTTGTAGTGTGTGTGTGTGTGTGTGTGT 3000  
 Db 2941 CTAGTGTCTGATCTCTTCTGCGCTTGTCTTGTAGTGTGTGTGTGTGTGTGTGTGT 3000  
 QY 3001 GCAAGCAGTGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3060  
 Db 3001 GCAAGCAGTGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3060  
 QY 3061 AAGAGATGT 3120  
 Db 3061 AAGAGATGT 3120  
 QY 3121 AAGCAAAAGATTTTGTAGATGATGATGATGATGATGATGATGATGATGATGATGAT 3180  
 Db 3121 AAGCAAAAGATTTTGTAGATGATGATGATGATGATGATGATGATGATGATGATGAT 3180  
 QY 3181 TGTATGTCCATCATACACAGCAAAATGTGGAAAGATCTTGTAGTCTTAAAGATTAAT 3240  
 Db 3181 TGTATGTCCATCATACACAGCAAAATGTGGAAAGATCTTGTAGTCTTAAAGATTAAT 3240  
 QY 3241 GGAATACAGAGT 3300  
 Db 3241 GGAATACAGAGT 3300  
 QY 3301 GATTCATGTCTATTTATTAACACCCAGCTTCTGACGTGTGTGTGTGTGTGTGTGTGT 3360  
 Db 3301 GATTCATGTCTATTTATTAACACCCAGCTTCTGACGTGTGTGTGTGTGTGTGTGTGT 3360  
 QY 3361 GATTCATGTCTATTTATTAACACCCAGCTTCTGACGTGTGTGTGTGTGTGTGTGTGT 3420  
 Db 3361 GATTCATGTCTATTTATTAACACCCAGCTTCTGACGTGTGTGTGTGTGTGTGTGTGT 3420  
 QY 3421 AGCAAGAGAAATCTGAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3480  
 Db 3421 AGCAAGAGAAATCTGAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3480  
 QY 3481 GCACCTGTAGAAAGACAGCCGCTAGTGAACCTGGAAGAACTTGAACCAAGACCTGT 3540  
 Db 3481 GCACCTGTAGAAAGACAGCCGCTAGTGAACCTGGAAGAACTTGAACCAAGACCTGT 3540  
 QY 3541 TTTACTGAGGCTGTGTCAAAAGATTTCAAGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3600  
 Db 3541 TTTACTGAGGCTGTGTCAAAAGATTTCAAGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3600  
 QY 3601 GGAAGAAAGATGT 3660  
 Db 3601 GGAAGAAAGATGT 3660  
 QY 3661 GAGACCTTCATTTGT 3720  
 Db 3661 GAGACCTTCATTTGT 3720  
 QY 3721 TATTTGTATCAGCAAGACATTAAGACAGATGATGATGATGATGATGATGATGATGAT 3780  
 Db 3721 TATTTGTATCAGCAAGACATTAAGACAGATGATGATGATGATGATGATGATGATGAT 3780  
 QY 3781 TACATTTTCATTTGT 3840  
 Db 3781 TACATTTTCATTTGT 3840





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|----|------|---|------|
| OY | 2884 | CGCGTGGTCAAGCATGTGCTTACTGTCTTCATGATGTCATGTGATTGAAACCTA          | 2943 |
| Db | 2851 | GTGTGTGTCAAGCCATGTGCTTACTGTCTTCATGATGTCATGTGATTGAAACCTA         | 2910 |
| OY | 2944 | GTGGCCCGAATCTCTTTCGCGCTGTGTMTGAGCATTTAGTGCAGACAAACCTTGCA        | 3003 |
| Db | 2911 | GTGGCCCGAATCTCTTTCGCGCTGTGTMTGAGCATTTAGTGCAGACAAACCTTGCA        | 2970 |
| OY | 3004 | GCCACTGATGATGATTAATGAATAATTCACAAATTCGCTGTGATAGATGCACAAA         | 3063 |
| Db | 2971 | GCCACTGATGATGATTAATGAATAATTCACAAATTCGCTGTGATAGATGCACAAA         | 3030 |
| OY | 3064 | GGAGTAGCTTATGTGAAAAGAAAATTTATGAATTTATCAACAGTCCTTCATTAGAAA       | 3123 |
| Db | 3031 | GGAGTAGCTTATGTGAAAAGAAAATTTATGAATTTATCAACAGTCCTTCATTAGAAA       | 3090 |
| OY | 3124 | CAAAAGATTTTATGATGAATAATTAACCCATGATGATATCAAAACAAAGAACAGTTGT      | 3183 |
| Db | 3091 | CAAAAGATTTTATGATGAATAATTAACCCATGATGATATCAAAACAAAGAACAGTTGT      | 3150 |
| OY | 3184 | ATGTCCATCATACARCAGAAATTTGGGAAGATCTTGACTATCTTTAAAGATGTAAATGGA    | 3243 |
| Db | 3151 | ATGTCCATCATACARCAGAAATTTGGGAAGATCTTGACTATCTTTAAAGATGTAAATGGA    | 3210 |
| OY | 3244 | ACTCAAGTGTATAGAACTGGCAGCAGTGTGAAAAATATCATTTATTTGATGAAGTAT       | 3303 |
| Db | 3211 | ACTCAAGTGTATAGAACTGGCAGCAGTGTGAAAAATATCATTTATTTGATGAAGTAT       | 3270 |
| OY | 3304 | TACATGTCAATTCATTAACAACCCCAAGTCTACGTGACCTGTACCAATTCCTGTAGAGAA    | 3363 |
| Db | 3271 | TACATGTCAATTCATTAACAACCCCAAGTCTACGTGACCTGTACCAATTCCTGTAGAGAA    | 3330 |
| OY | 3364 | TCGTACTTTGAAAAATTTTAAACACGGAAGACTTTTATGATGAATTCGGATCGGAAGAACG   | 3423 |
| Db | 3331 | TCGTACTTTGAAAAATTTTAAACACGGAAGACTTTTATGATGAATTCGGATCGGAAGAACG   | 3390 |
| OY | 3424 | AAAGAGAAATGATGATGAAGACATGACTATCAAGAGTAGACACTGTGACATCGCGCGA      | 3483 |
| Db | 3391 | AAAGAGAAATGATGATGAAGACATGACTATCAAGAGTAGACACTGTGACATCGCGCGA      | 3450 |
| OY | 3484 | CGTGTGAAGAAGAGCCCGTAGTGAACCGAAGAAACGTTGAAACACAGAGCTTTGTTTC      | 3543 |
| Db | 3451 | CGTGTGAAGAAGAGCCCGTAGTGAACCGAAGAAACGTTGAAACACAGAGCTTTGTTTC      | 3510 |
| OY | 3544 | ACTGAAGCGTGTGTACAAAGATTCAGATGTGTCAATCAATCAATGTGAAGAAGCAGAGA     | 3603 |
| Db | 3511 | ACTGAAGCGTGTGTACAAAGATTCAGATGTGTCAATCAATCAATGTGAAGAAGCAGAGA     | 3570 |
| OY | 3604 | AAACATATGATGGAACTGTGAAGAGAGCGTGTTCGGAATAGTTGAACATTAAGCTTTGAG    | 3663 |
| Db | 3571 | AAACATATGATGGAACTGTGAAGAGAGCGTGTTCGGAATAGTTGAACATTAAGCTTTGAG    | 3630 |
| OY | 3664 | ACCTTCATTTGTTTTCATGATTCCTCTTATGTAGTGGTGCCTGGCAATTGAATATATAT     | 3723 |
| Db | 3631 | ACCTTCATTTGTTTTCATGATTCCTCTTATGTAGTGGTGCCTGGCAATTGAATATATAT     | 3690 |
| OY | 3724 | ATTGATCAGCGAAAGACGATTAAGACGATTTGAAGATATGTGACAAAGCTTTTCACTTAC    | 3783 |
| Db | 3691 | ATTGATCAGCGAAAGACGATTAAGACGATTTGAAGATATGTGACAAAGCTTTTCACTTAC    | 3750 |
| OY | 3784 | ATTTTCATTTCTGGAANAATGTTCTTAAANATGGTGGCAGATATGCTATCAACATATTTCAAC | 3843 |
| Db | 3751 | ATTTTCATTTCTGGAANAATGTTCTTAAANATGGTGGCAGATATGCTATCAACATATTTCAAC | 3810 |
| OY | 3844 | AATGCGTGTGTGTGCTGGACTTCTTAATTTGATGTGTTTATTTGTCAGATTTTAACAGCA    | 3903 |
| Db | 3811 | AATGCGTGTGTGTGCTGGACTTCTTAATTTGATGTGTTTATTTGTCAGATTTTAACAGCA    | 3870 |
| OY | 3904 | AATGCTTTGGGTACTCAGAACTTGAGACCAATTCATCTCAGAGCACTTAAGACCTGTG      | 3963 |
| Db | 3871 | AATGCTTTGGGTACTCAGAACTTGAGACCAATTCATCTCAGAGCACTTAAGACCTGTG      | 3930 |
| OY | 3964 | AGACCTTAAGAGCCTTATCTCGATTTGAAGAGATGAGGCTGTGTGATATGCCCTTTTA      | 4023 |

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|---|------|---|------|
| D | 3931 | AGACCTCTAAGAGCTTATCTCATTTTGAAAGGATAGGGTGGTGTGAAAGGCCCTTTA     | 3995 |
| Q | 4024 | GGAGCAATTCATTCATCATGAATGTGCTTGTGGTTTGTCTTAATATTCGGCTAAATTTTC  | 4085 |
| D | 3991 | GGACCAATTCATTCATCAATGAATGTGCTTGTGGTTTGTCTTAATATTCGGCTAAATTTTC | 4085 |
| Q | 4084 | AGCATATGGGCGGAAATTTGTGTGGCAATTTCTACACTGTATTTAACACCAACT        | 4115 |
| D | 4051 | AGCATATGGGCGGAAATTTGTGTGGCAATTTCTACACTGTATTTAACACCAACT        | 4115 |
| Q | 4144 | GGTGACAGGTGTGCATATCGAAGACGTGAATATCATCTAGATGGCTTAACTAATAGAA    | 4225 |
| D | 4111 | GGTGACAGGTGTGCATATCGAAGACGTGAATATCATCTAGATGGCTTAACTAATAGAA    | 4225 |
| Q | 4204 | AGAAATGAGACTCTCGATGAGAAAAATGTGAAGTAACTTTGAAATATGATGATTTGGG    | 4285 |
| D | 4171 | AGAAATGAGACTCTCGATGAGAAAAATGTGAAGTAACTTTGAAATATGATGATTTGGG    | 4285 |
| Q | 4264 | TATCTCTTGTGTCAGTGTGCACATTTCAAAGATGATGATATATATGATAGCA          | 4325 |
| D | 4231 | TATCTCTTGTGTCAGTGTGCACATTTCAAAGATGATGATATATATGATAGCA          | 4325 |
| Q | 4324 | GTTGATTCAGAAATGTGAGACCTCAGGCTAAGTATGAAGAAATCTGTATATCTT        | 4385 |
| D | 4291 | GTTGATTCAGAAATGTGAGACCTCAGGCTAAGTATGAAGAAATCTGTATATCTT        | 4385 |
| Q | 4384 | TACTTGTATTTTCATCATCTTTGGGTCTTTCACCTTGAACCTGTTAATTTGGTTC       | 4445 |
| D | 4351 | TACTTGTATTTTCATCATCTTTGGGTCTTTCACCTTGAACCTGTTAATTTGGTTC       | 4445 |
| Q | 4444 | ATCATATATATTTCAACACGAGAAAAAGATTTGGAGGTCAAGACATCTTATAGCA       | 4505 |
| D | 4411 | ATCATATATATTTCAACACGAGAAAAAGATTTGGAGGTCAAGACATCTTATAGCA       | 4505 |
| Q | 4504 | GAGAACAGAGAAATATCATATATGCATGAAAAATTAGATGAAAAACCGCAAAAG        | 4565 |
| D | 4471 | GAGAACAGAGAAATATCATATATGCATGAAAAATTAGATGAAAAACCGCAAAAG        | 4565 |
| Q | 4564 | CCTATACCTCGACACAGAAACAAATTTCAAGAAATGGCTTTGACCTCGTAAACACAA     | 4625 |
| D | 4531 | CCTATACCTCGACACAGAAACAAATTTCAAGAAATGGCTTTGACCTCGTAAACACAA     | 4625 |
| Q | 4624 | GTTTTGACATATACATCATGATCTCATCTGTCTTAACATGGTCAACATGATGTGAA      | 4685 |
| D | 4591 | GTTTTGACATATACATCATGATCTCATCTGTCTTAACATGGTCAACATGATGTGAA      | 4685 |
| Q | 4684 | ACAGATGACCAAGAGAAATATGTACATACCAATTTGTACACGATCAATCTGTTCAT      | 4745 |
| D | 4651 | ACAGATGACCAAGAGAAATATGTACATACCAATTTGTACACGATCAATCTGTTCAT      | 4745 |
| Q | 4744 | GTCCTATTTACTGAGAGTGTACTGAAACTCATCTCTACGCCATATATATTTTACC       | 4805 |
| D | 4711 | GTCCTATTTACTGAGAGTGTACTGAAACTCATCTCTACGCCATATATATTTTACC       | 4805 |
| Q | 4804 | ATTGATGTAATTTTGTGATTTGTGTGTTCAATCTCTCAATTGTAGATATGTTCTT       | 4865 |
| D | 4771 | ATTGATGTAATTTTGTGATTTGTGTGTTCAATCTCTCAATTGTAGATATGTTCTT       | 4865 |
| Q | 4864 | GCCGAGCTGATAGAAAGATTTGGTCCCTACCTGTTCGAGTATCCGTCTGCT           | 4925 |
| D | 4831 | GCCGAGCTGATAGAAAGATTTGGTCCCTACCTGTTCGAGTATCCGTCTGCT           | 4925 |
| Q | 4924 | AGGATGGCCGAATCTTACGTCTATCAAAGAGACAAAGGAGATCCGACGCTGCTTT       | 4985 |
| D | 4891 | AGGATGGCCGAATCTTACGTCTATCAAAGAGACAAAGGAGATCCGACGCTGCTTT       | 4985 |
| Q | 4984 | GCTTTGATGATGCTCCTGCTGCTGTTTAAATCATGGGCTCTTACTCTTCTATGATG      | 5045 |
| D | 4951 | GCTTTGATGATGCTCCTGCTGCTGTTTAAATCATGGGCTCTTACTCTTCTATGATG      | 5045 |
| Q | 5044 | TTGCATACGCAATCTTTGGGATGTCAACTTTGCTTATGTTAAAGGAAAGTTGGATC      | 5105 |



Db 2011 GGAACACCTGAACTGAAATGAGAAAGAGTCACTTCTTCCACTTTCCTG 2070  
OY 2104 GACTTTCTAGAGATCTTCCCAAGGACAGCATGATATAGCCAGCATTTCTAACA 2163  
Db 2071 GACTTTCTAGAGATCTTCCCAAGGACAGCATGATATAGCCAGCATTTCTAACA 2130  
OY 2164 AATACAGTAAAGAACTTGAAGATTCAGGCAAGAAATCCCACTCTGTGTATTAATTT 2223  
Db 2131 AATACAGTAAAGAACTTGAAGAAATTCAGGCAAGAAATCCCACTCTGTGTATTAATTT 2190  
OY 2224 TCCAACTATCTTAACTGGGACCTGTCCTCAATATGTTTAAAGTAAACATGTTGTC 2283  
Db 2191 TCCAACTATCTTAACTGGGACCTGTCCTCAATATGTTTAAAGTAAACATGTTGTC 2250  
OY 2284 AACCTGTGTGATGAGACCACTTTGTGACCTGGCCATCACACTGTATTTCTTAAT 2343  
Db 2251 AACCTGTGTGATGAGACCACTTTGTGACCTGGCCATCACACTGTATTTCTTAAT 2310  
OY 2344 ACTCTTTCATGCGCATGAGCAGCATATCCAAATGACGCACTTTCAAATATGTGCTTACA 2403  
Db 2311 ACTCTTTCATGCGCATGAGCAGCATATCCAAATGACGCACTTTCAAATATGTGCTTACA 2370  
OY 2404 GTAGGAAACTTGTTTCTACTGAGATCTTACAGCAGAAATGTTTCTGAAAATTAATGTC 2463  
Db 2371 GTAGGAAACTTGTTTCTACTGAGATCTTACAGCAGAAATGTTTCTGAAAATTAATGTC 2430  
OY 2464 ATGATCTCTACTATTAATTTCCAAAGAGCTGATATCTTTGAGCGTTTATTTGAGAG 2523  
Db 2431 ATGATCTCTACTATTAATTTCCAAAGAGCTGATATCTTTGAGCGTTTATTTGAGAG 2490  
OY 2524 CTTAGCCGTGTAAAGAACTTGGACCTGCCCAATGGAAGATTAATCTGTTCTCCGTTCAAT 2583  
Db 2491 CTTAGCCGTGTAAAGAACTTGGACCTGCCCAATGGAAGATTAATCTGTTCTCCGTTCAAT 2550  
OY 2584 CGATTCGCTGCAAGTTTCAAGTTGSCAAATCTTGGCCAAAGTTAAATATGCTAATAAG 2643  
Db 2551 CGATTCGCTGCAAGTTTCAAGTTGSCAAATCTTGGCCAAAGTTAAATATGCTAATAAG 2610  
OY 2644 ATCATCGGCAATTCGCTGGGGGCTCTGGGAAATTTAACCTCTGCTTGGCCATCATGCTC 2703  
Db 2611 ATCATCGGCAATTCGCTGGGGGCTCTGGGAAATTTAACCTCTGCTTGGCCATCATGCTC 2670  
OY 2704 TTTCAATTTTGGCGTGTGGGATGAGACTCTTTGGTAAAGCTAACAAAGATTGTGTCTGC 2763  
Db 2671 TTTCAATTTTGGCGTGTGGGATGAGACTCTTTGGTAAAGCTAACAAAGATTGTGTCTGC 2730  
OY 2764 AAGATCGCAGATGTGTCACTCCACAGCTGGCAGATGAATGACTTCTTCCACTCTTC 2823  
Db 2731 AAGATCGCAGATGTGTCACTCCACAGCTGGCAGATGAATGACTTCTTCCACTCTTC 2790  
OY 2824 CTGATTTGTTCCGCGTCTGTGTGGGAGTGGATGAGACATGTGGACTGTATGAG 2883  
Db 2791 CTGATTTGTTCCGCGTCTGTGTGGGAGTGGATGAGACATGTGGACTGTATGAG 2850  
OY 2884 GTTGTGTGTCAGCAAGCATGTGCTTCACTGATGATGATGATGATGATGATGATGATGAT 2943  
Db 2851 GTTGTGTGTCAGCAAGCATGTGCTTCACTGATGATGATGATGATGATGATGATGATGAT 2910  
OY 2944 GTGTCTGTAATCTTCTGTGCGCTTGTGCTTGTGAGCTCATTTAGTGAACAACCTTGA 3003  
Db 2911 GTGTCTGTAATCTTCTGTGCGCTTGTGCTTGTGAGCTCATTTAGTGAACAACCTTGA 2970  
OY 3004 GCCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3063  
Db 2971 GCCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3030  
OY 3064 GGAGTGTGTTATGTAAGAAATATATGATTAATTTCAACAGTCTCTTATTAAGAAA 3123  
Db 3031 GGAGTGTGTTATGTAAGAAATATATGATTAATTTCAACAGTCTCTTATTAAGAAA 3090  
OY 3124 CAAAAGATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3183  
Db 3091 CAAAAGATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3150

OY 3184 ATGTCAATCATATACAGAAATTTGGAAAGATCTTACTATCTTAAAGATGATTAATGCA 3243  
Db 3151 ATGTCAATCATATACAGAAATTTGGAAAGATCTTACTATCTTAAAGATGATTAATGCA 3210  
OY 3244 ACTTCAAGTGTATAGGAACTGGCAGCAGTGTGAAAAATACATTAATTAATGAAAGTAT 3303  
Db 3211 ACTTCAAGTGTATAGGAACTGGCAGCAGTGTGAAAAATACATTAATTAATGAAAGTAT 3270  
OY 3304 TACATGCTATCATTAACAAACCCAGCTTACTGTGACTGTACCAATGCTGTATGAGAA 3363  
Db 3271 TACATGCTATCATTAACAAACCCAGCTTACTGTGACTGTACCAATGCTGTATGAGAA 3330  
OY 3364 TCTGACTTTGAAATTTTAAACACAGAACTTATAGTATGATGATGATGATGATGATGATGAT 3423  
Db 3331 TCTGACTTTGAAATTTTAAACACAGAACTTATAGTATGATGATGATGATGATGATGATGAT 3390  
OY 3424 AAAGAGAACTGAAATGAAAGCAGTATGATCATCAGAAAGTATGATGATGATGATGATGAT 3483  
Db 3391 AAAGAGAACTGAAATGAAAGCAGTATGATCATCAGAAAGTATGATGATGATGATGATGAT 3450  
OY 3484 CCTGTAGAGAAAGCCCGTATGATGAGAACTGAAAGAACTCTGTGAAACAGAGCTGTGTC 3543  
Db 3451 CCTGTAGAGAAAGCCCGTATGATGAGAACTGAAAGAACTCTGTGAAACAGAGCTGTGTC 3510  
OY 3544 ACTGAAAGCTGTGTACAAAGATTTCAAGTGTGTCAATGATGATGATGATGATGATGATGAT 3603  
Db 3511 ACTGAAAGCTGTGTACAAAGATTTCAAGTGTGTGTCAATGATGATGATGATGATGATGATGAT 3570  
OY 3604 AAACAAATGTGTGAACTGTGAGAGAGAGCTGTGTCGAAATGATGATGATGATGATGATGAT 3663  
Db 3571 AAACAAATGTGTGAACTGTGAGAGAGAGCTGTGTCGAAATGATGATGATGATGATGATGAT 3630  
OY 3664 ACCTTCAATTTGTTTCAATGATTTCTCTAGTATGATGATGATGATGATGATGATGATGAT 3723  
Db 3631 ACCTTCAATTTGTTTCAATGATTTCTCTAGTATGATGATGATGATGATGATGATGATGAT 3690  
OY 3724 ATTGATCAGCGAAAGAGATTTAGACGATGTTGGAATATCTGCAAGATTTTCACTTAC 3783  
Db 3691 ATTGATCAGCGAAAGAGATTTAGACGATGTTGGAATATCTGCAAGATTTTCACTTAC 3750  
OY 3784 ATTTTCATTTCTGGAATATGCTTTTAAATGAGTGTGATGATGATGATGATGATGATGATGAT 3843  
Db 3751 ATTTTCATTTCTGGAATATGCTTTTAAATGAGTGTGATGATGATGATGATGATGATGATGAT 3810  
OY 3844 AATGCTGTGTGTGCTGAGACTTCTTAATGTTGATGATGATGATGATGATGATGATGATGAT 3903  
Db 3811 AATGCTGTGTGTGCTGAGACTTCTTAATGTTGATGATGATGATGATGATGATGATGATGAT 3870  
OY 3904 AATGCTGTGTGTGCTGAGACTTGTGAGACATCAAAATCTGTCAAGACATCAAGAGCTGTG 3963  
Db 3871 AATGCTGTGTGTGCTGAGACTTGTGAGACATCAAAATCTGTCAAGACATCAAGAGCTGTG 3930  
OY 3964 AGACCTTGAAGAGCTTATCTCGATTTGAAAGGATGAGGCTGTGTGAAATGCTTTTAA 4023  
Db 3931 AGACCTTGAAGAGCTTATCTCGATTTGAAAGGATGAGGCTGTGTGAAATGCTTTTAA 3990  
OY 4024 GGAGCAATTTCCATCATCATGAAATGATGCTTCTGTGTTGCTTATATCTGCTGCTTAAATTTTC 4083  
Db 3991 GGAGCAATTTCCATCATCATGAAATGATGCTTCTGTGTTGCTTATATCTGCTGCTTAAATTTTC 4050  
OY 4084 AGCATATGAGGCGTAAATTTGTTTGTGCGAAATTTCAACAGTATTAACACACACACT 4143  
Db 4051 AGCATATGAGGCGTAAATTTGTTTGTGCGAAATTTCAACAGTATTAACACACACACT 4110  
OY 4144 GGTGACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4203  
Db 4111 GGTGACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4170  
OY 4204 AGAATGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4263  
Db 4171 AGAATGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4230







|   |   |      |   |      |
|---|---|------|---|------|
| D | b | 3828 | CACCAATGCGTGGTGTTGGCTGCACCTCTTAATTGTGTAGTGTTCATTGTGGTCAGTTBAC | 3887 |
| O | y | 3900 | AGCAAATGCTTGGGTACTCAGAACTTTGAGCCATCAAACTCTCAGAGACCTAAGAC      | 3959 |
| D | b | 3888 | AGCAAAATGCTTGGGTACTCAGAACTTTGAGCCATCAAACTCTCAGAGACCTAAGAC     | 3947 |
| O | y | 3960 | TCTGAGACCTCTAAGAGCCCTTATCTCGAATTTGAAGGATGAGGGTGTGTGATGCCCT    | 4019 |
| D | b | 3948 | TCTGAGACCTCTAAGAGCCCTTATCTCGAATTTGAAGGATGAGGGTGTGTGATGCCCT    | 4007 |
| O | y | 4020 | TTTTAGAGCAATTCANCCATCATAGAATGCTCTGCTGTTGCTCTAATACTGGCTAAT     | 4079 |
| D | b | 4008 | TTTTAGAGCAATTCANCCATCATAGAATGCTCTGCTGTTGCTCTAATACTGGCTAAT     | 4067 |
| O | y | 4080 | TTTAGACATATGGGCGCTAAATTTGTTGGTGSCAAATCTCACACTGATTAACACAC      | 4139 |
| D | b | 4068 | TTTAGACATATGGGCGCTAAATTTGTTGGTGSCAAATCTCACACTGATTAACACAC      | 4127 |
| O | y | 4140 | AACGTGTGACAGGTTTTSACATCGAACGTAAGTAATCATCTGATTCCTAAAACATAT     | 4199 |
| D | b | 4128 | AACGTGTGACAGGTTTTSACATCGAACGTAATCATCTGATTCCTAAAACATAT         | 4187 |
| O | y | 4200 | AGAAAGAAATGACCTCTCGATGGAAGAAATGTGAAGTAACTTTGATATATAGATAT      | 4259 |
| D | b | 4188 | AGAAAGAAATGACCTCTCGATGGAAGAAATGTGAAGTAACTTTGATATATAGATAT      | 4247 |
| O | y | 4280 | TGGGATATCTCTTGGTTCAGTTGCGCAATCAAGGATGATGATATATATATGAC         | 4319 |
| D | b | 4248 | TGGGATATCTCTTGGTTCAGTTGCGCAATCAAGGATGATGATATATATATGAC         | 4307 |
| O | y | 4320 | AGCAGTTGATTCGAGAAATGTGGAACCTCCAGCTAAGTATGAAGAAAGTCTGTACATGTA  | 4379 |
| D | b | 4308 | AGCAGTTGATTCGAGAAATGTGGAACCTCCAGCTAAGTATGAAGAAAGTCTGTACATGTA  | 4367 |
| O | y | 4380 | TCTTACTTCTTTATTTTCAATCTTTGGGTCTCTCACCCTTGAACCTGTATATGG        | 4439 |
| D | b | 4368 | TCTTACTTCTTTATTTTCAATCTTTGGGTCTCTCACCCTTGAACCTGTATATGG        | 4427 |
| O | y | 4440 | TGTCATCATATAGTAATTTTCAACACGAGAAAAAGAGTTGGAGGTCAAGACATCTTAT    | 4499 |
| D | b | 4428 | TGTCATCATATATATTTTCAACACGAGAAAAAGAGTTGGAGGTCAAGACATCTTAT      | 4487 |
| O | y | 4500 | GACAGAGAAACAGAGAAATACTATTAATGCAATGAAGAAAAATTTAGATGAGAAAAACGCA | 4559 |
| D | b | 4488 | GACAGAGAAACAGAGAAATACTATTAATGCAATGAAGAAAAATTTAGATGAGAAAAACGCA | 4547 |
| O | y | 4560 | AAAGCTTACTCTGACACAGAGAAACAATTTTCAAGAAATGTGTGATTCGTAAACAG      | 4619 |
| D | b | 4548 | AAAGCTTACTCTGACACAGAGAAACAATTTTCAAGAAATGTGTGATTCGTAAACAG      | 4607 |
| O | y | 4620 | ACAAATTTTGTGATTAAGATCATGATTCATCTGTCTTAACATGATCACAAATGATGT     | 4679 |
| D | b | 4608 | ACAAATTTTGTGATTAAGATCATGATTCATCTGTCTTAACATGATCACAAATGATGT     | 4667 |
| O | y | 4680 | GGAAACAGATGACCCAGAGTAAATGTGATACCAATTTTGTGACGATCAATCTGTGT      | 4739 |
| D | b | 4668 | GGAAACAGATGACCCAGAGTAAATGTGATACCAATTTTGTGACGATCAATCTGTGT      | 4727 |
| O | y | 4740 | CATTGTCTATTTACTGGAAGTGTGTACTGAAACATCATCTCTTACCCCATATATAT      | 4799 |
| D | b | 4728 | CATTGTCTATTTACTGGAAGTGTGTACTGAAACATCATCTCTTACCCCATATATAT      | 4787 |
| O | y | 4800 | TACCAATGATGATTAATTTTGTGATTTGTGTTGATCTCTCCATCTGATGAGTATGT      | 4859 |
| D | b | 4788 | TACCAATGATGATTAATTTTGTGATTTGTGTTGATCTCTCCATCTGATGAGTATGT      | 4847 |
| O | y | 4860 | TCTTGGCAGATGTATAGAAAGTATTTCTGTCTCCCTACCTGTTCCAGATGATCCGCT     | 4919 |
| D | b | 4848 | TCTTGGCAGATGTATAGAAAGTATTTCTGTCTCCCTACCTGTTCCAGATGATCCGCT     | 4907 |
| O | y | 4920 | TGCTAGATGTGGCGAAATCTTACGCTTATCAAAAGACAAAGGAGATCCGACGCTCT      | 4979 |

|    |      |   |      |
|----|------|---|------|
| Dd | 4908 | TGCTAGGATTTGGCCGAACTCCTAGCTCTGATCAAAAGACGAAAGGGGATCCGACGCTGCT   | 4967 |
| Qy | 4980 | CTTGTGCTTGATGATGTGCTCCCTCTCGGTGTGTTTAACATCGGCTCTCTCTCTGCTAGT    | 5039 |
| Dd | 4988 | CTTGTGCTTGATGATGATGCTCTCTCGGTGTGTTTAACATCGGCTCTCTCTCTGCTAGT     | 5027 |
| Qy | 5040 | CATGTTCACTACACCCATCTTTGGGATGTCCAACTTTGCCATATGTTAAGAGGGAAGTTGG   | 5099 |
| Dd | 5028 | CATGTTCACTACACCCATCTTTGGGATGTCCAACTTTGCCATATGTTAAGAGGGAAGTTGG   | 5087 |
| Qy | 5100 | GATGATGACACTGTGTCAACTTTAGAGACCTTTGGCAACACATGATCTGCTATTGCCAAT    | 5158 |
| Dd | 5088 | GATGATGACACTGTGTCAACTTTAGAGACCTTTGGCAACACATGATCTGCTATTGCCAAT    | 5147 |
| Qy | 5160 | TACAACTCTGCTGGCTGGGATGGATTCGTAGACACCACTTCTCAACAGTAAGCCACCGGA    | 5219 |
| Dd | 5148 | TACAACTCTGCTGGCTGGGATGGATTCGTAGACACCACTTCTCAACAGTAAGCCACCGGA    | 5207 |
| Qy | 5220 | CTGTGACCCCTTAATAAAGTAAACCTTGGAAAGCTCAGTTAAAGGAGACTGTGGAAACCCATC | 5279 |
| Dd | 5208 | CTGTGACCCCTTAATAAAGTAAACCTTGGAAAGCTCAGTTAAAGGAGACTGTGGAAACCCATC | 5267 |
| Qy | 5280 | TGTTGGAAATTTCTTTTTTGTCAAGTTACATCATATCTCTCTGTTGTGTGTACAT         | 5339 |
| Dd | 5268 | TGTTGGAAATTTCTTTTTTGTCAAGTTACATCATATCTCTCTGTTGTGTGTACAT         | 5327 |
| Qy | 5340 | GTACATGACGCGTATCCTGTGAGAACTCAAGTGTGTACTGAAAGAAATGGAAGACCTCT     | 5399 |
| Dd | 5328 | GTACATGACGCGTATCCTGTGAGAACTCAAGTGTGTACTGAAAGAAATGGAAGACCTCT     | 5387 |
| Qy | 5400 | GAGTGAAGATGACTTTGAGATGTGCTATGAGTTTGGGAAAGTTGATCCGATCGAAC        | 5459 |
| Dd | 5388 | GAGTGAAGATGACTTTGAGATGTGCTATGAGTTTGGGAAAGTTGATCCGATCGAAC        | 5447 |
| Qy | 5460 | TCACTTATATGAATTTGAAAAATATCTAGATGTTGCACTGCGCTTGAACCGCTCTCA       | 5519 |
| Dd | 5448 | TCACTTATATGAATTTGAAAAATATCTAGATGTTGCACTGCGCTTGAACCGCTCTCA       | 5507 |
| Qy | 5520 | TCTGCCACAACCAAACTCAGCTCATATGCGCATGATTTGCCATGATGTGAGTGGTGA       | 5579 |
| Dd | 5508 | TCTGCCACAACCAAACTCAGCTCATATGCGCATGATTTGCCATGATGTGAGTGGTGA       | 5567 |
| Qy | 5580 | CCGATCCACTGTCCTTGATATCTTAATTTGCTTTACAAAGCGGTTCTAGAGAGAGTGG      | 5639 |
| Dd | 5568 | CCGATCCACTGTCCTTGATATCTTAATTTGCTTTACAAAGCGGTTCTAGAGAGAGTGG      | 5627 |
| Qy | 5640 | AGAAATGATGCTCTACGAAATACAGATACAGATGGAAGAGGATTCATGCTTCCAT         | 5699 |
| Dd | 5628 | AGAAATGATGCTCTACGAAATACAGATACAGATGGAAGAGGATTCATGCTTCCAT         | 5687 |
| Qy | 5700 | GGTCTCTATCAGCAGATCACTCACTTAAAGGAAACAAAGGAAAGATATGCTGT           | 5759 |
| Dd | 5688 | GGTCTCTATCAGCAGATCACTCACTTAAAGGAAACAAAGGAAAGATATGCTGT           | 5747 |
| Qy | 5760 | CATTATTCAGCGTGTACAGAGACGCCACTTTTAAAGCACTGTAAACAAAGCTTCTT        | 5819 |
| Dd | 5748 | CATTATTCAGCGTGTACAGAGACGCCACTTTTAAAGCACTGTAAACAAAGCTTCTT        | 5807 |
| Qy | 5820 | TAGTCAATATATATATCAAAAGTGGGGCTAATCTTCTTATATATATATATATATAT        | 5879 |
| Dd | 5808 | TAGTCAATATATATATCAAAAGTGGGGCTAATCTTCTTATATATATATATATATAT        | 5867 |
| Qy | 5880 | AATTTGACAGATTAATGAAAGCTATTTCAGAAAAAATGATGACATGCTCACTGC          | 5939 |
| Dd | 5868 | AATTTGACAGATTAATGAAAGCTATTTCAGAAAAAATGATGACATGCTCACTGC          | 5927 |
| Qy | 5940 | AGCTTGTCACTTCTCTATGACCGGGTGAACAAGCAATTTGTAATAAATCATGACAGA       | 5999 |
| Dd | 5928 | AGCTTGTCACTTCTCTATGACCGGGTGAACAAGCAATTTGTAATAAATCATGACAGA       | 5987 |
| Qy | 6000 | AGGCAAAAGATGAAAAAGCCAAAGGAAATTA 6030                            |      |
| Dd | 5988 | AGGCAAAAGATGAAAAAGCCAAAGGAAATTA 6018                            |      |

RESULT 12  
AAD32841 standard; cDNA; 4329 BP.  
AAD32841;  
01-JUL-2002 (first entry)  
Human ion channel CDNA #3.  
Human; novel human protein; NHP; voltage-gated sodium channel;  
gene therapy; bioreactor; mental disorder; biological disorder;  
gene; medical disorder; ss.  
Homo sapiens.  
Key Location/Qualifiers  
CDS 1..4329  
/\*tag= a  
/product= "human ion channel protein #3"  
/transl\_except= (pos:2941..2943, aa:Xaa)  
/transl\_except= (pos:3166..3168, aa:Xaa)  
/note= "Xaa = any amino acid"

MO200214498-A2  
21-FEB-2002.  
15-AUG-2001; 2001NO-US25650.  
16-AUG-2000; 2000US-Z25989P.  
(LEXI-) LEXICON GENETICS INC.  
Turner CA, Mathur B, Mathur D;  
WPI; 2002-280757/32.  
P-PSDB; AAE20512.

Novel polynucleotides encoding human sodium channel proteins,  
particularly voltage-gated sodium channel proteins useful for drug  
screening, diagnosis and in gene therapy of biological disorders

Claim 1; Page 41-42; 83pp; English.

The present sequence is a cDNA encoding novel human protein (NHP), ion  
channel protein. NHP share structural similarity with mammalian sodium  
channel proteins particularly voltage-gated sodium channel proteins.  
NHP oligonucleotides are useful as hybridisation probes for screening  
libraries and assessing gene expression patterns. Sequences derived  
from regions adjacent to the intron/exon boundaries of NHP gene can be  
used to design primers for use in amplification assays to detect  
mutations within the exons, splice sites, introns that can be used in  
diagnostics and pharmacogenomics. NHP nucleotide sequences are useful  
for drug screening effective in the treatment of symptomatic or  
phenotypic manifestations of perturbing the normal function of NHP in  
the body, and nucleotide constructs encoding NHP products are useful  
genetically engineered host cells to express NHP products in vivo. These  
delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion  
protein to the body. Nucleotide construct encoding NHP products are  
also useful in gene therapy for modulating NHP expression and to  
produce genetically engineered host cells to express NHP products in  
vivo. NHP nucleotide sequences may also be used as part of ribozyme  
and/or triple helix sequences that are useful for generating antibodies.  
The NHP polypeptides are useful for generating other cellular gene  
reagents in diagnostic assays, for identifying other cellular gene  
products related to NHP and as reagents in assays for screening for  
compounds that are useful in the treatment of mental, biological or  
medical disorders and diseases.

| Seq | Sequence              | BP   | 1287 A       | 840 C    | 988 G       | 1211 T | 3 other: |
|-----|-----------------------|--|--------------|----------|-------------|--------|----------|
| 50  | Query Match           | 38.1%  | Score 2295   | DB 24    | Length 4329 |        |          |
|     | Best Local Similarity | 100.0%   | Pred. No. 0  |          |             |        |          |
|     | Matches 12295         | Conservative 0   | Mismatches 0 | Indels 0 | Gaps 0      |        |          |
| QY  | 2044                  | GGAAACAACCCGTAATCTGAAATGAAAGAAAGAAAGCTAAATCTCTTCCAGCTTCCAGT    | 2103         |          |             |        |          |
| DB  | 2011                  | GGAAACAACCCGTAATCTGAAATGAAAGAAAGAAAGCTAAATCTCTTCCAGCTTCCAGT    | 2070         |          |             |        |          |
| QY  | 2104                  | GACTTCTGAAAGATCCTTCCCAAAGGCAAGAGAAATGAAATAGGACATCTCAACA        | 2163         |          |             |        |          |
| DB  | 2071                  | GACTTCTGAAAGATCCTTCCCAAAGGCAAGAGAAATGAAATAGGACATCTCTCAACA      | 2130         |          |             |        |          |
| QY  | 2164                  | AATACAGTGAAGAACTTGAAGATCCAGGACAGAAATGCCACCCTTGTGTATAATTT       | 2223         |          |             |        |          |
| DB  | 2131                  | AATACAGTGAAGAACTTGAAGATCCAGGACAGAAATGCCACCCTTGTGTATAATTT       | 2190         |          |             |        |          |
| QY  | 2224                  | TCCAAACATATCTTAATCGGGACGTCTCCATATTTGGTTAAAAGTAAACATGTTGTC      | 2283         |          |             |        |          |
| DB  | 2191                  | TCCAAACATATCTTAATCGGGACGTCTCCATATTTGGTTAAAAGTAAACATGTTGTC      | 2250         |          |             |        |          |
| QY  | 2284                  | AACCTGGTGTGTGAGACCAATTTGTGACCGGGCCATCACATCTATTTGGCTTAAT        | 2343         |          |             |        |          |
| DB  | 2251                  | AACCTGGTGTGTGAGACCAATTTGTGACCGGGCCATCACATCTATTTGGCTTAAT        | 2310         |          |             |        |          |
| QY  | 2344                  | ACTCTTTTACGGCCATGGAGACATATCCATAGACAGCACTTTCATTAATGTGCTTACA     | 2403         |          |             |        |          |
| DB  | 2311                  | ACTCTTTTACGGCCATGGAGACATATCCATAGACAGCACTTTCATTAATGTGCTTACA     | 2370         |          |             |        |          |
| QY  | 2404                  | GTAGGAACCTGGTTTCTACTGGATCTTTACAGCAGAAATGTTCTGAAAATTAATGCC      | 2463         |          |             |        |          |
| DB  | 2371                  | GTAGGAACCTGGTTTCTACTGGATCTTTACAGCAGAAATGTTCTGAAAATTAATGCC      | 2430         |          |             |        |          |
| QY  | 2464                  | ATGAGATCCCTTACATTAATTTCCAAAGAGCGGAAATATCTTGAAGCTTATTTGGAGG     | 2523         |          |             |        |          |
| DB  | 2431                  | ATGAGATCCCTTACATTAATTTCCAAAGAGCGGAAATATCTTGAAGCTTATTTGGAGG     | 2490         |          |             |        |          |
| QY  | 2524                  | CTTAGCCTGGTAGAACCTTGGACTCGCCATGTGGAAGATTAATCTCTCCGTTCAATTT     | 2583         |          |             |        |          |
| DB  | 2491                  | CTTAGCCTGGTAGAACCTTGGACTCGCCATGTGGAAGATTAATCTCTCCGTTCAATTT     | 2550         |          |             |        |          |
| QY  | 2584                  | CGATTGCTGCGAGTTTCAAGTTGGCAAAATCTTGGCCAAAGTAAATATGCTAATTAAG     | 2643         |          |             |        |          |
| DB  | 2551                  | CGATTGCTGCGAGTTTCAAGTTGGCAAAATCTTGGCCAAAGTAAATATGCTAATTAAG     | 2610         |          |             |        |          |
| QY  | 2644                  | ATCATGGGCAATCCGCTGGGGGCTGTGGGAAATTAACCCGCTTGGGCCATCATCGTC      | 2703         |          |             |        |          |
| DB  | 2611                  | ATCATGGGCAATCCGCTGGGGGCTGTGGGAAATTAACCCGCTTGGGCCATCATCGTC      | 2670         |          |             |        |          |
| QY  | 2704                  | TTGATTTTGGCCGTGGTCCGATGAGGCTCTTGGTAAAGCTCAAAAGATGTGCTCG        | 2763         |          |             |        |          |
| DB  | 2671                  | TTGATTTTGGCCGTGGTCCGATGAGGCTCTTGGTAAAGCTCAAAAGATGTGCTCG        | 2730         |          |             |        |          |
| QY  | 2764                  | AAGATGCCAAGTATGTGTAATCCACGCTGGCCATGAATGACTTCTTCACTCCTTC        | 2823         |          |             |        |          |
| DB  | 2731                  | AAGATGCCAAGTATGTGTAATCCACGCTGGCCATGAATGACTTCTTCACTCCTTC        | 2790         |          |             |        |          |
| QY  | 2824                  | CTGATTTGTGTCGGGTGGTGTGTGTTGGGGAAGTGAATAGAGACATGTGGGACTGTATGGAG | 2883         |          |             |        |          |
| DB  | 2791                  | CTGATTTGTGTCGGGTGGTGTGTGTTGGGGAAGTGAATAGAGACATGTGGGACTGTATGGAG | 2850         |          |             |        |          |
| QY  | 2884                  | GTTGCTGGTCAAGCCATGTGCTTACTGTCTTCAATGATGGATGGATGGTAAACCTTA      | 2943         |          |             |        |          |
| DB  | 2851                  | GTTGCTGGTCAAGCCATGTGCTTACTGTCTTCAATGATGGATGGATGGTAAACCTTA      | 2910         |          |             |        |          |
| QY  | 2944                  | GTTGCTCTTAATCTCTTCTGGCTTGGCTTGTGACTCATTTAATGTCAGACAACCTTGA     | 3003         |          |             |        |          |
| DB  | 2911                  | GTTGCTCTTAATCTCTTCTGGCTTGGCTTGTGACTCATTTAATGTCAGACAACCTTGA     | 2970         |          |             |        |          |
| QY  | 3004                  | GCACAGTGAATGATTAATGAATTAATCTCCAAATTCGTGTGGATAGATGACACAAA       | 3063         |          |             |        |          |
| DB  | 2971                  | GCACAGTGAATGATTAATGAATTAATCTCCAAATTCGTGTGGATAGATGACACAAA       | 3030         |          |             |        |          |

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OY 3064 GGAGTACGTTATGTGAAAAAATATATGATTTATTCACAGCTCTTCTATTGGAAA 3123
DB 3031 GGAGTACGTTATGTGAAAAAATATATGATTTATTCACAGCTCTTCTATTGGAAA 3090
OY 3124 CAAAGATTTTGTGAAATTAACACATGATCTTAACACAGAAAGACAGTTGT 3183
DB 3091 CAAAGATTTTGTGAAATTAACACATGATCTTAACACAGAAAGACAGTTGT 3150
OY 3184 ATGTCCATCATACACACAGAAATTTGGAAAGATCTTGAATCTTAAGATTAATGGA 3243
DB 3151 ATGTCCATCATACACACAGAAATTTGGAAAGATCTTGAATCTTAAGATTAATGGA 3210
OY 3244 ACTACAGTGTATAGGAACTGGCAGCAGCTGTGAAAAATACATTATGATGAAGTGT 3303
DB 3211 ACTACAGTGTATAGGAACTGGCAGCAGCTGTGAAAAATACATTATGATGAAGTGT 3270
OY 3304 TACATGCTATTCATTAACAAACCCAGCTTACTGTGACGCTGCAATGCTTACAGAAA 3363
DB 3271 TACATGCTATTCATTAACAAACCCAGCTTACTGTGACGCTGCAATGCTTACAGAAA 3330
OY 3364 TCTGACTTGTGAATTTAAACACAGAGACTTATGATGATCGGATCTGGAAGAAAGC 3423
DB 3331 TCTGACTTGTGAATTTAAACACAGAGACTTATGATGATCGGATCTGGAAGAAAGC 3390
OY 3424 AAGAGAACTGATGAAAGACAGTACCTCATGAGAGAGTACGCTGTGACATCGGCGCA 3483
DB 3391 AAGAGAACTGATGAAAGACAGTACCTCATGAGAGAGTACGCTGTGACATCGGCGCA 3450
OY 3484 CCTGTGAAGAAACGCGCTAGTGAACCTGGAAGAACTCTTGAACCGAACACTGTTTC 3543
DB 3451 CCTGTGAAGAAACGCGCTAGTGAACCTGGAAGAACTCTTGAACCGAACACTGTTTC 3510
OY 3544 ACTGAAGCGTGTACAAAGATTCAGTGTCTCAATCATATGATGGAAGAGCAGAGGA 3603
DB 3511 ACTGAAGCGTGTACAAAGATTCAGTGTCTCAATCATATGATGGAAGAGCAGAGGA 3570
OY 3604 AACAATGTGTGAACTGTGAAGAGCAGTGTTCGCAATAGTTGAACATTAAGTGTGAG 3663
DB 3571 AACAATGTGTGAACTGTGAAGAGCAGTGTTCGCAATAGTTGAACATTAAGTGTGAG 3630
OY 3664 ACCCTGATGTTTCAATGATTCCTTACTAGTGGTCTGCGCATTTGAATATATAT 3723
DB 3631 ACCCTGATGTTTCAATGATTCCTTACTAGTGGTCTGCGCATTTGAATATATAT 3690
OY 3724 ATGTATCAGCAGAAAGACGATTAAGACGATGTTGAATATGCTGACAGAGTTTCACTTAC 3783
DB 3691 ATGTATCAGCAGAAAGACGATTAAGACGATGTTGAATATGCTGACAGAGTTTCACTTAC 3750
OY 3784 ATTTTCATTTCTGGAATGCTTCTAATAATGGTGGCATATGCTATCAACATATTTTAC 3843
DB 3751 ATTTTCATTTCTGGAATGCTTCTAATAATGGTGGCATATGCTATCAACATATTTTAC 3810
OY 3844 AATGCTGTGTTGGTGTGACTTCTAATGTTGATGTTTCAATGTTGCTAAGTTTACAGGA 3903
DB 3811 AATGCTGTGTTGGTGTGACTTCTAATGTTGATGTTTCAATGTTGCTAAGTTTACAGGA 3870
OY 3904 AATGCTGTGTTGGTGTGACTTCTAATGTTGATGTTTCAATGTTGCTAAGTTTACAGGA 3963
DB 3871 AATGCTGTGTTGGTGTGACTTCTAATGTTGATGTTTCAATGTTGCTAAGTTTACAGGA 3930
OY 3964 AGACCTCTAAGACCTTATCTGATTTGAAGGATGAGGGTGTGTGATGCCCTTTTA 4023
DB 3931 AGACCTCTAAGACCTTATCTGATTTGAAGGATGAGGGTGTGTGATGCCCTTTTA 3990
OY 4024 GGAGCAATTCATCATCATGATGATGCTGCTGCTTCAATATTCGCTAATTTTC 4083
DB 3991 GGAGCAATTCATCATCATGATGATGCTGCTGCTTCAATATTCGCTAATTTTC 4050
OY 4084 AGCATCATGCGGTAAATTTGTTGCTGGCAATTTCTACACAGTATTAACACCAACT 4143
DB 4051 AGCATCATGCGGTAAATTTGTTGCTGGCAATTTCTACACAGTATTAACACCAACT 4110

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OY 4144 GGTGACAGTTGTGACATCGGAAGCGTGAATATCTACTGATTTGCTTAAACTATAGAA 4203
DB 4111 GGTGACAGTTGTGACATCGGAAGCGTGAATATCTACTGATTTGCTTAAACTATAGAA 4170
OY 4204 AGAATGAGACTGCTCGATGGAAGAAATGTGAAGTGAATCTTGAATATGATGATTTGG 4263
DB 4171 AGAATGAGACTGCTCGATGGAAGAAATGTGAAGTGAATCTTGAATATGATGATTTGG 4230
OY 4264 TATCTCTCTTTCCTTCAAGTTGCCACATTCAGAGATGATGATATATATGATGACCA 4323
DB 4231 TATCTCTCTTTCCTTCAAGTTGCCACATTCAGAGATGATGATATATATGATGACCA 4290
OY 4324 GTTGATTCAGAAAT 4338
DB 4291 GTTGATTCAGAAAT 4305

RESULT 13
AD32842 standard; CDNA; 4146 BP.
AD32842;
01-JUL-2002 (first entry)
Human Ion channel CDNA #4.
Human; novel human protein; NHP; voltage-gated sodium channel;
gene therapy; bioreactor; mental disorder; biological disorder;
KW gene; medical disorder; ss.
OS Homo sapiens.
XX
XX FH Location/Qualifiers
XX FT 1..4146
XX FT CDS
XX
XX /product= "Human Ion channel protein #4"
XX /transl_except= (pos:2941..2943, aa:xaa)
XX /note= "Xaa = any amino acid"
XX
XX WO200214498-A2.
XX
XX 21-FEB-2002.
XX
XX 15-AUG-2001; 2001WO-US25650.
XX
XX 16-AUG-2000; 2000US-225989P.
XX
XX (LEXI-) LEXICON GENETICS INC.
XX
XX Turner CA, Mathur B, Mathur D;
XX
XX WPI. 2002-280757/32.
XX P-PSDB; AAE20513.
XX
XX Novel polynucleotides encoding human sodium channel proteins,
XX particularly voltage-gated sodium channel proteins useful for drug
XX screening, diagnosis and in gene therapy of biological disorders
XX
XX Claim 1; Page 46-47; 83pp; English.
XX
XX The present sequence is a cDNA encoding novel human protein (NHP), ion
XX channel protein. NHP share structural similarity with mammalian sodium
XX channel proteins particularly voltage-gated sodium channel proteins.
XX NHP oligonucleotides are useful as hybridisation probes for screening
XX libraries and assessing gene expression patterns. Sequences derived
XX from regions adjacent to the intron/exon boundaries of NHP gene can be
XX used to design primers for use in amplification assays to detect
XX mutations within the exons, splice sites, introns that can be used in
XX diagnostics and pharmacogenomics. NHP nucleotide sequences are useful
XX for drug screening effective in the treatment of symptomatic or
XX phenotypic manifestations of perturbing the normal function of NHP in

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the body, and nucleotide constructs encoding NHP products are useful to genetically engineer host cells to express NHP products in vivo. These genetically engineered cells function as bioreactors in the body delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion protein to the body. Nucleotide constructs encoding NHP products are also useful in gene therapy for modulating NHP expression and to produce genetically engineered host cells to express NHP products in vivo. NHP nucleotide sequences may also be used as part of ribzyme and/or triple helix sequences that are useful for NHP gene regulation. The NHP polypeptides are useful for generating antibodies, as reagents in diagnostic assays, for identifying other cellular gene products related to NHP and as reagents in assays for screening for compounds that are useful in the treatment of mental, biological or medical disorders and diseases.

Sequence 4146 BP; 1226 A; 810 C; 951 G; 1156 T; 3 other;

Query Match 35.0%; Score 2109; DB 24; Length 4146;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|    |      |   |      |
|----|------|---|------|
| OY | 2044 | GGAAACACCTGAACTGAATGAGAAAGAGAGTCAGTCTTCCAGCTTCCATG        | 2103 |
| DB | 2011 | GGAAACACCTGAACTGAATGAGAAAGAGAGTCAGTCTTCCAGCTTCCATG        | 2070 |
| OY | 2104 | GACCTTCTGAAAGATCCTTCCCAAGCAAGCAAGATGATGACGACATCTTACA      | 2163 |
| DB | 2071 | GACCTTCTGAAAGATCCTTCCCAAGCAAGCAAGATGATGACGACATCTTACA      | 2130 |
| OY | 2164 | AATACAGTGAAGAACTGGAAGATCCAGGCAAGAAATGCCCTGTGTATAAATT      | 2223 |
| DB | 2131 | AATACAGTGAAGAACTGGAAGATCCAGGCAAGAAATGCCCTGTGTATAAATT      | 2190 |
| OY | 2224 | TCCAAATATCTTATCTGGAGCTGTTCTCATATTTGTTAAAGTGAATGTTGTC      | 2283 |
| DB | 2191 | TCCAAATATCTTATCTGGAGCTGTTCTCATATTTGTTAAAGTGAATGTTGTC      | 2250 |
| OY | 2284 | AACCTGTGTGATGAGACCCATTTGTGACCTGACCATCACCATCTGATTTCTTAAT   | 2343 |
| DB | 2251 | AACCTGTGTGATGAGACCCATTTGTGACCTGACCATCACCATCTGATTTCTTAAT   | 2310 |
| OY | 2344 | ACTCTTCATGGCCATGGAGCATTCCTCAATGAGGACATTTCAATATGCTTACA     | 2403 |
| DB | 2311 | ACTCTTCATGGCCATGGAGCATTCCTCAATGAGGACATTTCAATATGCTTACA     | 2370 |
| OY | 2404 | GTAGGAAATCTGTTTCACTGGATCTTTACAGCAGAAATGTTCTGAAAATTAATGTC  | 2463 |
| DB | 2371 | GTAGGAAATCTGTTTCACTGGATCTTTACAGCAGAAATGTTCTGAAAATTAATGTC  | 2430 |
| OY | 2464 | ATGATTCCTTATTAATTTCCAGAGGCTGGAATATCTTGAAGGTTTATTTGACG     | 2523 |
| DB | 2431 | ATGATTCCTTATTAATTTCCAGAGGCTGGAATATCTTGAAGGTTTATTTGACG     | 2490 |
| OY | 2524 | CTTACCGCTGTAAGACTTGGATCCGCAATGAGAGATATCTGTTCTCCGTTCAATT   | 2583 |
| DB | 2491 | CTTACCGCTGTAAGACTTGGATCCGCAATGAGAGATATCTGTTCTCCGTTCAATT   | 2550 |
| OY | 2584 | CGATTCGTCGAGTTTCAAGTTGSCAAATCTTGCCCAAGCTTAATATGTTAATAG    | 2643 |
| DB | 2551 | CGATTCGTCGAGTTTCAAGTTGSCAAATCTTGCCCAAGCTTAATATGTTAATAG    | 2610 |
| OY | 2644 | ATCATGCGCAATTCGCTGGGGGCTCTGGGAAATTTAACCTCGTCTGGCCATCATGTC | 2703 |
| DB | 2611 | ATCATGCGCAATTCGCTGGGGGCTCTGGGAAATTTAACCTCGTCTGGCCATCATGTC | 2670 |
| OY | 2704 | TTTCATTTTGGCGTGGGATGACGCTTTGTGTAAGAGTACAAAGATTTGTCTGC     | 2763 |
| DB | 2671 | TTTCATTTTGGCGTGGGATGACGCTTTGTGTAAGAGTACAAAGATTTGTCTGC     | 2730 |
| OY | 2764 | AAGATCGCAGATGATGCAACTCCAGCGGCGACATGAAGATTTCTCCACCTCCTC    | 2823 |
| DB | 2731 | AAGATCGCAGATGATGCAACTCCAGCGGCGACATGAAGATTTCTCCACCTCCTC    | 2790 |

|    |      |  |      |
|----|------|--|------|
| OY | 2824 | CTGATTTGTTCCGGCTGCTGTGGGAGTGAATAGACCATGTGGACTGTATGAG     | 2883 |
| DB | 2791 | CTGATTTGTTCCGGCTGCTGTGGGAGTGAATAGACCATGTGGACTGTATGAG     | 2850 |
| OY | 2884 | GTGCTGTCAAGCCATGCTTACTGTCTTCAATGATGATGATGATTTGAACCTA     | 2943 |
| DB | 2851 | GTGCTGTCAAGCCATGCTTACTGTCTTCAATGATGATGATGATTTGAACCTA     | 2910 |
| OY | 2944 | GTGGCTCGAATTCCTTCTGGCCTGCTGTGAGCTCATTTAGTGCAGACCTTGA     | 3003 |
| DB | 2911 | GTGGCTCGAATTCCTTCTGGCCTGCTGTGAGCTCATTTAGTGCAGACCTTGA     | 2970 |
| OY | 3004 | GCCACTGATGATGAATGAATGAATATCTCCAAATGCTGTGATGATGATGACAAA   | 3063 |
| DB | 2971 | GCCACTGATGATGAATGAATGAATATCTCCAAATGCTGTGATGATGATGACAAA   | 3030 |
| OY | 3064 | GGAGTACCTTATGTAAGAAAGAAATATGAAATTTATCAACAGTCTTATAGAAA    | 3123 |
| DB | 3031 | GGAGTACCTTATGTAAGAAAGAAATATGAAATTTATCAACAGTCTTATAGAAA    | 3090 |
| OY | 3124 | CAAAAGATTTATGATGAATTAACCACTGATGATGATTAACCAAGAAAGACATTT   | 3183 |
| DB | 3091 | CAAAAGATTTATGATGAATTAACCACTGATGATGATTAACCAAGAAAGACATTT   | 3150 |
| OY | 3184 | ATGTCAATCATACACAGAAATTTGGGAAAGATCTGACATCTTAAAGATGTAATGA  | 3243 |
| DB | 3151 | ATGTCAATCATACACAGAAATTTGGGAAAGATCTGACATCTTAAAGATGTAATGA  | 3210 |
| OY | 3244 | ACTACAGTGTATAGAACTGCGACAGTGTGAAAAATACATTAATGATGAAGTAT    | 3303 |
| DB | 3211 | ACTACAGTGTATAGAACTGCGACAGTGTGAAAAATACATTAATGATGAAGTAT    | 3270 |
| OY | 3304 | TACATGTCATCATTAACCAACCCAGTCTTACTGTGATGATGATGATGATGATG    | 3363 |
| DB | 3271 | TACATGTCATCATTAACCAACCCAGTCTTACTGTGATGATGATGATGATGATG    | 3330 |
| OY | 3364 | TCTGACTTTGAAATTTAAACAGGAAAGACTTGTGATGATGATGATGATGATG     | 3423 |
| DB | 3331 | TCTGACTTTGAAATTTAAACAGGAAAGACTTGTGATGATGATGATGATGATG     | 3390 |
| OY | 3424 | AAAAGAAATCTGAATGAAGAGTACTCATCAGAGGATGACACTGTGACATGCGCA   | 3483 |
| DB | 3391 | AAAAGAAATCTGAATGAAGAGTACTCATCAGAGGATGACACTGTGACATGCGCA   | 3450 |
| OY | 3484 | CCTGTAGAGAAAGCCCGTGTGGAACCTGGAACCTGGAACCTGGAACCTGGAAC    | 3543 |
| DB | 3451 | CCTGTAGAGAAAGCCCGTGTGGAACCTGGAACCTGGAACCTGGAACCTGGAAC    | 3510 |
| OY | 3544 | ACTGAAGCTGTGTACAAAGATTCAGTGTGCAATGCAATGGAAGAGCAGAGGA     | 3603 |
| DB | 3511 | ACTGAAGCTGTGTACAAAGATTCAGTGTGCAATGCAATGGAAGAGCAGAGGA     | 3570 |
| OY | 3604 | AAACAAATGCTGAACTGAGAGAGAGCTGTTCCGAATAGTTGAACATTAAGTGTGAG | 3663 |
| DB | 3571 | AAACAAATGCTGAACTGAGAGAGAGCTGTTCCGAATAGTTGAACATTAAGTGTGAG | 3630 |
| OY | 3664 | ACCTTCATTTGTTTCATGATCTCTCTAGTGTGCTCTGGATTTGAAGATATAT     | 3723 |
| DB | 3631 | ACCTTCATTTGTTTCATGATCTCTCTAGTGTGCTCTGGATTTGAAGATATAT     | 3690 |
| OY | 3724 | ATTGATCAGCAAGAGATTAAGACATGTTGAAATATGCTGCAAGGTTTCACTTAC   | 3783 |
| DB | 3691 | ATTGATCAGCAAGAGATTAAGACATGTTGAAATATGCTGCAAGGTTTCACTTAC   | 3750 |
| OY | 3784 | ATTTTCATTTGGAATAGCTTCTAAATGAGTGGCATATGAGCATTAATTTACCC    | 3843 |
| DB | 3751 | ATTTTCATTTGGAATAGCTTCTAAATGAGTGGCATATGAGCATTAATTTACCC    | 3810 |
| OY | 3844 | AATGCTGTGTTTGGCTGAGCTTCTTAATGTTGATGTTTCAATGTTTCAAGCA     | 3903 |
| DB | 3811 | AATGCTGTGTTTGGCTGAGCTTCTTAATGTTGATGTTTCAATGTTTCAAGCA     | 3870 |
| OY | 3904 | AATGCTGTGTTTACTGAGAACTTGAAGCATTAATCTGCAAGGAACTAAGAGCTCTG | 3963 |

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DB 3871 AAGCCTGGGTACTACAGACTGAGGCATCAATCTCTGAGACATGAAGCTCTG 3930
OY 3964 AGACCTTAAGACCTTATCTGATTTGAAGGATAGGGTGGTTGAATGCCCTTTA 4023
DB 3931 AGACCTTAAGACCTTATCTGATTTGAAGGATAGGGTGGTTGAATGCCCTTTA 3990
OY 4024 GGAGCAATTCATCCATCAATGAATGCTTCTGTTGCTTATATTCGGCTAATTTTC 4083
DB 3991 GGAGCAATTCATCCATCAATGAATGCTTCTGTTGCTTATATTCGGCTAATTTTC 4050
OY 4084 AGCATCATGGGCTAATTTGTTGCTGGCAATTCACACATGATTAACACACAACT 4143
DB 4051 AGCATCATGGGCTAATTTGTTGCTGGCAATTCACACATGATTAACACACAACT 4110
OY 4144 GGTGACAGG 4152
DB 4111 GGTGACAGG 4119

RESULT 14
AAD32843
ID AAD32843 standard; cDNA; 4164 BP.
XX
AC AAD32843;
XX
DT 01-JUL-2002 (first entry)
DE Human ion channel cDNA #5.
XX
DE Human ion channel cDNA #5.
XX
KM Human; novel human protein; NHP; voltage-gated sodium channel;
KW gene therapy; bioelectro; mental disorder; biological disorder;
XX
OS Homo sapiens.
XX
FH Location/Qualifiers
FT CDS 1..4164
FT FT /tag= a
FT FT /product= "human ion channel protein #5"
FT FT /transl_except= (pos:2941..2943, aa:Xaa)
FT FT /transl_except= (pos:3166..3168, aa:Xaa)
FT FT /note= "Xaa - any amino acid"
XX
PN MO20021498-A2.
XX
PD 21-FEB-2002.
XX
PF 15-AUG-2001; 2001MO-US25650.
XX
PR 16-AUG-2000; 2000US-225989P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Turner CA, Mathur B, Mathur D;
XX
DR WPI; 2002-280757/32.
XX
DR P-PSDB; AAE20514.
XX
PT Novel polynucleotides encoding human sodium channel proteins,
PT particularly voltage-gated sodium channel proteins useful for drug
PT screening, diagnosis and in gene therapy of biological disorders
XX
PS Claim 1; Page 51-52; 83pp; English.
XX
XX The present sequence is a cDNA encoding novel human protein (NHP), ion
XX channel protein. NHP share structural similarity with mammalian sodium
XX channel proteins particularly voltage-gated sodium channel proteins.
XX NHP oligonucleotides are useful as hybridisation probes for screening
XX libraries and assessing gene expression patterns. Sequences derived
XX from regions adjacent to the intron/exon boundaries of NHP gene can be
XX used to design primers for use in amplification assays to detect
XX mutations within the exons, splice sites, introns that can be used in

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CC diagnostics and pharmacogenomics. NHP nucleotide sequences are useful
CC for drug screening effective in the treatment of symptomatic or
CC phenotypic manifestations of perturbing the normal function of NHP in
CC the body, and nucleotide constructs encoding NHP products are useful to
CC genetically engineer host cells to express NHP products in vivo. These
CC genetically engineered cells function as bioelectrodes in the body
CC delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion
CC protein to the body. Nucleotide construct encoding NHP products are
CC also useful in gene therapy for modulating NHP expression and to
CC produce genetically engineered host cells to express NHP products in
CC vivo. NHP nucleotide sequences may also be used as part of ribozyme
CC and/or triple helix sequences that are useful for NHP gene regulation.
CC The NHP polypeptides are useful for generating antibodies, as
CC reagents in diagnostic assays, for identifying other cellular gene
CC products related to NHP and as reagents in assays for screening for
CC compounds that are useful in the treatment of mental, biological or
CC medical disorders and diseases.
XX
SQ Sequence 4164 BP; 1219 A; 816 C; 958 G; 1168 T; 3 other;
Query Match 33.3%; Score 2011; DB 24; Length 4164;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2011; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ATGGAGCAACAGTGGTTTACACAGAGCCTGACAGTTTAACTTCTTCCAGAGAA 60
DB 1 ATGGAGCAACAGTGGTTTACACAGAGCCTGACAGTTTAACTTCTTCCAGAGAA 60
OY 61 TCTCTTGGCGGTATTTGAAGAGCAGATTGAGAAAGAAAGCAATGCCAAGCAGAC 120
DB 61 TCTCTTGGCGGTATTTGAAGAGCAGATTGAGAAAGAAAGCAATGCCAAGCAGAC 120
OY 121 AAAAAAGATGACGAGAAATGCCCCAAAGCCAAATAGTACTGAGAGCTGAAAGAAC 180
DB 121 AAAAAAGATGACGAGAAATGCCCCAAAGCCAAATAGTACTGAGAGCTGAAAGAAC 180
OY 181 GTTCATTTATTTATGAGACATTCCTCCAGAGATGCTGACAGCCCTGGAGAGCTG 240
DB 181 GTTCATTTATTTATGAGACATTCCTCCAGAGATGCTGACAGCCCTGGAGAGCTG 240
OY 241 GACCCCTACTATATCATATAGAAACTTTTATAGTATTAATAGAGAGGAGCCATCTTC 300
DB 241 GACCCCTACTATATCATATAGAAACTTTTATAGTATTAATAGAGAGGAGCCATCTTC 300
OY 301 CGGTTGAGTGCACAGCTGCGCTGATATTTAACTCCCTTCAATCTTATAGAAATA 360
DB 301 CGGTTGAGTGCACAGCTGCGCTGATATTTAACTCCCTTCAATCTTATAGAAATA 360
OY 361 GGTATTAAGATTTGGTACATTCATTTATGACAGTCTAATATGTCATTTTGGACA 420
DB 361 GGTATTAAGATTTGGTACATTCATTTATGACAGTCTAATATGTCATTTTGGACA 420
OY 421 AACTGTGTTTATGACATGATGATTAACCTGCTGATGAGCAAGAAAGTAAATACACC 480
DB 421 AACTGTGTTTATGACATGATGATTAACCTGCTGATGAGCAAGAAAGTAAATACACC 480
OY 481 TTCACAGAAATATATCTTTTGAATCACTTATTAATAATTTATGCAAGGGGATCTGTTA 540
DB 481 TTCACAGAAATATATCTTTTGAATCACTTATTAATAATTTATGCAAGGGGATCTGTTA 540
OY 541 GAAATTTTACCTTCTTGGGATCCAGAACTGGCTGATTTGACGTCTATCAATTT 600
DB 541 GAAATTTTACCTTCTTGGGATCCAGAACTGGCTGATTTGACGTCTATCAATTT 600
OY 601 GGTACGTCACAGAGTTTGTGACCTGGGCAATGCTGGCATTTAGAAATTCAGAGTT 660
DB 601 GGTACGTCACAGAGTTTGTGACCTGGGCAATGCTGGCATTTAGAAATTCAGAGTT 660
OY 661 CTCGAGCATTTAAGAGATTTTCAATTCAGAGCTGAAACCATTTGTGGAGCCCTG 720
DB 661 CTCGAGCATTTAAGAGATTTTCAATTCAGAGCTGAAACCATTTGTGGAGCCCTG 720
OY 721 ATCCAGTCTGTGAAGAGCTCTCAAGTATGATCTGACTGTCTGTCTGAGCGTA 780

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Db 721 ATTCAGTCTGTGAAGAGCTCAGATGTATATCTCTGACTGTCTCTGAGCGTA 780
OY 781 TTGGCTATATGGGCGTGCATGTCANGGGGAACCTGAGGAATAATATACATGG 840
Db 781 TTGGCTATATGGGCGTGCATGTCANGGGGAACCTGAGGAATAATATACATGG 840
OY 841 CCTCCACCAATGCTCTCTGGAGGAACATAGTATAGAAAAGAAATTAATCTGAATTA 900
Db 841 CCTCCACCAATGCTCTCTGGAGGAACATAGTATAGAAAAGAAATTAATCTGAATTA 900
OY 901 AATGTAACATTAATAATGAAGTGTCTTGAATGAGTGAAGTCAATATTCAGAT 960
Db 901 AATGTAACATTAATAATGAAGTGTCTTGAATGAGTGAAGTCAATATTCAGAT 960
OY 961 TCAAGATATCATATTTCCGGAGGGTTTTTATGATGCACTACTATATGGAATACCT 1020
Db 961 TCAAGATATCATATTTCCGGAGGGTTTTTATGATGCACTACTATATGGAATACCT 1020
OY 1021 GATGAGGCCAATGTCAGAGGATATATGTGTGAAAGCTGTAGAAATCCCAATTAT 1080
Db 1021 GATGAGGCCAATGTCAGAGGATATATGTGTGAAAGCTGTAGAAATCCCAATTAT 1080
OY 1081 GGCTACACAAGCTTTGATACCTTCAGTGGCTTTTGTCTGTTGCTGACTAATGACT 1140
Db 1081 GGCTACACAAGCTTTGATACCTTCAGTGGCTTTTGTCTGTTGCTGACTAATGACT 1140
OY 1141 CAGGACTCTGGGAAAAATCTTATCAACTACATFACGTCTCTCTGGAAAAAGTACATG 1200
Db 1141 CAGGACTCTGGGAAAAATCTTATCAACTACATFACGTCTCTCTGGAAAAAGTACATG 1200
OY 1201 AATATTTTGTGTGCTATTTCTGTGGGCTCATTTCTACCTAATAATTTGATCCGGCT 1260
Db 1201 AATATTTTGTGTGCTATTTCTGTGGGCTCATTTCTACCTAATAATTTGATCCGGCT 1260
OY 1261 GTGGTGCCATGGCTACGAGGAACAGAAATCAGGCCACCTTGGAGAGCAGAAACAGAAA 1320
Db 1261 GTGGTGCCATGGCTACGAGGAACAGAAATCAGGCCACCTTGGAGAGCAGAAACAGAAA 1320
OY 1321 GAGGCCGAATTTCAAGCATGATTTGAACAGACTTAAAAAGCAACAGAGGAGCTCAGCAG 1380
Db 1321 GAGGCCGAATTTCAAGCATGATTTGAACAGACTTAAAAAGCAACAGAGGAGCTCAGCAG 1380
OY 1381 GAGCAAGGCACTGGCTCAGAACATTCAGAGAGGCCAGTCCAGAGGAGGAGGCTCTCA 1440
Db 1381 GAGCAAGGCACTGGCTCAGAACATTCAGAGAGGCCAGTCCAGAGGAGGAGGCTCTCA 1440
OY 1441 GAGAGCTCATCTGAAGCTCTAAGTTGAGTTCCAAAGATGCTTAAGGAAAGAAATCGG 1500
Db 1441 GAGAGCTCATCTGAAGCTCTAAGTTGAGTTCCAAAGATGCTTAAGGAAAGAAATCGG 1500
OY 1501 AGGAGAAAAAGAAAACAGAAAGAGAGCTGTGTGGGAGAGAAAGATGAGATGAAATTC 1560
Db 1501 AGGAGAAAAAGAAAACAGAAAGAGAGCTGTGTGGGAGAGAAAGATGAGATGAAATTC 1560
OY 1561 CAAAAATCTGAATCTGAGCAGCATCAGGAGGAAAAAGTTTTGGCTTCCATTTGAAGGG 1620
Db 1561 CAAAAATCTGAATCTGAGCAGCATCAGGAGGAAAAAGTTTTGGCTTCCATTTGAAGGG 1620
OY 1621 AACCGATGACATATGAAAAGAGTACTCTCCCAACAGAGTCTTGTGTGAGCATCCGT 1680
Db 1621 AACCGATGACATATGAAAAGAGTACTCTCTCCCAACAGAGTCTTGTGTGAGCATCCGT 1680
OY 1681 GGTCTCCATATTTTACCAAGGCAATAGCAGAAAGCCTTTTACGCTTTAGAGGGCGA 1740
Db 1681 GGTCTCCATATTTTACCAAGGCAATAGCAGAAAGCCTTTTACGCTTTAGAGGGCGA 1740
OY 1741 GCAAGGATGTGGATCTGAGAGGAGCTTGAGATGATGAGAGACGACCTTGGAGAT 1800
Db 1741 GCAAGGATGTGGATCTGAGAGGAGCTTGAGATGATGAGAGACGACCTTGGAGAT 1800
OY 1801 AAGGAGCGGTAGAGATTCCTTGTGTGTCCTCCGAGCAGACGAGAGAGACGCAACAGC 1860

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Db 1801 AAGGAGCGGTAGAGATTCCTTGTGTGTCCTCCGAGCAGACGAGAGAGACGCAACAGC 1860
OY 1861 AACCTGAGTCACACACAGTAGTATGATATCCCGAGATGCTGTCCTCCAGCAATGGGAG 1920
Db 1861 AACCTGAGTCACACACAGTAGTATGATATCCCGAGATGCTGTCCTCCAGCAATGGGAG 1920
OY 1921 ATGACAGCAGCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
Db 1921 ATGACAGCAGCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
OY 1981 ACATGCTCTGTTGGACAGCTTCTGCCAGAG 2011
Db 1981 ACATGCTCTGTTGGACAGCTTCTGCCAGAG 2011

RESULT 15
AAK02861/C
ID AAK02861 standard; DNA; 1992 BP.
XX
AC AAK02861;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe SEQ ID NO: 2852.
XX
KW Human; brain expressed exon; gene expression analysis; probe;
KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW epilepsy; cancer; ss.
XX
OS Homo sapiens.
XX
PN M0200157275-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00067.
XX
PR 04-FEB-2000; 2000US-0180312.
XX
PR 26-MAY-2000; 2000US-0207456.
XX
PR 30-JUN-2000; 2000US-0608408.
XX
PR 03-AUG-2000; 2000US-0632366.
XX
PR 21-SEP-2000; 2000US-0234687.
XX
PR 27-SEP-2000; 2000US-0236359.
XX
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483446/52.
XX
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains -
XX
XX Example 4: SEQ ID NO: 2852; 650bp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX brain. They can be used to measure gene expression in brain cell samples,
XX which may enable the diagnosis and improved treatment of nervous system
XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX epilepsy and cancers. The present sequence is one of the probes of the
XX invention.
XX
XX Sequence 1992 BP; 589 A; 399 C; 384 G; 620 T; 0 other;
XX
XX
XX Query Match 19.6%; Score 1181; DB 22; Length 1992;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 1181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4850 TAGGTATGTTCTTGGCCAGTGTAGTAAAGTATTTGCTGCTTCCCTACCTGTTCCGAG 4909
Db 1447 TAGGTATGTTCTTGGCCAGTGTAGTAAAGTATTTGCTGCTTCCCTACCTGTTCCGAG 1388

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|    |      |  |      |
|----|------|--|------|
| Oy | 4910 | TGACCGCTTGGTAGAGATTGGCCGAATGCTACGCCTCATCAAAAGACAAGGGAGATTC     | 4969 |
| Db | 1387 | TGATCCGTCTGGTAGAGATTGGCCGAATGCTACGCCTCATCAAAAGACAAGGGAGATTC    | 1328 |
| Oy | 4970 | GCAAGCGTCCTTTGGCTTGATGATGTCCTCCCTCCTGCGCTGTTAACATCGGCCCTCTAC   | 5029 |
| Db | 1337 | GCACGCGTCCTTTGGCTTGATGATGTCCTCCCTCCTGCGCTGTTAACATCGGCCCTCTAC   | 1268 |
| Oy | 5030 | TCTTCACAGCATGTCATCTACCTACGCCACTGTTGGGATGTCACAAGCTCCGATCTTAGA   | 5089 |
| Db | 1267 | TCTTCACAGCATGTCATCTACGCCACTGTTGGGATGTCACAAGCTCCGATCTTAGA       | 1208 |
| Oy | 5090 | GGGAAGTTGGGATGATGATGACATGTTCAACTTTGAGACCTTTGGCAAACAGCATGATCGCC | 5149 |
| Db | 1207 | GGGAAGTTGGGATGATGATGACATGTTCAACTTTGAGACCTTTGGCAAACAGCATGATCGCC | 1148 |
| Oy | 5150 | TATTCGAAAATAACAACCTCGCTGGCGTGGGATGAGATGTCAGACCCTCTGTCACAGTA    | 5209 |
| Db | 1147 | TATTCGAAAATAACAACCTCGCTGGCGTGGGATGAGATGTCAGACCCTCTGTCACAGTA    | 1088 |
| Oy | 5210 | AGCCACCCGACTGTGACCCCTAATAAAGTTAACCTCGGAAGCTCATGTTAAGGAGACGTGTG | 5269 |
| Db | 1087 | AGCCACCCGACTGTGACCCCTAATAAAGTTAACCTCGGAAGCTCATGTTAAGGAGACGTGTG | 1028 |
| Oy | 5270 | GGAACCATCTGTTGGAAATTTTTTTTTTGTCAGTTACATCATATATCCTTCTGTTG       | 5329 |
| Db | 1037 | GGAACCATCTGTTGGAAATTTTTTTTTTGTCAGTTACATCATATCCTTCTGTTG         | 968  |
| Oy | 5330 | TGGTGAACATGTATACATGGCGGTATCCTCGTGAAGAATCTGTTCTCTACTGAAAGATG    | 5389 |
| Db | 967  | TGGTGAACATGTATACATGGCGGTATCCTCGTGAAGAATCTGTTCTCTACTGAAAGATG    | 908  |
| Oy | 5390 | CAGAACCTCTGATGAGAGATGACTTTGAATGTTCTATGAGGTTTGGAGAAAGTTGATC     | 5449 |
| Db | 907  | CAGAACCTCTGATGAGAGATGACTTTGAATGTTCTATGAGGTTTGGAGAAAGTTGATC     | 848  |
| Oy | 5450 | CCGANTCAACACTGTCATGGAATTTGAAAAATATATCAGTTTGACACTCGCGCTGAC      | 5509 |
| Db | 847  | CCGANTCAACACTGTCATGGAATTTGAAAAATATATCAGTTTGACACTCGCGCTGAC      | 788  |
| Oy | 5510 | CGCCTCTCAATCTCCCAACAACAACAACCTCAGCTCATTTGCCATGATTTGGCCATCG     | 5569 |
| Db | 787  | CGCCTCTCAATCTCCCAACAACAACAACCTCAGCTCATTTGCCATGATTTGGCCATCG     | 728  |
| Oy | 5570 | TGATGGTGACCGGATCTCACTGCTCTGATATCTTATTTCTCTTTTCAAAAGCGGTTCTAG   | 5629 |
| Db | 727  | TGATGGTGACCGGATCTCACTGCTCTGATATCTTATTTCTCTCTTTTCAAAAGCGGTTCTAG | 668  |
| Oy | 5630 | GAGAGAGTGGAGATGATGATGCTCTCAAGATACAGATGGAAGAGGATCATAGGCTTCCA    | 5689 |
| Db | 667  | GAGAGAGTGGAGATGATGATGCTCTCAAGATACAGATGGAAGAGGATCATAGGCTTCCA    | 608  |
| Oy | 5690 | ATCCTTCCAAAGTCTCCTATCACCAATCATACTACTTTAAAGGAAAACAAGAGGAG       | 5749 |
| Db | 607  | ATCCTTCCAAAGTCTCCTATCACCAATCATACTACTTTAAAGGAAAACAAGAGGAG       | 548  |
| Oy | 5750 | TATCTGCTGTCATATTTACAGCGTGTCTTACAGACGCCACTTTTAAAGGAAGTGTAAAC    | 5809 |
| Db | 547  | TATCTGCTGTCATATTTACAGCGTGTCTTACAGAGGCCACTTTTAAAGGAAGTGTAAAC    | 488  |
| Oy | 5810 | AAGCTTCCTTACGTACAAATAAATAACAATAACAAGTGGGGCTATCTCTTATAAAG       | 5869 |
| Db | 487  | AAGCTTCCTTACGTACAAATAAATAACAATAACAAGTGGGGCTATCTCTTATAAAG       | 428  |
| Oy | 5870 | AAAGATGATTAATTGACAGAAATAAATGAAAATCTATTACAGAAAAAACTGATCTGACCA   | 5929 |
| Db | 427  | AAAGATGATTAATTGACAGAAATAAATGAAAATCTATTACAGAAAAAACTGATCTGACCA   | 368  |
| Oy | 5930 | TGTCACAGTGAAGCTTGTCACACTTCCATGATACGGGGTGAACAAGCAATGTGGAANAAC   | 5989 |
| Db | 367  | TGTCACAGTGAAGCTTGTCACACTTCCATGATACGGGGTGAACAAGCAATGTGGAANAAC   | 308  |

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Oy 5990 ATGACCAAGAAAGCGCAAAAGTGTAAAAAGCCAAAGCGCAAAATTA 6030
Db 307 ATGACCAAGAAAGCGCAAAAGTGTAAAAAGCCAAAGCGCAAAATTA 267

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Search completed: April 22, 2003, 14:24:28  
Job time : 798 secs

GenCore version 5.1.4\_p5\_4578  
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OM nucleic - nucleic search, using sw model

Run on: April 22, 2003, 13:39:49 ; Search time 5066 Seconds  
(without alignments)  
19277.297 Million cell updates/sec

Title: US-09-930-871-11

Perfect score: 6030  
Sequence: 1 atgagcaacaacagctgtctt.....aaaagccaagggaaatca 6030

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST:  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estcom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1          | 559   | 9.3         | 579    | 14 | BM718214    |
| 2          | 548   | 9.1         | 562    | 14 | BM682680    |
| 3          | 427   | 7.1         | 683    | 13 | BI667397    |
| 4          | 348   | 5.8         | 951    | 9  | AL533359    |
| 5          | 285   | 4.7         | 455    | 9  | AA912739    |
| 6          | 264   | 4.4         | 710    | 9  | AL707423    |

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 7          | 213   | 3.5         | 717    | 12 | BG724147    |
| 8          | 173   | 2.9         | 382    | 12 | BG208320    |
| 9          | 164   | 2.7         | 598    | 14 | BM726341    |
| 10         | 154   | 2.6         | 774    | 13 | BI488799    |
| 11         | 148   | 2.5         | 482    | 13 | BI032903    |
| 12         | 146   | 2.4         | 735    | 13 | BI488967    |
| 13         | 135   | 2.2         | 672    | 17 | AG054756    |
| 14         | 115   | 1.9         | 450    | 9  | AL120392    |
| 15         | 107   | 1.8         | 325    | 9  | AA214661    |
| 16         | 98    | 1.6         | 343    | 14 | P07776      |
| 17         | 98    | 1.6         | 873    | 12 | BF527027    |
| 18         | 80    | 1.3         | 402    | 13 | BM484672    |
| 19         | 79    | 1.3         | 304    | 12 | BG181807    |
| 20         | 79    | 1.3         | 618    | 10 | BE566126    |
| 21         | 79    | 1.3         | 892    | 12 | BG215777    |
| 22         | 79    | 1.3         | 982    | 14 | BM905527    |
| 23         | 76    | 1.3         | 731    | 9  | AT796228    |
| 24         | 70    | 1.2         | 602    | 9  | AL706368    |
| 25         | 65    | 1.1         | 674    | 12 | BG342331    |
| 26         | 64    | 1.1         | 260    | 12 | BG227970    |
| 27         | 62    | 1.0         | 577    | 9  | AU067361    |
| 28         | 62    | 1.0         | 581    | 10 | BB644560    |
| 29         | 62    | 1.0         | 800    | 9  | AU066802    |
| 30         | 62    | 1.0         | 900    | 9  | AU067321    |
| 31         | 52    | 0.9         | 693    | 17 | AG178030    |
| 32         | 50    | 0.8         | 438    | 12 | AZ495334    |
| 33         | 50    | 0.8         | 490    | 12 | BF391260    |
| 34         | 50    | 0.8         | 928    | 14 | BO715936    |
| 35         | 48    | 0.8         | 561    | 12 | BF076296    |
| 36         | 47    | 0.8         | 325    | 12 | BF471558    |
| 37         | 47    | 0.8         | 373    | 10 | AM456773    |
| 38         | 47    | 0.8         | 379    | 12 | BE947431    |
| 39         | 47    | 0.8         | 386    | 12 | BE944106    |
| 40         | 47    | 0.8         | 437    | 10 | AM495598    |
| 41         | 47    | 0.8         | 495    | 12 | BE563427    |
| 42         | 47    | 0.8         | 547    | 12 | BF470392    |
| 43         | 47    | 0.8         | 618    | 10 | BB622500    |
| 44         | 47    | 0.8         | 721    | 17 | BH035847    |
| 45         | 45    | 0.7         | 293    | 12 | BG183871    |

## ALIGNMENTS

RESULT 1  
BM718214 579 bp mRNA linear EST 01-MAR-2002  
UI-E-EJ1-ajf-a-09-0-UI-r1 UI-E-EJ1 Homo sapiens CDNA clone  
DEFINITION  
BM718214  
LOCUS  
ACCESSION  
BM718214  
VERSION  
BM718214.1 GI:19036382  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens  
human.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 579)  
Bonaldo, M.F., Lennon, G. and Soares, M.B.  
Normalization and subtraction: two approaches to facilitate gene  
discovery  
JOURNAL  
Genome Res. 6 (9), 791-806 (1996)  
MEDLINE  
97044477  
COMMENT  
Contact: Soares, MB  
Program for Rat Gene Discovery and Mapping  
University of Iowa  
451 Eckstein Medical Research Building Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: msoares@blue.weeg.uiowa.edu  
Tissue Procurement: Dr. Gregg Hageman  
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).  
 Seq primer: M13 Reverse.  
 Location/Qualifiers  
 1. 579  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="UI-E-E1-a-09-0-UI"  
 /tissue\_type="fetal eyes, lens, eye anterior segment, optic nerve, retina, Retina Foveal and Macular, RPE and Choroid"  
 /dev\_stage="fetal and adult"  
 /lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
 /note="Organ: eye; Vector: p773-Pac (Pharmacia) with a modified polylinker; Site.1: EcoR I; Site.2: Not I; UI-E-E1 is a subcloned cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGAATCAGA ; lens, CGATTAGCGA; eye anterior segment, AATGCCCAT; optic nerve, CCATTAGTG; retina, CCGCG; Retina Foveal and Macular, GTCC; RPE and Choroid, ACCCA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

BASE COUNT 168 a 123 c 125 g 163 t  
 ORIGIN

Query Match 9.3%; Score 559; DB 14; Length 579;  
 Best Local Similarity 100.0%; Pred No. 1.9e-278; Indels 0; Gaps 0;  
 Matches 559; Conservative 0; Mismatches 0;

QY 5270 GGAACCCATCTGTTGGAATTTCTTTTGTGCAATCATCATCATCTCTGTTG 5329  
 DB 1 GGAACCCATCTGTTGGAATTTCTTTTGTGCAATCATCATCATCTCTGTTG 60  
 QY 5330 TGGTGAACATGTCACATCGCGTCATCTCGAGAACTTCACTGCTACGAAAGAGTG 5389  
 DB 61 TGGTGAACATGTCACATCGCGTCATCTCGAGAACTTCACTGCTACGAAAGAGTG 120  
 QY 5390 CAGAGCCTCGAGTGGAGTACCTTGAGATGTTCTATGAGGTTGGAGAGTTGATC 5449  
 DB 121 CAGAGCCTCGAGTGGAGTACCTTGAGATGTTCTATGAGGTTGGAGAGTTGATC 180  
 QY 5450 CCGATGCAATCTGTCATGGAATTTGAAAATTTATCTCAGTTTGACGTCGCTTGAC 5509  
 DB 181 CCGATGCAATCTGTCATGGAATTTGAAAATTTATCTCAGTTTGACGTCGCTTGAC 240  
 QY 5510 CGCCTTCATATGTCACAAACAAACAACTCCAGCTATGCGCATGATGGCCATGG 5569  
 DB 241 CGCCTTCATATGTCACAAACAAACAACTCCAGCTATGCGCATGATGGCCATGG 300  
 QY 5570 TGAAGTGGACCGGATCCAGTCTGATATCTTATTTGTTTACAAAGGGGTTCTAG 5629  
 DB 301 TGAAGTGGACCGGATCCAGTCTGATATCTTATTTGTTTACAAAGGGGTTCTAG 360  
 QY 5630 GAGAGTGGAGATGATGCTCTACGAATACAGATGGAAGAGCATGCTGCTTCCA 5689  
 DB 361 GAGAGTGGAGATGATGCTCTACGAATACAGATGGAAGAGCATGCTGCTTCCA 420  
 QY 5690 ATCTCTCAAGGCTCTCTATACGCAATCACTACTTTTAAACGAAAGAGAGAG 5749  
 DB 421 ATCTCTCAAGGCTCTCTATACGCAATCACTACTTTTAAACGAAAGAGAGAG 480  
 QY 5750 TATCTGCTGATATTCAGGCTTACAGAGCCACCTTTTAAAGGAACGTAAAC 5809  
 DB 481 TATCTGCTGATATTCAGGCTTACAGAGCCACCTTTTAAAGGAACGTAAAC 540

QY 5810 AAGCTTCTTACGTACCA 5828  
 DB 541 AAGCTTCTTACGTACCA 559

RESULT 2  
 LOCUS BM682680/c 562 bp mRNA linear EST 27-FEB-2002  
 DEFINITION UI-E-E1-a-09-0-UI.s1 UI-E-E1 Homo sapiens cDNA clone  
 UI-E-E1-a-09-0-UI 3', mRNA sequence.  
 ACCESSION BM682680  
 VERSION BM682680.1 GI:18992576  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 562)  
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.  
 TITLE Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 JOURNAL Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE 97044477  
 COMMENT Contact: Soares, MB  
 Program for Rat Gene Discovery and Mapping  
 University of Iowa  
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: msoares@blue.weeg.uiowa.edu  
 Tissue Procurement: Dr. Gregg Hageman  
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).  
 Seq primer: M13 Forward  
 POLYA=yes.

FEATURES  
 source

1. 562  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="UI-E-E1-a-09-0-UI"  
 /clone\_lib="UI-E-E1"  
 /tissue\_type="fetal eyes, lens, eye anterior segment, optic nerve, retina, Retina Foveal and Macular, RPE and Choroid"  
 /dev\_stage="fetal and adult"  
 /lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
 /note="Organ: eye; Vector: p773-Pac (Pharmacia) with a modified polylinker; Site.1: EcoR I; Site.2: Not I; UI-E-E1 is a subcloned cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGAATCAGA ; lens, CGATTAGCGA; eye anterior segment, AATGCCCAT; optic nerve, CCATTAGTG; retina, CCGCG; Retina Foveal and Macular, GTCC; RPE and Choroid, ACCCA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).  
 TAG\_LIB=UI-E-E1  
 TAG\_TISSUE=Foveal and Macular Retina  
 TAG\_SEQ=GTCC"  
 BASE COUNT 161 a 121 c 118 g 162 t  
 ORIGIN

Query Match 9.1%; Score 548; DB 14; Length 562;  
 Best Local Similarity 100.0%; Pred. No. 9.8e-273; Indels 0; Gaps 0;  
 Matches 548; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5281 GTTGAATTTCTTTTCTTCTAGTACATCATATCCCTCCGTTGGTGTGAACATG 5340  
 |||||  
 DB 562 GTTGAATTTCTTTTCTTCTAGTACATCATATCCCTCCGTTGGTGTGAACATG 503

QY 5341 TACATCCGGTCTCTCGGAGAACTTCACTGTTGCTCTCTAGAGAAATGCAAGCCTCTG 5400  
 |||||  
 DB 502 TACATCCGGTCTCTCGGAGAACTTCACTGTTGCTCTCTAGAGAAATGCAAGCCTCTG 443

QY 5401 AGTGAAGATGCTTGTGATGTTCTATGAGATTTGGAGAAAGTTGATCCGATGCAACT 5460  
 |||||  
 DB 442 AGTGAAGATGCTTGTGATGTTCTATGAGATTTGGAGAAAGTTGATCCGATGCAACT 383

QY 5461 CAGTTTCAATGAAATTTGAAAAATATCTCACTTTGACCTGCGCTGTAACCGCTCTCAAT 5520  
 |||||  
 DB 382 CAGTTTCAATGAAATTTGAAAAATATCTCACTTTGACCTGCGCTGTAACCGCTCTCAAT 323

QY 5521 CTGCGACACCAACCAAACTCCAGCTCATGTCATGATTTGCCATGTTGATGTTGAC 5580  
 |||||  
 DB 322 CTGCGACACCAACCAAACTCCAGCTCATGTCATGATTTGCCATGTTGATGTTGAC 263

QY 5581 CGGATCCACTGCTGTGATCTTATCTTATTTGCTTTTCAAAAGGGGTTCTAGAGAGAGTGA 5640  
 |||||  
 DB 262 CGGATCCACTGCTGTGATCTTATCTTATTTGCTTTTCAAAAGGGGTTCTAGAGAGAGTGA 203

QY 5641 GAGATGATGCTCTACAGATATACAGATGGAAGAGGATTCATGCTTCCATCCCTCCAG 5700  
 |||||  
 DB 202 GAGATGATGCTCTACAGATATACAGATGGAAGAGGATTCATGCTTCCATCCCTCCAG 143

QY 5701 GTCTCTATGACCAATCACTACTACTTAAACGAAAGAGAGATGCTGTC 5760  
 |||||  
 DB 142 GTCTCTATGACCAATCACTACTACTTAAACGAAAGAGAGATGCTGTC 83

QY 5761 ATATTTAGCGTGTCTACAGACGCACTTTTAAAGGAAGTGTAAACAGCTCTT 5820  
 |||||  
 DB 82 ATATTTAGCGTGTCTACAGACGCACTTTTAAAGGAAGTGTAAACAGCTCTT 23

QY 5821 ACGTACAA 5828  
 |||||  
 DB 22 ACGTACAA 15

RESULT 3  
 B1667397 683 bp mRNA linear EST 12-SEP-2001  
 LOCUS 603292118F1 NIH\_MGC\_96 Homo sapiens cDNA clone IMAGE:511627 5',  
 mRNA sequence.  
 ACCESSION B1667397  
 VERSION B1667397.1 GI:15581630  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 683)  
 NIH-MGC http://mgs.ncl.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-remail.nih.gov  
 Tissue Procurement: Miklos Palokovits, M.D., Ph.D.  
 CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shitaki  
 Toshiyuki and Piero Carninci (RIKEN)  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: L16M1789 row: k column: 20  
 High quality sequence stop: 681.

FEATURES  
 source Location/Qualifiers  
 1.683  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_image="511627"  
 /clone\_id="NIH\_MGC\_96"  
 /tissue\_type="hypothalamus"  
 /lab\_host="DH10B"  
 /note="Organ: Brain; Vector: pBluescript (modified  
 pBluescript KS+); Site\_1: BamHI; Site\_2: SalI-XhoI (gtcgag  
 ); Oligo-dt primed using primer 5'-TTTTTTTTTTTTTNN-3',  
 size-selected for average insert size 2.3 kb and  
 normalized to 10^5. This is a primary library enriched  
 for full-length clones and constructed using the  
 cap-trapper method (Carninci, in preparation). Library  
 constructed by M. Brownstein (NHGRI/NHRI, National  
 Institutes of Health). Note: this is a NIH-MGC library."

BASE COUNT 236 a 136 c 139 g 172 t

Query Match 7.1%; Score 427; DB 13; Length 683;  
 Best Local Similarity 100.0%; Pred. No. 8.1e-210; Indels 0; Gaps 0;  
 Matches 427; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5587 CACTGCTTGATATCTTATTTGCTTTTACAAAGCGGTTCTAGAGAGATGAGAGATG 5646  
 |||||  
 DB 6 CACTGCTTGATATCTTATTTGCTTTTACAAAGCGGTTCTAGAGAGATGAGAGATG 65

QY 5647 GATGCTCTACAGATACAGATGGAAGAGCGATTCATGCTTCCATCCCTCCAGTCTCC 5706  
 |||||  
 DB 66 GATGCTCTACAGATACAGATGGAAGAGCGATTCATGCTTCCATCCCTCCAGTCTCC 125

QY 5707 TATCAGCAATCACTACTACTTAAACGAAAGAGAGATGCTGCTGCTATAT 5766  
 |||||  
 DB 126 TATCAGCAATCACTACTACTTAAACGAAAGAGAGATGCTGCTGCTATAT 185

QY 5767 CACGCGCTTACAGAGCGCCACTTTTAAAGCAACTGTAAACAGCTTCTTACGTAC 5826  
 |||||  
 DB 186 CACGCGCTTACAGAGCGCCACTTTTAAAGCAACTGTAAACAGCTTCTTACGTAC 245

QY 5827 ATATTAACCAATCAAAAGTGGGCTATCTTCTTAAAGAGACATGATATATGAC 5886  
 |||||  
 DB 246 ATATTAACCAATCAAAAGTGGGCTATCTTCTTAAAGAGACATGATATATGAC 305

QY 5887 AGATTAATGAAACTCTATATACGAAAAAAGTATGACATGTCACACTGACGCTGT 5946  
 |||||  
 DB 306 AGATTAATGAAACTCTATATACGAAAAAAGTATGACATGTCACACTGACGCTGT 365

QY 5947 CCACCTTCTATGACCGCGGTGACAAAGCCAAATGTGAAAAACATGACCAAGGCAAA 6006  
 |||||  
 DB 366 CCACCTTCTATGACCGCGGTGACAAAGCCAAATGTGAAAAACATGACCAAGGCAAA 425

QY 6007 GATGAAA 6013  
 |||||  
 DB 426 GATGAAA 432

RESULT 4  
 AL533359 951 bp mRNA linear EST 13-FEB-2001  
 LOCUS AL533359  
 DEFINITION AL533359 L11\_F015\_Brn1 Homo sapiens cDNA clone CSODN0041F22 5  
 prime, mRNA sequence.  
 ACCESSION AL533359  
 VERSION AL533359.1 GI:12796852  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 951)  
 L11\_F015\_Brn1, Gruber, C., Jesse, J., and Polyes, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)



| REFERENCE                                | AUTHORS   | TITLE  | JOURNAL   | COMMENT   |
|--|---|--|---|---|
| 1 (bases 1 to 717)                       | NIH-MGC   | http://mgc.ncl.nih.gov/.                           | National Institutes of Health, Mammalian Gene Collection (MGC)  | Unpublished (1999)  |
| Contact: Robert Strausberg, Ph.D.        | Email: cgapds-remail.nih.gov  | Tissue Procurement: Mikiros Palkovits, M.D., Ph.D. | CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shitaki Toshitaka and Piero Carninci (RIKEN)           | CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)   |
| DNA sequencing by: Incyte Genomics, Inc. | Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.lnl.gov | Plate: LLM10749                                    | Row: C  | Column: 17  |
| High quality sequence stop: 712.         | Location/Qualifiers   | 1. 717   | /organism="Homo sapiens"  | /db_xref="taxon:9606"   |
| /clone_image="4829512"                   | /clone_id="NIH.MGC.97"  | /lab_host="DH10B"                                  | /note="Organ: testis; Vector: pBluescript (modified pBluescript KS+); Site.1: BamHI; Site.2: SalI-XhoI (glucag) | ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.2 kb and normalized to R0F 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH-MGC Library." |
| BASE COUNT                               | 180 a   | 182 c  | 151 g   | 204 t   |
| ORIGIN                                   |   |  |   |   |
| Query Match                              | 3.5%  | Score 213:   | DB 12:  | Length 717:   |
| Best Local Similarity                    | 100.0%  | Prod. No. 1.4e-96;                                 |   |   |
| Matches 213;                             | Conservative 0;   | Mismatches 0;                                      | Indels 0;   | Gaps 0;   |
| QY 3200                                  | CAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAATGAACTACAACTAGGTATAG   | 3259   |   |   |
| DB 612                                   | CAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAATGAACTACAACTAGGTATAG   | 553  |   |   |
| QY 3260                                  | GAACTGGCAGCAGTGTGAAAATACATTATGTAGGAAGAAGTATTCATGTCATTCATTA  | 3319   |   |   |
| DB 552                                   | GAACTGGCAGCAGTGTGAAAATACATTATGTAGGAAGAAGTATTCATGTCATTCATTA  | 493  |   |   |
| QY 3320                                  | ACAACCCCGCTTCTGCTGACTGTACCAATGCTGTAGGAGAATCTGACTTGAATTT   | 3379   |   |   |
| DB 492                                   | ACAACCCCGCTTCTGCTGACTGTACCAATGCTGTAGGAGAATCTGACTTGAATTT   | 433  |   |   |
| QY 3380                                  | TAAACACGGAAGACTTTAGTAGTCGATC 3412   |  |   |   |
| DB 432                                   | TAAACACGGAAGACTTTAGTAGTCGATC 400  |  |   |   |
| RESULT 8                                 | 382 bp  | mRNA   | linear  | EST 21-APR-2001   |
| LOCUS                                    | RG208320/c  |  |   |   |
| DEFINITION                               | RG272812  | Athersys RAGE Library                              | Homo sapiens cDNA, mRNA sequence.   |   |
| ACCESSION                                | RG208320  |  |   |   |
| VERSION                                  | RG208320.1  | GI:13730007  |   |   |
| KEYWORDS                                 | EST.  |  |   |   |
| SOURCE                                   | human.  |  |   |   |
| ORGANISM                                 | Homo sapiens  |  |   |   |
| REFERENCE                                | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;   |  |   |   |
| AUTHORS                                  | Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.   |  |   |   |
|  | 1 (bases 1 to 382)  |  |   |   |
|  | Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,  |  |   |   |
|  | Cahn, S., Leverette, C., Thornton, M., Ramchandran, R., Whittington, J.,  |  |   |   |
|  | Lerner, L., Costanzo, D., McElligott, K., Booser, S., Mays, R., Smith   |  |   |   |
|  | , E., Veloso, N., Kliska, A., Hess, J., Colthen, K., Lo, K., Offenbacher  |  |   |   |
|  | , J., Danzig, J., and Ducat, M.,  |  |   |   |



TITLE Creation of genome-wide protein expression libraries using random activation of gene expression  
 JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)  
 MEDLINE 21227151  
 COMMENT Contact: Scott J. Cain  
 Athersys, Inc.  
 3201 Carnegie Ave, Cleveland, OH 44115, USA  
 Tel: 216 431 9900  
 Fax: 216 361 9596  
 Email: sca@atersys.com  
 High quality sequence stop: 382.  
 Location/Qualifiers

FEATURES  
 source  
 1. 382  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="Athersys RAGE Library"  
 /cell\_line="HT1080"  
 /note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

BASE COUNT 103 a 104 c 82 g 91 t 2 others

Query Match 2.9%; Score 173; DB 12; Length 382;  
 Best Local Similarity 99.6%; Pred. No. 7.6e-78;  
 Matches 223; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1661 AGCTTTGTGAGATCCGTGCTCCCTATTTCACCAAGCGAATATGAGACAAGCC 1720  
 DB 327 AGCTTTGTGAGATCCGTGCTCCCTATTTCACCAAGCGAATATGAGACAAGCC 268  
 QY 1721 TTTTCACCTTTAGAGCGCGAGCAAGATGTGGATGTGAAACGACTTGGCAGATGATG 1780  
 DB 267 TTTTCACCTTTAGAGCGCGAGCAAGATGTGGATGTGAAACGACTTGGCAGATGATG 208  
 QY 1781 AGCAGACACCTTTGAGATACAGAGCGGTGAGATCTGTTGTGCCCCGAGAC 1840  
 DB 207 AGCAGACACCTTTGAGATACAGAGCGGTGAGATCTGTTGTGCCCCGAGAC 148  
 QY 1841 ACGGAGAGAGACGACACGACCTGATGACAGACCAAGATGCA 1884  
 DB 147 ACGGAGAGAGACGACACGACCTGATGACAGACCAAGATGCA 104

RESULT 9 598 bp mRNA linear EST 01-MAR-2002  
 BM726341

LOCUS UT-E-EJ0-ah-n-09-0-UT.r1 UT-E-EJ0 Homo sapiens cDNA clone  
 DEFINITION UT-E-EJ0-ah-n-09-0-UT 5', mRNA sequence.  
 ACCESSION BM726341  
 VERSION BM726341.1 GI:19047674  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 598)  
 Bernaldo, M.F., Lennon, G. and Soares, M.B.  
 Normalization and subtraction: two approaches to facilitate gene  
 discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE 97044477  
 COMMENT Contact: Soares, MB  
 Program for Rat Gene Discovery and Mapping  
 University of Iowa  
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: msoares@blue.weeg.uiowa.edu  
 Tissue Procurement: Dr. Gregg Hageman

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research  
 Genetics (www.resgen.com).  
 Seq primer: M13 Reverse.  
 Location/Qualifiers

FEATURES  
 source  
 1. 598  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="UT-E-EJ0-ah-n-09-0-UT"  
 /clone\_lib="UT-E-EJ0"  
 /tissue\_type="fetal eyes, lens, eye anterior segment,  
 optic nerve, retina, Retina Foveal and Macular, RPE and  
 choroid"  
 /dev\_stage="fetal and adult"  
 /lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
 /note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a  
 modified polylinker; Site: 1: EcoR I; Site: 2: Not I;  
 UT-E-EJ0 is a subtracted cDNA library constructed  
 according to Bernaldo, Lennon and Soares, Genome Research,  
 6:791-806, 1996. First strand cDNA synthesis was primed  
 with an oligo-dT primer containing a Not I site. Double  
 stranded cDNA was ligated to an EcoR I adaptor, digested  
 with Not I, and cloned directionally into pT73-Pac  
 vector. The oligonucleotide used to prime the synthesis of  
 first-strand cDNA contains a library tag sequence that is  
 located between the Not I site and the (GT)<sub>18</sub> tail. The  
 sequence tags for this library are: fetal eyes, AGATACAGA  
 ; lens, CGATTACGGA; eye anterior segment, ATGCGCAT;  
 optic nerve, CCATTAGATG; retina, CCGCG; Retina Foveal and  
 Macular, GTCC; RPE and Choroid, ACCCTA. This library was  
 created for the program, Gene Discovery in the Visual  
 System, supported by National Eye Institute (NEI)."

BASE COUNT 160 a 125 c 142 g 170 t 1 others

Query Match 2.7%; Score 164; DB 14; Length 598;  
 Best Local Similarity 100.0%; Pred. No. 4e-73;  
 Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5293 TTTTGTGAGTATCATATATCTCTGTTGTGTGTAACATGATCGGGTC 5352  
 DB 37 TTTTGTGAGTATCATATATCTCTGTTGTGTGTAACATGATCGGGTC 96  
 QY 5353 ATCTGAGAACTTCACTGCTACTGAAGAAAGTCAGAGCTTGTAGTATGAC 5412  
 DB 97 ATCTGAGAACTTCACTGCTACTGAAGAAAGTCAGAGCTTGTAGTATGAC 156  
 QY 5413 TTTGAGATGTTCTATGAGTTTGGAGAGTTGATCCGATGC 5456  
 DB 157 TTTGAGATGTTCTATGAGTTTGGAGAGTTGATCCGATGC 200

RESULT 10 774 bp mRNA linear EST 28-AUG-2001

LOCUS B1488799  
 DEFINITION 603021384F1 NIH\_MGC\_114 Homo sapiens cDNA clone IMAGE:5192206 5',  
 mRNA sequence.  
 ACCESSION B1488799  
 VERSION B1488799.1 GI:15328027  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 774)  
 NIH-MGC http://mgs.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cga@bbs-r@mail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.

JOURNAL  
 MEDLINE  
 COMMENT

| REFERENCE  | LOCUS    | DEFINITION  | ACCESSION | VERSION | KEYWORDS    | SOURCE | ORGANISM |
|--|----------|---|-----------|---------|-------------|--------|----------|
| 1 (bases 1 to 482)   | BI032903 | MR-NNO205-220101-202-a12 NNO205 Homo sapiens CDNA, mRNA sequence. | BI032903  | EST.    | GI:14439529 | human. |          |
| Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R., Nagai, M. A., da Silva, W. J., Zago, M. A., Bordin, S., Costa, F. F., Goldmann, G. H., Carvalho, A. F., Matukuma, A., Bala, G. S., Simpson, D. H., Brunstein, A., deOliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. K., Reis, L. F., de Souza, S. J. and Simpson, A. J. G. |          |   |           |         |             |        |          |
| Shotgun sequencing of the human transcriptome with ORF expressed sequence tags   |          |   |           |         |             |        |          |
| Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)   |          |   |           |         |             |        |          |
| Contact: Simpson A.J.G.  |          |   |           |         |             |        |          |
| Laboratory of Cancer Genetics  |          |   |           |         |             |        |          |
| Ludwig Institute for Cancer Research   |          |   |           |         |             |        |          |
| Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil   |          |   |           |         |             |        |          |
| Tel: +55-11-2704922  |          |   |           |         |             |        |          |

RESULT 12  
 BI488967  
 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

BI488967 735 bp mRNA linear EST 28-AUG-2001  
 603021693F01 NIH\_MGC\_114 Homo sapiens cDNA clone IMAGE:5192182 5',  
 mRNA sequence.  
 BI488967  
 BI488967.1 GI:15328195  
 EST.  
 human.  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 735)  
 NIH-MGC <http://mgc.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgapds-remail.nih.gov](mailto:cgapds-remail.nih.gov)  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNLN at:  
<http://image.lnl.gov>  
 Plate: L1AM11480 Row: J Column: 23  
 High quality sequence stop: 728.  
 location/Qualifiers  
 1. 735  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"

```

/clone="IMAGE:5192182"
/clone_lib="NH_MGC_114"
/lab host="DH10B"
/Note="Organ: brain; Vector: PCMV-SPORE6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yo. Library is 0.19g-dt
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Institut für Genetik, Universität Köln). Note:
this is a NH_MGC Library."

BASE COUNT      164 a      173 c      175 g      223 t
ORIGIN

Query Match      2.4%; Score 146; DB 13; Length 735;
Best Local Similarity 100.0%; Pred. No. 9.6e-64;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5287 ATTTCTTTTGTGACATCATCATATCCCTCTGCTGTGTGATGATGATCATC 5346
|||||
DB 393 ATTTCTTTTGTGACATCATCATATCCCTCTGCTGTGTGATGATGATCATC 452
|||||

QY 5347 GCGGTCACTCTGAGAACTCAGTGTGCTACTGAGAGAAAGCAGAGCCTCTGAGTGA 5406
|||||
DB 453 GCGGTCACTCTGAGAACTCAGTGTGCTACTGAGAGAAAGCAGAGCCTCTGAGTGA 512
|||||

QY 5407 GATGACTTGTGAGATGCTTATGAGGT 5432
|||||
DB 513 GATGACTTGTGAGATGCTTATGAGGT 538
|||||

RESULT 13
AG054756/c 672 bp DNA linear GSS 02-NOV-2001
LOCUS Pan troglodytes DNA, clone: PTB-040113.R, genomic survey sequence.
AG054756
VERSION AG054756.1 GI:16592199
KEYWORDS GSS.
SOURCE Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC library clone:PTB-040113.R.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Pan troglodytes
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.
REFERENCE
1 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,
Toto, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of library PTB
Unpublished
2 (bases 1 to 672)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,
Toto, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: chimbes@gs.c.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
PRIMERS
Sequencing: M13Rev
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
Location/Qualifiers
1. 672
/organism="Pan troglodytes"
/db_xref="taxon:9596"
/clone="PTB-040113.R"
/sex="male"

FEATURES
SOURCE

BASE COUNT      105 a      103 c      105 g      132 t      5 others
ORIGIN

Query Match      1.9%; Score 115; DB 9; Length 450;
Best Local Similarity 100.0%; Pred. No. 1.1e-47;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5328 TGTGCGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5387
|||||
DB 169 TGTGCGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 228
|||||

QY 5388 TGCAGAGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5442
|||||

```

Db 229 TGCAGAGCCCTGAGTGAAGATGACTTTGAGATGTTCTATGAGGTTGGAGAG 283

## RESULT 15

LOCUS AA214661 225 bp mRNA linear EST 12-MAR-1998

DEFINITION zq9809.r1 Stratagene hnt neuron (#937233) Homo sapiens cDNA clone IMAGE:649192 5' similar to gb:U94055 SODIUM CHANNEL PROTEIN, BRAIN

ACCESSION AA214661 GI:1813315

VERSION EST.

KEYWORDS human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

## REFERENCE

AUTHORS

1 (bases 1 to 225)  
Hiller, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,  
Kritzman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Maira, M., Martin,  
J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,  
White, Y., Wylie, T., Waterston, R. and Wilson, R.  
WashU-NCI human EST Project  
Unpublished (1997)

## COMMENT

Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810

Email: estewatson.wustl.edu

This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.

Insert Length: 1023 Std Error: 0.00

Seq primer: -28m13 rev1 ET from Amersham

High quality sequence stop: 125.

## FEATURES

## Source

1.225  
/organism="Homo sapiens"  
/db\_xref="GDB:5278471"  
/db\_xref="taxon:9606"  
/clone="IMAGE:649192"  
/dev\_stage="Stratagene hnt neuron (#937233)"  
/lab\_host="hnt neurons"  
/note="Vector: SOLR (kanamycin resistant)"  
Xhol: Cloned unidirectionally. Primer: Oligo dT.  
differentiated, post mitotic hnt neurons. Average insert  
size: 1.5 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5'  
GAATTCGGCAGAG 3' -3' adaptor sequence: 3'  
CTCGAGCTTTTCTTTTCTTTT 3'

BASE COUNT 54 a 39 c 59 g 72 t 1 others

Query Match 1.88; Score 107; DB 9; Length 225;  
Best Local Similarity 100.0%; Pred. No. 1.4e-43;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5287 ATTTCCTTTTTCATGATCATCATATCCCTTCGTTGGTGGAGACATGATACATC 5346

Db 34 ATTTCCTTTTTCATGATCATCATATCCCTTCGTTGGTGGAGACATGATACATC 93

QY 5347 GCGGTCACTCTGAGAACTTCAGTGTGCTACTGAGAGAAAGTCGAGA 5393

Db 94 GCGGTCACTCTGAGAACTTCAGTGTGCTACTGAGAGAAAGTCGAGA 140

Search completed: April 22, 2003, 18:36:12  
Job time : 5110 secs